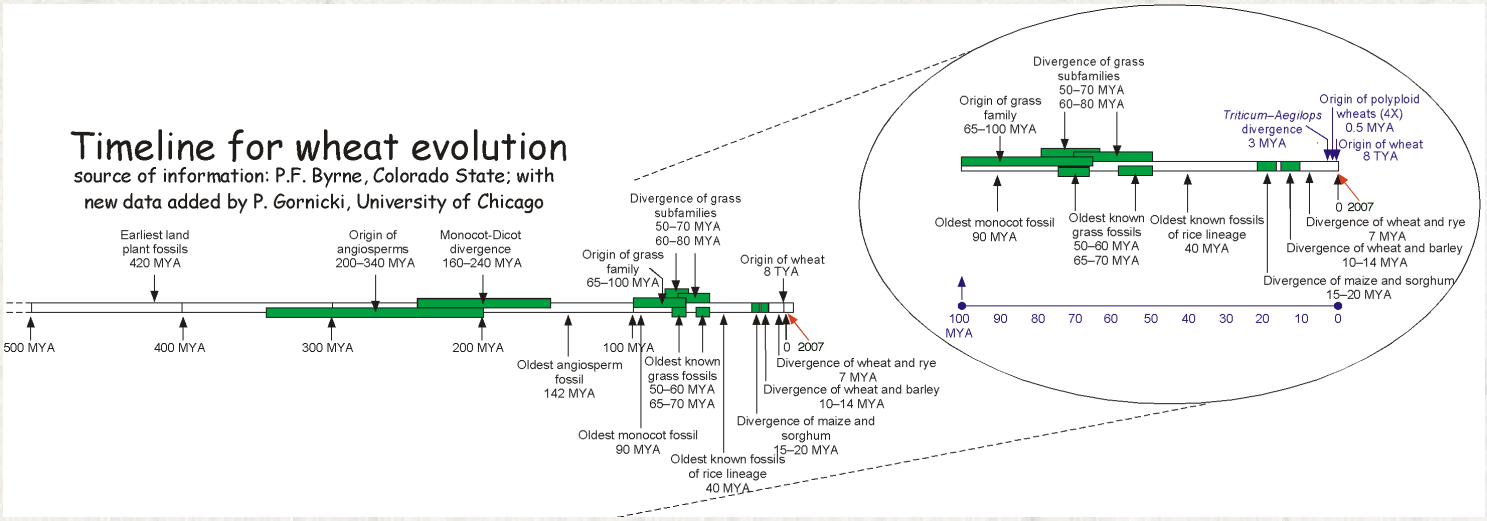
ANNUAL WHEAT NEWSLETTER

Volume 56



Contribution no. 11-023-D from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

ANNUAL WHEAT NEWSLETTER

Volume 56

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IN DEDICATION TO PROF. MICHAEL D. GALE FRS

Professor Mike Denis Gale, a world-leading plant geneticist, died suddenly on the 18 July, 2009. Mike made numerous seminal contributions to genetics and genomics research on cereals, particularly wheat.

Mike was born on 25 August, 1943, and brought up on a diary farm in the West Country of England. He went onto Birmingham University as an undergraduate where he specialized in genetics. The close connection at that time between the Birmingham Genetics Department and the Agricultural Botany Department at the University of Wales, Aberystwyth, resulted in Mike moving there in 1965 for a Ph.D. under the supervision of Prof. Hubert Rees. Mike's dissertation was on the 'Cytological and biometrical studies in the Gramineae'. Following this, he was offered a job in 1968 at the Plant Breeding Institute (PBI) in Cambridge by Prof. Sir Ralph Riley, then Head of the Cytogenetics Department. The PBI employed Mike as a geneticist and encouraged him into developmental genetics and physiology. Mike thrived at the PBI and started on a path that would lead him to make ground-breaking discoveries on the genetics of height and preharvest sprouting, and later in wheat genomics. His contributions to agricultural research led to the award of the Royal Agricultural Society of England's gold medal for research in 1994.

In the mid to late 1980s, Mike was becoming increasingly interested in genetics at the protein and DNA level and started programs to discover genetic marker polymorphisms. He started an extensive program to discover and exploit isozyme polymorphisms and published extensively in this area. At the end of the 1980s, his interest turned to DNA polymorphisms, which led to the development of the first comprehensive genetic maps of wheat.

In 1990, following the privatization of the breeding activities of the PBI, Prof. Gale, together with his colleagues on the research side of the PBI, moved to Norwich. Mike became Head of Cereal Genetics in 1988, and Associate Research Director of the new John Innes Centre (JIC) in 1994. The years that followed were the most scientifically productive of Mike's research career. Mike's research group, in collaboration with Graham Moore, extended the DNA marker work to analyze the genetic relationships between wheat and other grass species, particularly rice. This led to the seminal discovery that despite being separated by many millions of years of evolution, the genetic content and gene order in the major grasses had been conserved over time, which in turn led to the 'lego model' and 'crop circles' concepts, where the genomes of all grass species could be aligned into a common framework. For this work, he was awarded the Rank Prize in Nutrition in 1997, and with Graham Moore, the Royal Society Darwin Medal in 1998. For his accumulated scientific discoveries and achievements, Mike was elected a Fellow of the Royal Society in 1996. He also took on a greater administrative load at JIC and rose to become Director of the JIC.

Mike was always interested in international agricultural research. During the 1980s and 1990s, he had become an important figure in the Rockefeller Rice Biotechnology Program and also worked extensively for the Plant Breeding Division of the International Atomic Energy Agency in Vienna. This led him to express a passionate view that science, and genetics in particular, has a major role to play in alleviating world food shortages and poverty. Mike became increasingly involved with the Consultative Group on International Agricultural Research (CGIAR) and in 2004 was elected to the Science Council, the major group that directs the strategic directions of the CGIAR Institutes. In this role, Mike played a major role in the directions that international agricultural research has taken over the last few years with respect to crop improvement strategies.

Mike officially retired from the JIC in 2003, but became an Emeritus John Innes Foundation Professor in the Crop Genetics Department. Following retirement, he kept busy continually working or travelling for business and pleasure. As well as his CGIAR role, he worked as a consultant to numerous national and international organizations, public and private, involved in agricultural science.

Prof. Gale passed away from a heart attack while attending the Latitude Festival in Suffolk on 18 July, 2009, following a game of golf in the morning and catching up with the British Open Tournament, which he always enjoyed.

IN DEDICATION TO DR. TOM L. HARVEY

Tom Larkin Harvey was born in Nebraska in 1926 and served as a rifleman in the 38th Infantry Division during the Philippine Islands campaign in the Pacific theatre of WWII. After the war, Tom joined the Naval Reserve and rose to the rank of Commander in the Medical Service Corps where he remained active for many years. He obtained his Bachelor and Master of Science degrees from Kansas State University in 1950 and 1951, respectively. Following graduation, he spent several years as an Instructor of Entomology at New Mexico State University before returning to serve at KSU in the same capacity. In 1957, he was hired as Assistant Professor of Entomology at KSU and was posted to the Fort Hays Experiment Station (now the Agricultural Research Center–Hays). A sabbatical leave afforded him the opportunity to complete his Ph.D dissertation at Oklahoma State University in 1963. His thesis documented the evolution of resistance to Bt, at the time a novel microbial insecticide, in the house fly, the first recorded case of resistance to Bt (previously, he had shown that feeding Bt spores to cattle could prevent development of house flies in manure). Tom was promoted to Associate Professor in 1964 and full Professor in 1970 and spent virtually his entire career at Kansas State, where he authored and co-authored some 120 publications and numerous crop variety registrations. In addition to membership in several scientific societies, he was a member of the Entomological Society of America for 57 years.

Tom was a true pioneer of entomology on the High Plains and his interests reflect how well attuned he was to the entomological needs of agriculture in the region; plant resistance to insects, veterinary entomology, insecticide application technologies, and resistance evolution. He believed deeply in public service, and his research was always designed to yield benefits for others. For example, he measured the weight loss in steers caused by horn fly feeding to demonstrate to farmers the importance of controlling them. He dyed white cows black on one side to show that biting flies were more attracted to dark animals. Watching the behavior of cattle, Tom soon realized that treatment of only a few animals could control flies in the whole herd, and that attaching ear tags to nursing calves protected also their mothers. Tom's 1970 invention of the ear tag is the kind of innovation that would have been patented and sold to a private company in today's research environment, but Tom made the technology freely available and never received a dime while chemical companies made millions from it. This was just one of many techniques that he developed for applying insecticides to cattle. Others included pickup-mounted sprayers, backrubbers, impregnated strips and wax bars, and the use of a chin ball attached to a bull to treat cows. Decades before paintball became a popular sport, Tom was shooting cows from a pickup with insecticide-loaded paintballs from an air pistol. This solved the problem of having to stress cattle with mid-summer round-up to replace ear-tags as their efficacy waned. The technique was very effective, but filling the paintballs with insecticide was time-consuming and he was never able to obtain commercial support for their production. When horn flies evolved resistance to pyrethroid ear tags in 1985, Tom was the first to report it and suggest management solutions.

As a former student of Reginald Painter, a founding father of plant resistance to insects, Tom was instrumental in the development of many insect-resistant varieties of field crops. He was the first to document insects impacting alfalfa seed production in Kansas and, when the spotted alfalfa aphid became invasive in the 1950s, Tom collaborated with Painter and others to produce cultivars resistant to both alfalfa and pea aphids. When plant breeders introduced wheat with pubescent leaves to improve resistance to cereal leaf beetle, Tom showed that these cultivars collected more wheat curl mites because the leaf hairs made it easier for airborne mites to gain purchase on the plants. Tom was instrumental in documenting the evolution of a long succession of greenbug 'biotypes' on wheat, recognized by their ability to overcome specific sources of resistance, and developed the aphid-rearing protocols and bioassays that we still use today. When greenbugs began attacking sorghum in 1968, Tom worked with sorghum breeders to develop the first greenbug resistant cultivar in 1975 and showed that increasing plant density could reduce seedling infestation. He also discovered sources of wheat resistance to Russian wheat aphid in the 1990s that enabled development of some of the earliest locally-adapted resistant cultivars. Tom demonstrated that the wheat curl mite was responsible for vectoring several virus diseases of wheat, and his final projects were focused on the development of mite-resistance wheat cultivars and understanding the nature of simultaneous transmission of different viruses by the mites.

When I succeeded Tom at ARCH in 2002, I spent several winter months poring over the library of resources he left me that charted the history of his career. In semi-retirement, he was always outgoing, helpful, and a valuable resource as I learned the ropes of crop protection on the High Plains. He was an exceptionally humble and humanitarian person, reminding me in many ways of my own father. In 2005, Tom received a plaque from the governor of Kansas to commemorate his 50 years of service to KSU and the state of Kansas. He retired fully three years later, spending winters with his wife Joan in their house in Sun City, Florida, and returning to Hays in the summer where he continued to volunteer his time at the research station, assisting with studies of virus transmission by mites. It was on such a summer afternoon that his car was struck broadside by a semi-trailer as he crossed an intersection in front of the research station – on his way to check on his mites. He is survived by his wife, two daughters, five sons, and numerous grandchildren.

Written by J.P. Michaud, Associate Professor of Entomology, Kansas State University, Agricultural Research Center–Hays.

WHEAT WORKER'S CODE OF ETHICS

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

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

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

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

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

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

IWGSC: PHYSICAL MAPPING STANDARD PROTOCOLS WORKSHOP

Plant and Animal Genome Meeting, San Diego, CA, USA
Tuesday, 12 January, 2010.

Workshop report.

Rudi Appels, Eduard Akhunov, Michael Alaux, Mario Caccamo, Federica Cattonaro, Jaroslav Dolezel, David Edwards, Ming-Cheng Luo, Dave Matthews, Nicolas Guilhot, Etienne Paux, Thomas Wicker, Kellye Eversole, and Catherine Feuillet.

On 12 January, 2010, the International Wheat Genome Sequencing Consortium (IWGSC) organized a workshop to develop and discuss protocols and standards for the physical mapping of the hexaploid wheat genome and develop a consensus. In addition, the workshop surveyed the sequencing efforts undertaken within the consortium to coördinate the studies carried out in member laboratories. The goal was to ensure homogeneity in the procedures used for constructing the wheat physical maps by providing guidelines developed in expert laboratories and distributing these to the groups participating in the physical mapping and sequencing of bread wheat chromosomes under the auspice of the IWGSC.

The road map for achieving a high-quality reference sequence of the bread wheat genome established by the IWGSC includes, as a first step, the construction of physical maps in hexaploid wheat using a chromosome-specific strategy. This approach relies on recent improvements in chromosome sorting and BAC library construction technologies that have allowed the construction of chromosome-specific BAC libraries (Dolezel et al. 2007). The first physical map has been achieved for the largest wheat chromosome, 3B (1 Gb) (Paux et al. 2008; http://urgi.versailles.inra.fr/projects/Triticum/index.php) and its sequencing has been initiated this year in the framework of an ANR flagship project (3BSEQ). Physical mapping and sequencing project leaders have been secured for all of the bread wheat chromosomes (Fig. 1), and a number of projects are in the initial phases of fingerprinting and contig assembly (see http://wheat.pw.usda.gov/ggpages/awn/55/TEXTFILES/IWGSC_REPORT.pdf).

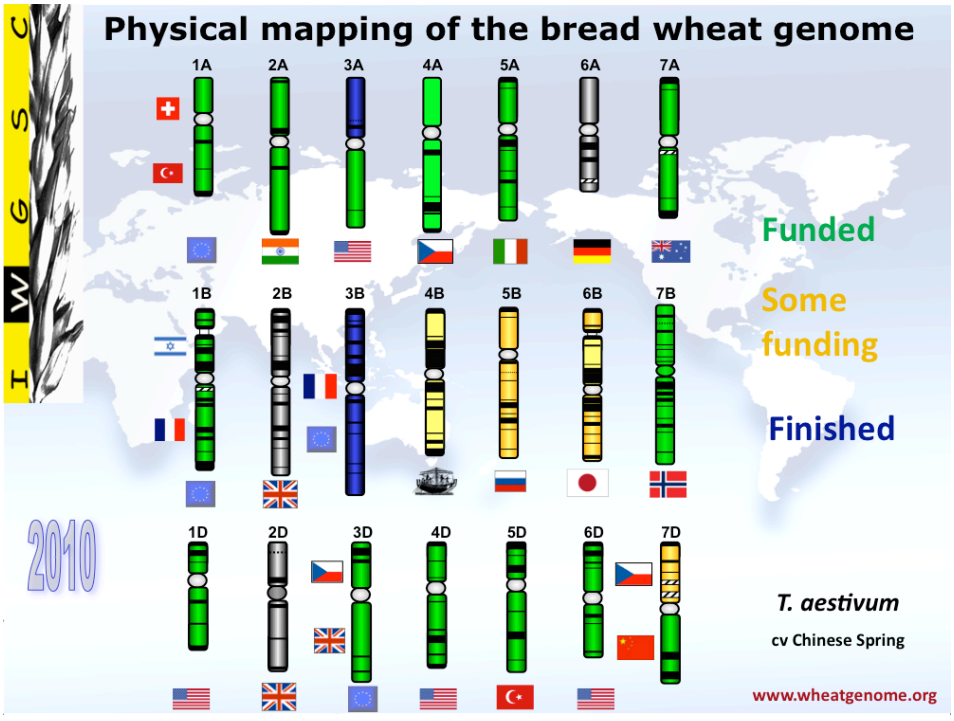

Fig. 1. Status of the IWGSC physical mapping projects as of January 2010.

The workshop was organized in five sessions of 45 minutes each that covered the following topics:
• Fingerprinting (Ming-Cheng Luo and Federica Cattonaro)

- Contig assembly (Etienne Paux and Ming-Cheng Luo)
- Anchoring (Eduard Akhunov and Etienne Paux)
- Sequencing with next generation technologies for marker development (Thomas Wicker and David Edwards)
- Databases and online tools for displaying the anchored physical maps (Michael Alaux and Dave Mathews)

In an introduction to the workshop, Jaroslav Dolezel (Institute of Experimental Botany (IEB), Czech Republic), who pioneered the chromosome sorting approach, presented the methods used to construct chromosome-specific BAC libraries and the effort required to produce high-quality DNA from sorted chromosomes. About 5 μg DNA, which corresponds to 5–10 million chromosomes, sorted during about 6–8 weeks of work by the team at IEB is needed to construct one library. Except for chromosome 3B that can be sorted directly from Chinese Spring, specific cytogenetic stocks (ditelosomic, telosomic lines) are used for sorting the different chromosome arms. About 10,000–20,000 seeds of good quality are needed to construct each BAC library. The contamination of sorted fractions by other chromosomes is generally low (5–15%) and does not interfere with the subsequent analyses as the contamination represents a mixture of unrelated chromosomes. To date, BAC libraries have been constructed and delivered to the lead laboratories for 12 chromosomes (1A, 2A, 3A, 4A, 5A, 1B, 3B, 1D, 3D, 4D, 6D, and 7D; see Table 1 for details) and another six will be completed this year. Recently, constructed libraries are cloned in phage-resistant bacteria, and their average insert size is about 120 Kb. All BAC libraries are constructed with the *Hin*dIII restriction site. Two low-coverage libraries (1, 4, 6D, and 3B) were constructed with the *Eco*RI cloning site as well. Finally, the demand is increasing for chromosomal DNA to perform whole-chromosome (arm), shotgun sequencing by next-generation technologies for chromosome composition surveys and marker development. This is performed now routinely in different projects with DNA amplified from flow-sorted chromosomes and chromosome arms. Typically, 50 seeds are needed to isolate sufficient numbers of chromosome arms to produce 3–5 μg DNA after whole-genome amplification with the GenomiPhi V2 DNA Amplification Kit (GE Healthcare). The available data indicate representative amplification with only several-fold quantitative differences in the rate of amplification of various genomic loci.

Table 1. List of chromosome-specific BAC libraries currently available.

Chromosome	Country sponsor/lead	Library name	Insert size	Coverage
1D, 4D, 6D	USA	TaaCsp146eA	110 kb	1.3 x
1D, 4D, 6D	CZ, FR	TaaCsp146hA	85 kb	3.4 x
1D, 4D, 6D	USA	TaaCsp146hB	102 kb	6.9 x
1D, 4D, 6D	USA	TaaCsp146hC	116 kb	7.4 x
1AL	EU/TR	TaaCsp1ALhA	103 kb	8.0 x
1AL	EU/TR	TaaCsp1ALhB	109 kb	7.7 x
1AS	EU/CH	TaaCsp1AShA	111 kb	11.8 x
1BL	EU/FR	TaaCsp1BLhA	114 kb	15.4 x
1BS	EU/IL	TaaCsp1BShA	113 kb	15.7 x
2AS	IND	TaaCsp2AShA	123 kb	15.4 x
3AL	USA	TaaCsp3ALhA	106 kb	10.2 x
3AL	USA	TaaCsp3ALhB	114 kb	5.2 x
3AS	USA	TaaCsp3AShA	80 kb	10.9 x
3AS	USA	TaaCsp3AShB	115 kb	15.9 x
3B	EU/FR	TaaCsp3BFeA	107 kb	1.9 x
3B	CZ/FR	TaaCsp3BFhA	103 kb	6.2 x
3B	EU/FR	TaaCsp3BFhB	126 kb	9.1 x
3DL	EU/UK	TaaCsp3DLhA	105 kb	12.2 x
3DS	EU/CZ	TaaCsp3DShA	110 kb	11.0 x
4AL	CZ	TaaCsp4ALhA	126 kb	17.4 x
4AS	CZ	TaaCsp4AShA	131 kb	16.6 x
5AL	I	TaaCsp5ALhA	123 kb	18.3 x
5AS	I	TaaCsp5AShA	120 kb	16.5 x
7DL	CZ/PRC	TaaCsp7DLhA	115 kb	14.8 x
7DS	CZ	TaaCsp7DShA	114 kb	12.2 x
1BS	USA	TaaPav1BShA	82 kb	14.5 x
3B	CZ/AUS	TaaHop3BFhA	78 kb	6.0 x

The first session, led by Ming-Cheng Luo (University of California, Davis, USA) and Frederica Cattonaro (IGA, Italy), was dedicated to presenting and discussing 'Fingerprinting protocols'. The labs of Ming-Cheng Luo and Jan Dvorak have pioneered the use of the SNaPshot kit to perform BAC fingerprinting (Luo et al., 2003) and have used it to develop a physical map of *Ae. tauschii* (http://wheatdb.ucdavis.edu), the ancestral D-genome donor of hexaploid wheat. This D-genome progenitor map will serve as a framework to support the assembly of the D-genome physical map of hexaploid wheat cultivar Chinese Spring. The SNaPshot protocol is the basis for all physical mapping projects in wheat as well as in other species, including *Brachypodium distachyon*, soybean, cowpea, cassava, walnut, banana,

and citrus. The laboratory of Federica Cattonaro has been involved in physical mapping several plant species, including grape wine, as a basis for genome sequencing. To date, the Cattonaro laboratory has fingerprinted all of the wheat BAC libraries (1AS, 1AL, 1BS, 1BL, 3DS, 3DL, and 3Bv2) of the European project TriticeaeGenome (www.trticeae-geome.eu). The Luo and Cattonaro laboratories presented their working protocols and latest improvements in terms of DNA isolation, SNaPshot reaction, and electrophoresis on capillary sequencers. The main differences between the two protocols concerned the type of size marker that was used (GS500Liz vs. GS1200Liz), and a consensus was reached on the fact that the use of the GS1200Liz is recommended to gain more fingerprint information. The main message from the two specialists was that although fingerprinting a few clones is not so complicated both theoretically and technically, it is one of the most complex tasks when fingerprints have to be generated over months or years and for these fingerprints to remain comparable in a large mapping and sequencing project.

A number of steps are critical for producing high quality fingerprints:

- the bacterial growth conditions need to be carefully determined before starting the production phase;
- it is recommended that the DNA preparations should not be done all at the same time before starting with fingerprinting because the conditions are not always stable and, sometimes, need to be re-optimized during the production phase;
- it is critical to use fresh β-mercaptoethanol and BSA;
- high-fidelity restriction enzymes and a good control of the digestion conditions (temperature, buffer) need to be used to avoid star activity (reaction volume should not be too small); and
- the running conditions for electrophoretic analyses need to be optimized.

Thus, to ensure the construction of high-quality and homogenous physical maps within the IWGSC, the consortium requires that the labs involved in the physical maps project use one of the two protocols developed by Ming-Cheng Luo and Federica Cattonaro. These protocols are available on the IWGSC website at http://www.wheatgenome.org/News-and-Reports/General-reports/Physical-mapping-standard-protocol-workshop.

The second session was led by Etienne Paux (INRA, France) and Ming-Cheng Luo (UC Davis, USA) and concerned the 'assembly of the physical contigs' from the fingerprints. Both experts presented the critical parameters that need to be taken into account to ensure reliable and robust assemblies. Paux presented a detailed protocol for contig assembly using FPC that was developed by the European project TriticeaeGenome. The protocol provides a step-by-step description of the assembly starting from the BAC naming convention to be adopted for the IWGSC projects to the MTP selection. The protocol includes the recently developed FPB software that permits the elimination of spurious background noise (Scalabrin et al. 2009; available at http://www.appliedgenomics.org/tools.php). Some of the critical parameters and processes were discussed, and there was agreement on the fact that the assembly needs to be performed first with high stringency, which reduces the risk of spurious assemblies due to the 10–20% of bands that are shared randomly between BACs, reflecting the repetitive nature of the wheat genome composition. Luo mentioned that some of the parameters need to be adjusted accordingly, especially the cut-off value (Sulston Score), which varies with the number of clones in assembly, the average number of fragments, fragment sizing range, and the value of tolerance (instrument sizing precision). A general consensus was established to use the guideline established by the TriticeaeGenome project and implement it with parameter settings that can be applied depending on the size of the project. The guideline is available through the IWGSC website at http://www.wheatgenome.org/News-and-Reports/General-reports/Physical-mapping-standard-protocol-workshop.

Finally, Paux mentioned a new algorithm called LTC (for Linear Topography Contig) that has been developed by A. Korol's group at the Institute of Evolution in Haifa and tested on the 3B physical contigs. The first results are very encouraging and indicate that LTC improves the quality of the assembly by identifying and resolving nonlinear topological structures. LTC enables the construction of highly reliable and longer contigs, the detection of 'weak' connections in contigs, and their 'repair', as well as the elongation of contigs obtained by other assembly methods such as FPC. A publication is underway, and A. Korol is willing to help colleagues use LTC for their physical assembly.

The third session, led by Etienne Paux (INRA, France) and Ed Akhunov (Kansas State University, Manhattan, USA), was dedicated to the different options available for 'anchoring the physical maps to the genetic maps'. Paux presented different strategies for pooling BAC libraries and MTPs that need to be screened with different markers. He then described the three approaches that can be used to anchor the physical contigs to the genetic maps: (1) by using markers (SSR, DArT, EST, and SNPs) already localized on genetics maps (forward approach) to screen the BAC contigs (pools) by PCR (individual PCR or through the hybridization of BAC pools on marker arrays); (2) by developing markers from

the BAC contigs (through BAC end sequencing) and mapping those on genetic maps (reverse approach); or (3) by developing markers from whole-chromosome or genome shotgun sequencing) to map them on genetic maps and screen the BAC pools (hybrid approach). To support these approaches, a number of scripts have been developed by INRA Clermont-Ferrand to define SSR and ISBP markers from 454 sequences obtained from sorted chromosome sequences or BAC end sequences (Paux et al. 2010). These are available publicly upon request to Frederic Choulet (fchoulet@clermont.inra.fr). One of the main conclusions from the experience of the initial wheat projects is that there is little overlap between the different type of markers used so far (EST, SSR, and ISBPs) and that it is better to use a diverse set of markers to ensure that most of the contigs will be anchored by at least one marker and that all regions of the chromosome are covered. The high-throughput platforms such as the Illumina bead express for SNPs or EST arrays that are emerging for marker genotyping in wheat should be used to improve the cost efficiency of the process. New platforms are currently under development (e.g., ISBPs on chip) and will continue to improve the efficiency of the anchoring. Akhunov presented the strategy planned for chromosome 3A that uses the sequences generated by 454 sequencing of BAC pools representing the chromosome 3A minimum tiling path (MTP) to develop molecular markers for anchoring. The major type of markers to be used for anchoring 3A is SNPs due to their amenability to high-throughput detection using various genotyping technologies. Development of SNP markers will be performed by targeted resequencing of low-copy genomic regions in the parents of mapping populations. The products of selective amplification generated using the PCR primers designed on the basis of MTP sequences will be pooled for 454 sequencing and variant discovery. Polymorphic sites and their flanking sequences will be submitted to Illumina for the design of 1536-plex Oligo Pool Assay (OPA). The data generated by genotyping of mapping populations on BeadArray platform using Illumina's GoldenGate assay will be utilized for the anchoring of chromosome 3A MTP.

A discussion followed on the genetic material that can be used for anchoring in wheat. Recombination mapping will be very useful to support map based cloning projects but will remain limited because 50% of the chromosomal regions do not show high levels of recombination. A number of populations are now available for anchoring including a large RIL of 2,000 individuals from a cross between Chinese Spring and Renan that will be publicly available through the TriticeaeGenome project in 2011 and a new large (1,600 RILs) ITMI population that is developed by M. Sorrels and C. Qualset. In addition, deletion mapping with the series of deletion lines that are available for the 21 wheat chromosomes is recommended and these can be ordered by contacting Bikram Gill at Kansas State University (bsgill@k-state.edu). Even if the resolution obtained with these lines is rather low due to the large size of the deletion bins, the lines provide valuable information of the location of centromeric and pericentromeric contigs that cannot be obtained by meiotic mapping. To increase the mapping resolution with a technique that does not rely on recombination and polymorphism, S. Kianian (North Dakota State University, Fargo, USA) has developed radiation hybrids in wheat (Hossain et al. 2004). A first panel has been developed for chromosome 3B (Paux et al. 2008) and the results indicated that a resolution of about 263 kb can be achieved with RH panels. RH populations will be developed now for the D-genome physical mapping project and other chromosomes are planned for the IWGSC. The main limitation at the moment is the greenhouse space required to develop the first generation of RH plants.

Thomas Wicker (University of Zurich, Switzerland) and David Edwards (University of Queensland, Australian Centre for Plant Functional Genomics, Australia) chaired the fourth session on sequencing with next generation technologies for marker development'. They first presented a survey of the ongoing efforts at the international level to produce sequence from wheat using next generation techniques. A number of projects are underway to either produce sequence surveys from whole genomes (A, D, and ABD) or from individual chromosomes and chromosome arms (Table 2). Wicker and Edwards will update the information regularly and request that the IWGSC members keep them informed about new projects to avoid redundancy and increase coordination and collaborations within the consortium. It is also im-

Table 2. Projects underway to produce sequence surveys from whole genomes or individual chromosomes and chromosome arms.

Country	Target	Coverage	Technique
United Kingdom	WGS	5x	454 Titanium
United Kingdom	3DL	75x	GAII PE
TriticeaeGenome	Group 1	1.5x	454 Titanium
France	3B	2x	GAII
Australia	WGS	0.2x	GAII PE
Australia	7DS	16x	GAII PE
United States	3A	2x	454 Titanium
Italy	5A	2x	454 Titanium
Switzerland	A/B/D ancestors and R(ye)	0.1x each	454 Titanium
China	D (*Ae. tauschii)*	40x	GAII PE
China	A (*T. urartu*)	40x	GAII PE

portant to gain more details about the methods that have been used for library production (Native or amplified DNA, Cp DNA contamination, WGS DNA library preparation, PE library features, etc…) as well as the quality controls that were applied on the sequence. This is essential to evaluate potential bias and assess the quality of the data produced. A 'WIKI type' platform will be established by Edwards and Wicker the IWGSC website to store and access all information related to the sequence data produced and the contact persons within the consortium. Edwards also presented the visualization tools he has developed for displaying short reads and using them for SNP discovery (see PowerPoint presentation online). He is happy to distribute them upon request (dave.edwards@uq.edu.au). Edwards also hosts a web tool, TAGdb, for searching paired read information for targeted assembly and cloning in wheat, which is available at http://flora.acpfg.com.au/tagdb.

The last session was dedicated to 'databases and online tools for displaying the anchored physical maps' and it was led by Michael Alaux (INRA URGI, France) and Dave Mathews (Cornell University, Ithaca, NY, USA). Mathews presented the different tools and resources available at GrainGenes (http://graingenes.org), where the physical maps and the contigs are displayed using a CMap interface. Links to the deletion bins are lacking in this representation, but this can be done in collaboration with Alaux and the URGI who have developed a Gbrowse interface that can display the bins along the chromosomes (http://urgi.versailles.inra.fr/projects/Triticum/deletionBin.php). The URGI-Gbrowse interface has a clickable link to the BAC contigs assigned to each bin (http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/) and the subsequent information about each BAC contig (markers, sequence etc…). Mario Caccamo presented the PGP-viewer, a set of software tools, databases and interfaces developed to assist the work of the pig and zebrafish genome projects at the Sanger Institute (UK). The system integrates, in one platform, data from different sources including whole-genome assemblies, genetic markers, and expression information. The PGP-viewer interface extends the Ensembl browser with customized tracks that use a colour-based schema to distinguish robust versus more unstable sequences. The information is stored in an underlying database that can be used to access the data programmatically and also is attached to other interfaces, such as GBrowse. Caccamo mentioned that BACs excluded as singletons during the FPC assembly could be recovered at the sequence stage by using information provided by the alignment of BAC ends. The same information was used to guide the selection of BACs to close or extend over gaps in the underlying physical maps. One of the most valuable tools was a 'punch list' that provided an interface to the users for getting requests and tracking comments from the community. These comments were taken into account by the curators to improve the versions of the sequence release. It was decided that such a 'punch list' should be put in place for the IWGSC. Finally, Caccamo mentioned the genome reference consortium (http://www.ncbi.nlm.nih.gov/projects/genome/assembly/grc/) that was established to curate the human and mouse genomes and can be followed as an example for the wheat sequencing effort.

The PowerPoint slides that were presented by the different speakers are available as PDF files on the IWGSC website at http://www.wheatgenome.org/News-and-Reports/General-reports/Physical-mapping-standard-protocol-workshop.

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SPEAKER AND POSTER ABSTRACTS

2010 U.S. Wheat Genomics Workshop

9–10 MARCH, 2010
UNIVERSITY OF NEBRASKA–LINCOLN

SESSION I: MARKER-BASED BREEDING STRATEGIES

Marker-assisted breeding and the harsh reality of cultivar development.

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The promise envisioned decades ago for marker-assisted selection (MAS) in plant breeding has been only partially realized. First proposed as a means to improve complex traits with low heritability, MAS has been primarily employed for improving traits with simple inheritance and high heritability. This talk will address using MAS in the present for simple traits and the potential utilization for complex traits in the near future. The Ohio State University wheat breeding program currently uses MAS for improving some key traits where single genes or major QTL are available and effective. The program primarily uses an aggressive backcrossing (BC) scheme where backcrossing is initiated early in the variety-development phase using many recurrent parents. The annual fate of any BC population depends on the performance of the recurrent parent in ongoing cultivar-development evaluations. This scheme and the reasons for using it will be presented.

Most key traits for Ohio, such as yield, are truly quantitative and there are few, if any, useful QTL such that traditional MAS has had little impact. A recent analysis of yield gain in the U.S. indicates that the rate of yield improvement needs to be increased by 25 to 50% to increase yield by 35% in 25 years. A plan to utilize historical trends, association analysis, and genomic selection to attain that rate of gain will be presented.

Implementing marker-assisted selection in wheat variety development.

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Marker-assisted selection (MAS) has become a routine part of wheat breeding, enabling efficient backcross breeding, pyramiding of genes, and creation of isolines that allow for the genetic dissection of traits. The wheat genetics group at Montana State University has developed markers and implemented MAS for traits of importance to our state. One successful example of marker development and implementation is with markers for white seed. Resources for breeding programs in much of the Great Plains largely have been directed to hard red wheat development and, as a result, agronomic performance of hard white wheat varieties has tended to be inferior. Based on demands from the Montana wheat industry, we developed markers for white kernel color and used these to convert our best hard red wheat varieties into hard white. Development of markers for white seed required analysis of three mapping populations, each segregating for one of the three controlling loci. Once identified, the markers linked to white seed color pose several challenges in application to variety development. Because white is recessive and controlled by three genes, red-seeded plants have unknown genotypes, so that the breeder does not know how many genes need to be converted. Also, a certain sized band is not diagnostic of all white-seeded lines. Despite these caveats, we were able to use the markers in a backcrossing program to covert the best hard red wheat varieties into hard white isolines. These hard white wheat lines are currently being tested in breeding trials, with the expectation that agronomic performance will equal that of the hard red varieties. In addition, the ability to develop isolines with red versus white kernel color provides the opportunity for experiments that are otherwise difficult to conduct. Our experience with the markers for white kernel color, and with markers for other traits, has provided insights that have helped us refine marker implementation in variety development.

Breeding wheat somewhere between the poverty level and the 99% confidence level.

Brett Carver and Liuling Yan. Department of Plant and Soil Sciences, Oklahoma State University, Stillwater, OK 74078, USA.

The Oklahoma State University (OSU) wheat breeding program has operated continually for the past 60 years but not without significant shifts in financial base support and breeding strategy in only the last decade. The next shift, already in motion, will invoke gene-targeted selection among inbred lines as a means to reduce costs and/or maximize selection gains for adaptation traits relevant to the southern Great Plains. The USDA–CSREES–CAP population, 'Jagger/2174', provided OSU's cornerstone for QTL discovery and mapping of critical traits for reproductive development patterns (stem elongation, heading, and physiological maturity) and disease reaction (leaf rust, stripe rust, and powdery mildew). As a result of their alignment with phenotypic-based selection in our program, most informative among these markers are *VRNA1*, *PPD-D1*, *VRN-D3*, *Lr34*, *Pm3*, and a novel gene on chromosome 2A that confers adult-plant resistance to stripe rust. Little variation was found among elite lines in the OSU wheat breeding program at *VRNA1*, a major locus that regulates the timing of stem elongation, apparently is consequential to intense selection pressure in prior generations against precocious winter dormancy release. All of the gene markers enable selection pressure for traits that may not be consistently measurable from year to year or traits that have very low heritability due to human error. Their high diagnostic capability provides a healthy balance between costs and confidence.

MAS and the future of cereal breeding: how should the genotyping centers fit in ?

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The concept of regional genotyping centers providing marker-assisted selection (MAS) analysis for genetic selection has become ingrained in the U.S. wheat and barley breeding strategies. To remain relevant to the breeding community, the genotyping centers must move past the current paradigm one-gene MAS and toward efficient holistic selection strategies. A chip-based, single nucleotide polymorphism (SNP) marker system applied to genomic breeding is the obvious next step. The transition away from single-gene selection and towards genomic breeding is conceptually easy to understand. The realization of genomic breeding is much more difficult to achieve. To make this leap, the SNPs linked to adaptation, agronomic, and quality traits must be identified for each breeding program. The public U.S. cereal breeding community currently is lacking in genomic information essential to implement the next generation MAS platforms. The USDA genotyping labs, in association with university partners, are currently identifying new SNPs useful in wheat. Identification of SNPs beneficial in specific germplasm also is being developed for PNW programs. Future work will require integrated efforts between genotyping centers and cereal geneticists to discover useful SNPs, identify and implement appropriate marker platforms, and elucidate the association between markers and haplotypes essential in the breeding programs. With the current rate of technological development, now is the time to establish a concerted effort to develop the markers, detection platforms, and the bioinformatics.

SESSION II: APPLICATION OF PHYSICAL MAPS/GENOME SEQUENCE TO BREEDING

The future impact of genomics assisted approaches in maize breeding.

Pierre Dubreuil, Mickaël Bosio, Laurent Décousset, Jeremy Derory, Morgan Renault, Marie-Hélène Tixier, Olivier Dugas, Frédéric Sapet, Jorge Duarte, and **Sébastien Praud**. BIOGEMMA ZI du Brézet - 8, rue des frères Lumière Cédex 2 Clermont-Ferrand, France.

The U.S. maize community initiated a huge three-step project in 1998, including the sequencing of the maize genome, to obtain the complete sequence and structure of all maize genes and their locations on both the genetic and physical maps of maize. All the information generated is made available to the community, via the maizegenome.org website, and from the EBI database in Europe. Now the maize genome is almost fully sequenced, which is great news for genomics, and so for maize breeding!

Having access to the genome contributes to crop improvement because comparative genomic approaches make links using the gene information already available on model species, to understand and identify more easily the function of key genes and complex biological mechanisms involved in the agronomic traits of crops. The assembled genome sequence provides a good basis for developing a large number of markers (wet lab or *in silico*) in candidate genes or within gene-rich regions that can be used in genetic studies (QTL and association mapping). Such tools facilitate and stimulate germplasm and allelic diversity characterization and increase breeding efficiency by marker-assisted selection. Traits can then be bred directly (selection of the favorable alleles only). Bioinformatics is an essential component of such studies, because it connects data from very diverse origins (genetic, transcriptomic, phenotypic, and mutants) to the genome sequences, to generate valuable information to be used in applied programs. All this, associated with the new high-throughput and low-cost technologies now available (in sequencing and genotyping), already is speeding up the identification of the most interesting genetic factors involved in agronomic traits, thus improving marker-assisted selection. Breeders need to encourage all the initiatives that aim at sequencing our genomes of interest.

Using genetic diversity to understand phenotypic variation in maize.

Michael McMullen [1] and the Maize Diversity Project [2].

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One of the goals of the Maize Diversity Project is the development of genetic resources for conducting joint linkage-association analysis in maize. We have designated our main genetic resource as nested association mapping (NAM). NAM is constructed from 26 inbred lines chosen to maximize genetic diversity. NAM has a reference design with B73 as the common parent and consists of 25 families of 200 RILs each from B73 crossed by 25 diverse lines (25DL). The broad sampling of allelic diversity and the 136,000 recombination events captured in NAM gives the population extensive power to describe the genetic architecture of agronomic traits for maize. For example, flowering time in maize is controlled by numerous, small-effect QTL that are shared among families, with multiple allelic effects segregating among the founder lines. The true power of NAM is based on ability to project polymorphism from the founder lines onto the RILs allowing genome wide association analysis for maize.

SESSION III: WHEAT TRANSFORMATION

Transgenic solutions to wheat biotic stresses.

Harold N. Trick [1], J.P. Fellers [2], M.S. Chen [2], J. Shah [3], L. Cruz [1], X. Liu [2], and V. Nalam [3].

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Although conventional breeding approaches will always play a major role in varietal development, transgenic technologies will become an increasingly valuable tool for our wheat breeders in the near future. The current climate for accepting biotech wheat is changing slowly to a more favorable position. Although it is unlikely that transgenic wheat will be released in the next few years, it is important to proceed with transgenic wheat research so that products can be readily deployed after the biotech wheat issue has been resolved. Providing resistance to biotic stresses is one area where transgenic wheat can make a significant impact. Highlighted in this presentation are collaborative efforts providing possible solutions for various biotic stresses including wheat streak mosaic virus, *Triticum* mosaic virus, Fusarium head blight, and Hessian fly resistance.

SESSION IV: BIOINFORMATICS

GrainGenes, the Triticeae Genome Database.

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The GrainGenes database has been serving genomic and genetic data for the Triticeae since 1993. It includes genetic and physical maps, probes used for mapping, nucleotide sequences, bibliographic references, and an address book of colleagues. The GrainGenes website includes additional information and publications, such as the Catalogue of Gene Symbols for Wheat, the *Barley Genetics Newsletter*, and the *Annual Wheat Newsletter*. Recent additions to the database are the physical/genetic map of wheat chromosome 3B, the OPA barley consensus map, and the OPA/DArT map of the Oregon Wolfe Barley population. A new GrainGenes service is TAWG, the Triticeae Annotation Working Group, a public repository for annotated genomic sequences of wheat and barley. Soon, GrainGenes will host The Hordeum Toolbox (THT), a database for genotyping and phenotyping data from the U.S. Barley CAP project.

Brachypodium distachyon: a new model to study Triticeae genomes.

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Brachypodium distachyon (*Brachypodium*) is being developed as a new model organism for structural and functional genomics of temperate grasses because of its several desirable attributes for plant biology research, such as easy growth requirements, small stature, short generation time, and small genome size. With the recent completion of the *Brachypodium* genome sequence, along with the established *Agrobacterium*-mediated, high-efficiency transformation system for T-DNA insertional mutagenesis and other genomics resources, tools are now available for exploiting the utility of *Brachypodium* in facilitating wheat research. Comparative mapping of several disease resistance genes indicated that wheat retains colinearity of disease gene orthologs with *Brachypodium*. Such colinearity is not present between wheat and rice, suggesting that *Brachypodium* will be more useful in map-based cloning of rapid or recent evolving genes such as wheat resistance genes. Higher colinearity between wheat and *Brachypodium* also is observed in genomic regions harboring wheat prolamin genes. Expression of wheat promoters and genes in *Brachypodium* provides direct evidence supporting the usefulness of *Brachypodium* in functional characterization of important genes or traits of wheat. A collection of over 6,000 T-DNA insertional mutant lines is now available for public access at website http://brachypodium.pw.usda.gov/TDNA/. These lines are indexed through flanking sequence tags that facilitate mapping of the T-DNA insertions within the *Brachypodium* genome. Several other useful websites for comparative and functional *Brachypodium* genomics will also be discussed.

SESSION V: EARLY CAREER SCIENTISTS

Identification of a novel QTL for Fusarium head blight resistance on wheat chromosome 7A.

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Fusarium head blight (FHB), caused by *Fusarium graminearum,* is an important cereal disease worldwide. Resistance to disease spread within a spike (type II) is the more stable type of resistance. A previous study identified a Chinese Spring (CS)–Sumai 3 chromosome 7A substitution line having a high level of type-II resistance, but an associated quantitative trait locus (QTL) on 7A has never been reported. In this study, we developed CS–Sumai 3 7A chromosome recombinant inbred lines (CRIL) from a cross between CS and CS–Sumai 3 7A disomic substitution lines. A genome-wide marker analysis with 72 chromosome-specific simple sequence repeats (SSR) confirmed that entire 7A chromosome and a small fragment from chromosome 3BS were from Sumai 3 and all other chromosomes were from CS. A total of 191 F_5 CRIL were evaluated for type-II, FHB resistance using single-spikelet inoculation in 2009. The proportion of symptomatic spikelets (PSS) for each CRIL was calculated to measure FHB resistance. The frequency distribution of PSS was bimodal, ranging from 6% to 84%. Out of 75 SSR markers screened from chromosome 7A, 33 were polymorphic and only 7 of 30 SSR markers and 30 sequence tagged sites from 3BS chromosome were polymorphic. The linkage maps for chromosome 7A spans a distance of 181.7 cM and for 3BS, over 2 cM. Composite interval mapping feature of Qgene software was used for QTL mapping with a LOD score threshold of 2.0 ($P < 0.005$) to claim a significant QTL based on 1,000 simulations. A new, major QTL for type-II FHB resistance was detected on the short arm of chromosome 7A with a LOD score of 11, flanked by markers *Xwmc17* and *Xwmc9*. FHB1, a previously reported major QTL on 3BS, also was detected in this study. Both QTL explained 24% (7A) and 45% (FHB1) of the phenotypic variation. An additive effect was observed between the two QTL. Replacement of both alleles of CS with these of Sumai 3 resulted a 66 % reduction in disease severity. Therefore, the QTL from CS 7A is a new major QTL for FHB resistance and can be used for enhancing FHB resistance in breeding.

Wheat–rye T2BS·2BL-2RL recombinants conferring resistance to Hessian fly (H21).

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The Hessian fly, *Mayetiola destructor* (Say), is a destructive insect pest of bread wheat *Triticum aestivum* L. worldwide. Although 32 genes conferring resistance to Hessian fly have been identified, only a few of them are still effective. One such highly effective gene is *H21*, which was transferred to wheat from Chaupon rye via a compensating T2BS·2R#2L Robertsonian, whole-arm, wheat–rye translocation. This translocation also has a locus for field resistance to powdery mildew. To broaden the use of T2BS·2R#2L in wheat improvement, we attempted to transfer both resistance loci, via homologous recombination, to a T2BS·2BL-2R#2L chromosome. The *H21* locus was linked closely to the telomere; the powdery mildew locus was distal, but closely linked, to the translocation breakpoint in T2BS·2BL-2R#2L. Recovered short-segment, rye translocation chromosomes confer resistance to Hessian fly; no crossover event in the desirable configuration was recovered to produce a short-segment, wheat–rye translocation with both *H21* and the powdery mildew resistance gene present. The T2BS·2BL-2R#2L recombinant chromosome has been transferred to adapted winter and spring wheat cultivars.

An adult-plant resistance gene to stripe rust is located on chromosome 2AS in the hexaploid wheat cultivar Jagger.

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Stripe rust is one of the most common and persistent wheat diseases worldwide. With the continuous evolution of different pathogen races, new resistance genes are needed to defend against the mutated pathogens. In this study, we report that a major quantitative trait locus (QTL) for stripe rust resistance was located on the short arm of chromosome 2A (*QYr.osu.2A*) in a population of recombinant inbred lines (RILs) generated from a cross between Jagger and 2174, two prominent winter wheat cultivars in the southern Great Plains, USA. *QYr.osu.2A* was mapped when this population was tested at two sites in Washington where stripe rust frequently occurs and in Beijing, PR China, where CYR32 was inoculated on adult plants. *QYr.osu.2A* explained 81 to 85% of the total phenotypic variation in relative area under the disease progress curve (rAUDPC) value, showing its nearly complete resistance against natural field infection of stripe rust on adult plants in Washington. Stripe rust races included PST-100, PST-114, PST-116, and PST-138, which frequently occur in Washington and other regions of the U.S. such as the Great Plains. *QYr.osu.2A* also accounted for 36% of the total phenotypic variation, showing its partial resistance to CYR32, currently one of the predominant Chinese races and virulent to 80% of commercial cultivars and germplasm in China. In addition, a minor QTL was mapped on the long arm of chromosome 5A (*QYr.osu.5A*), explaining 22 to 30% of the total phenotypic variation across years and locations. Jagger carried a resistant allele at both *QYr.osu.2A* and *QYr.osu.5A*, whereas 2174 carried a susceptible allele at both loci. Our findings suggest that the *de novo* resistance gene at *QYr.osu.2A* in Jagger can provide consistent and broad-spectrum, adult-plant protection to stripe rust. Resistance in Jagger has remained effective during the 15 years since its release, and we recommend this source of resistance be used in breeding applications in conjunction with the molecular markers. This study also demonstrated that many resistance genes present in local cultivars and available mapping populations can be identified and characterized when they are tested in diverse geographical areas of wheat worldwide.

Toward cloning of a major QTL for preharvest sprouting resistance in white wheat.

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Preharvest sprouting (PHS) is a major constraint to white wheat production. Previously, we mapped a major quantitative trait loci (QTL) for preharvest sprouting resistance in the U.S. white wheat Rio Blanco and located the QTL in the distal end of 3AS using a recombinant inbred line (RIL) population derived from the cross 'Rio Blanco/NW97S186'. To validate and fine map the QTL, a new segregation population consisting of 1,874 F_2 lines was developed by selfing the progenies of a RIL (RIL25) that was heterozygous for the three SSR markers in the QTL region. The segregation ratio of PHS resistance in the population fits monogenic inheritance. Plants with all Rio Blanco marker alleles at the three marker loci were resistant to PHS, whereas those with all NW97S186 alleles were susceptible. The additive effect of the QTL played major role on PHS resistance with dominant effect was also observed. Fifty-six recombinants among the three SSR markers were identified in the population to produce homozygous recombinants. Fine mapping delimited the QTL in the region close to *Xbarc57* flanked by *Xbarc321* and *Xbarc12*. The QTL region was further saturated by 11 AFLP and seven wheat EST-derived markers. Microcolinearity was established between the QTL region and the corresponding region on rice chromosome 1 according to the EST information. The QTL was narrowed down to a region about 0.4 cM after analyzing the PHS resistance of the homozygous recombinants. A physical map of the QTL region was constructed by screening a Chinese Spring chromosome 3AS arm-specific BAC library with markers flanking the QTL. Two contigs were identified to span the QTL region. Sequence analysis of these contigs is underway.

POSTER SESSION ABSTRACTS

Poster 1. Saturation and comparative mapping of the Tsc2 region in hexaploid wheat.

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Ptr ToxB is a proteinanceous, host-selective toxin produced by the tan spot fungus, *Pyrenophora tritici-repentis*, capable of causing chlorosis in susceptible wheat (*Triticum aestivum* L.) cultivars. Sensitivity to Ptr ToxB is governed by the *Tsc2* gene located at the distal end of wheat chromosome arm 2BS. *Tsc2* was initially mapped in the International Triticeae Mapping Initiative (ITMI) mapping population, which was derived from the synthetic hexaploid wheat W-7984 and the hexaploid variety Opata 85. The main objectives of this study were to validate the chromosomal location of *Tsc2* and its effects in an intervarietal hexaploid wheat population, develop or identify user-friendly PCR-based markers suitable for marker-assisted selection (MAS) against toxin sensitivity conferred by the *Tsc2* locus, and determine the utility of rice and *Brachypodium* genomic sequences for fine-mapping of the *Tsc2* region. A population consisting of 121 $F_{2:7}$ recombinant inbred lines derived from a cross between the Ptr ToxB-sensitive hexaploid wheat cultivar Katepwa and the Ptr ToxB-insensitive hexaploid landrace Salamouni was used for mapping and phenotypic analysis. SSR markers known to map to 2BS and sequence tagged site (STS) primers developed for 2BS-bin mapped ESTs were mapped in the 'Salamouni/Katepwa' (SK) population. Monomorphic EST–STSs were further mapped as RFLPs. To date, the 2BS map developed in the SK population consists of 32 SSR, 9 EST–STS, and 3 RFLP markers. The SSR marker *Xmag681* and RFLP marker *XBE444541* flanked the *Tsc2* locus at distances of 2.8 cM and 2.6 cM, respectively. *Xmag681* will be suitable in MAS schemes and efforts are underway to convert *XBE444541* to a PCR-based marker as well. Results regarding the effects of the *Tsc2* locus on conferring tan spot susceptibility, comparative analysis of the *Tsc2* region with rice and *Brachypodium*, and discussion regarding the usefulness of using the genomic information from rice and *Brachypodium* for developing additional markers, genomic analysis, and map-based cloning of *Tsc2* will be presented.

Poster 2. Development, mapping, and haplotype analysis of EST-based SNPs for wheat Fusarium head blight resistance QTL Fhb1.

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Fusarium head blight (FHB) is a destructive disease that reduces wheat grain yield and quality. The Chinese variety Sumai3 and its derivatives such as Ning 7840 have a high level of resistance to FHB symptom spread within a spike (type-II resistance) and have been widely used as resistant parents in breeding programs worldwide. The quantitative trait locus (QTL) in chromosome 3BS (*Fhb1*) from Sumai3 has been identified to have the largest effect on FHB resistance to date. This QTL has been linked to restriction fragment length polymorphism, simple sequence repeat (SSR), amplified fragment length polymorphism, and sequence tagged site (STS) markers. Single nucleotide polymorphism (SNP) is the most common form of genetic variation, and SNP may be the next generation marker system for mapping and marker-assisted selection (MAS). In this study, we developed SNP markers based on wheat expressed sequence tags (ESTs) associated with the 3BS QTL region. A total of 131 SNPs were identified between Ning 7840 (FHB resistant) and Clark (susceptible) based on the sequences of ten ESTs. SNPs were analyzed in 71 'Ning 7840/Clark' BC_7F_7 populations using the single-base extension method. Seven SNP markers mapped between *Xgwm533* and *Xgwm493*; SSR markers flanking *Fhb1* in 3BS. Five of these SNP markers clustered with four other SSR/STS markers and covered a 7.4-cM interval, 12.9 cM from *Xgwm533*. This marker-dense region gave the highest R^2 (40–54%) and LOD values (9.16–11.80) and is the most likely location of *Fhb1*. Haplotype analysis of 63 lines from eight countries based on EST sequence (SNP), SSR, and STS markers associated with *Fhb1* identified four major groups: (1) Clark, (2) Asian, (3) Ernie, and (4) Chinese Spring. The Asian group consisted of Chinese and Japanese lines that carry the *Fhb1* resistance QTL and one *Xsnp-11* marker haplotype could differentiate these lines from lines in other groups. All Sumai3-related lines formed a subcluster within the Asian group, and an *Xsnp3BS-8* marker haplotype is specific for these lines. The SNP markers identified in this study should be useful for fine-mapping and MAS of *Fhb1*.

Poster 3. The International Wheat Genome Sequencing Consortium: a genome sequence-based platform to accelerate wheat improvement.

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Bread wheat is grown on over 95% of the wheat-growing area, and its sequence holds the key to genetic improvements necessary to meet the increasing demands for high-quality food and feed produced in an environmentally sensitive, sustainable, and profitable manner. Furthermore, because of its recent history, hexaploid wheat is a very good model to study polyploidy, a driving force for plant genome evolution. The International Wheat Genome Sequencing Consortium (IWGSC) was established by plant scientists, breeders, and growers who are dedicated to sequencing the wheat genome to enhance our knowledge of its structure and function and deploy state-of-the-art molecular tools to accelerate wheat improvement and meet the challenges of the 21st century. The Consortium is committed to ensuring that the wheat genome sequence, and the resulting DNA-based tools are available for all to use without restriction. To achieve the vision of a sequenced wheat genome, the IWGSC develops strategic plans with short- and mid-term goals; defines areas of coordination; facilitates and coordinates research projects and funding efforts at the national and international levels; develops and supports the design of research proposals; provides a framework for the establishment of common guidelines, protocols, and resources; and organizes scientific meetings and workshops. The IWGSC is governed by six co-chairs, a Coordinating Committee, and an executive director. General membership is open to any individual, laboratory, or entity with an active interest in meeting IWGSC objectives. The mission, goals, organizational structure, projects, and online membership registration are available at http://www.wheatgenome.org.

Poster 4. RNAi-mediated viral resistance in transgenic wheat.

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Wheat streak mosaic virus (WSMV) and *Triticum* mosaic virus (TriMV), are two of the major viruses in the Great Plains of the United States. Cultural practices, mite vector control, and deployment of resistant varieties are the primary methods of disease management; however, they are not fully effective. We evaluated the use of interference RNA, recognized as a natural defense mechanism, as a biotech approach to generate resistance to these wheat viruses. RNAi expression vectors were independently created from the sequences of the coat proteins (CP) of both WSMV and TriMV. Immature embryos of the wheat cultivar Bobwhite were independently co-transformed by biolistic particle-delivery system with these RNAi expression vectors and pAHC20, which contains the bar gene for glufosinate selection. After tissue culture, putative transformed plants were analyzed through PCR for the presence of the appropriate RNAi CP gene. Transgenic T_1 seeds were collected and each line was tested for transgene expression via RT-PCR. To determine viral resistance, T_1 progeny were mechanically inoculated with the corresponding virus. Viral presence was established by ELISA. In the T_1 generation, resistance was seen in up to 60% of the plants evaluated for both constructs, although some events that showed transgene presence did not exhibited resistant phenotype. Analyses of transgene presence and expression in the T_2 generation evidenced events of transgene silencing and deletion. Regardless of these phenomena, consistent resistance response in two lines of WSMV CP construct and one TriMV CP transgenic line was found.

Poster 5. QTL detection and factor analysis of yield and adaptive traits in winter wheat.

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The relationships between yield components, adaptive traits, and molecular markers were investigated in two populations of recombinant inbred lines (RILs) using QTL analysis and factor analysis. The RIL populations were derived from single crosses with Tubbs, an Oregon soft white winter wheat variety, with two western European hard red winter wheat varieties. The populations were grown in two replications at two locations in Oregon. Each plot was evaluated for total grain yield, yield components, measures of maturity, and other important traits. The values of all traits were broadly distributed and transgressive segregates were observed in both populations. The yield components most highly correlated with yield were fertile spikelets/spike and seeds/spike in both populations. In one population, these correlations ranged from 0.4 to 0.47. They ranged from 0.21 to 0.25 in the other population. Flowering time was inversely correlated with yield in both populations, ranging from -0.17 to -0.32. Heritabilities were determined for each population across locations. The heritabilities for yield components ranged from 0.44 to 0.84. Heritability for grain-fill duration varied the most between populations, ranging from 0.33 to 0.54. The interrelatedness of the traits was examined by factor analysis of each population at each location using the principle-component method. Five factors, accounting for 69.7% to 73.4% of the total variance, were selected. Important factors were observed for head fertility, tillering, and maturity. Genetic linkage maps composed of DArT and SSR markers were used to detect putative QTL, and their locations are presented. The extension of QTL analysis to factor scores was investigated.

Poster 6. Establishment of a double-haploid production technique using microspore culture for Midwestern U.S. wheat varieties.

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Double haploids (DH) are genetically 100% homozygous plants. Microspore culture is the method of production of DHs from microspores (immature pollen) by androgenesis in a single step. Success of DH plant production is determined by the genotype and health of the donor plant, environmental conditions under which it is grown, staging of the microspore, pretreatment methods, and composition of induction and regeneration media. The objective of this study is to establish a DH-production technique using microspore culture for the Midwestern U.S. wheat varieties. We used Macon, a Washington spring wheat variety, as a check and three Nebraska winter wheat varieties, Anton, Millennium, and Pronghorn, as representatives of the U.S. Midwest. Plants were grown in the greenhouse with 16 hrs of light at 21–25°C and an 8-hr dark period at 16±2°C. Two pretreatment methods (0.4 M mannitol at 4ºC and solution B containing 0.3 M mannitol with inorganic components at room temperature) and one regeneration media was used. We have standardized the staging of microspores and established the steps of the technique (pretreatment, induction, and regeneration) in our laboratory conditions. We were able to produce DH plants for Macon. The microspore culture technique for the winter wheat varieties is in progress. The DH-production technique will be useful in wheat-breeding programs throughout the U.S. Midwest.

Poster 7. Towards a sequence-ready, physical map of chromosomes 1D, 4D, and 6D of hexaploid wheat.

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A physical map is a prerequisite for sequence assembly of large genomes such as that of wheat (*Triticum aestivum* L). Because of the high repeat content and genome triplication, assembly of a high-quality, whole-genome sequence may be difficult. Fortunately, flow cytometry allows the division of wheat chromosomes into three fractions based on size (fraction I: 1D, 4D, 6D; fraction II: 1A, 3A, 6A, 2D, 3D, 5D, 7D; and fraction III: 2A, 4A, 5A, 7A, 1B, 2B, 4B, 5B, 6B, 7B) in addition to an individual chromosome 3B. We have developed fraction-I physical maps of chromosomes 1D, 4D, and 6D and three BAC libraries (312,576 clones) from Chinese Spring fraction-I, with a total coverage of 15.3x of the chromosome length. The BAC clones are being fingerprinted with SNaPshot HICF technology. Fingerprinting of first BAC library (*Eco*RI) with 26,112 clones has been completed and fingerprinting of the *Hind*III BAC libraries is in progress. In total, 70,112 clones (3.5x chromosome coverage) have been fingerprinted with a success rate of 96% and are being used for the initial assembly with FPCv9.3. Progress on the assemblies will be discussed. Mapping populations have been developed to anchor, order, and orient the FPC contigs.

Poster 8. Threading the line between GrainGenes and other genome resources.

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GrainGenes (graingenes.org) has long used molecular markers for the comparison of genomes between its related grass species, mainly those of the Triticeae and *Avena*. Available tools have mainly focused on the CMap and GBrowse (gmod.org) displays. New genome sequence data from other grass species adds to the utility of comparative mapping between the grass species.

With a growing interest in the study of temperate cereals and forage grasses, a new model for the grasses, *Brachypodium distachyon*, has evolved within the research community, some of it leveraged toward bioenergy research. Resources for *Brachypodium* to date include a whole-genome sequence, ESTs, SNPs, a high-density genetic linkage map, and germplasm resources. The high-efficiency transformation system of *Brachypodium* using *Agrobacterium tumefaciens* has yielded a resource of T-DNA insertional mutant lines. Greater than 4,300 T_0 lines have been generated to date, and from these, flanking sequence tag (FSTs) data yielded 1,601 (46.2%) shown to contain *Brachypodium* genomic sequences. As work continues to visually and physically screen these for mutant phenotypes, protocols for working with *Brachypodium*, information about the T-DNA project, and links to seed resources is now available from a website (brachypodium.pw.usda.gov).

Sequencing the wheat genome is now underway in one form or another. There is a need to develop molecular markers for this complex genome. The complexity of the wheat genome has been leveraged against the abundance of randomly mobilized repetitive sequences, many represented by transposable elements (TE). Software, TEPrimers (wheat.pw.usda.gov/demos), was built to recognize this complexity and define candidate repeat junction-junction markers (RJJM) sites, which could predictively be used as unique marker sites. The software has been tested using BAC end sequences and 'next-generation' sequences (Roche 454) of wheat. These and other resources that help bind the genomes together will be presented.

Poster 9. Development and characterization of wheat–alien translocation lines conferring stem rust resistance from Aegilops searsii and Ae. geniculata.

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is potentially one of the most damaging wheat diseases. Although crop loss to stem rust has been infrequent in the past several decades, the emergence of the Ug99 lineage of stem rust races now threatens a large proportion of the wheat acres in the world. Exploiting novel genes effective against Ug99 from wild relatives of wheat is one of the most promising strategies for the protection of wheat production. In this study, resistance to Ug99 was identified on the short arm of $3S^s$ of *Ae. searsii* (2n=2x=14, S^sS^s) and long arm of $5M^g$ of *Ae. geniculata* (2n=2x=28, U^gM^g) by testing of a disomic and ditelosomic addition lines with the chromosomes. To transfer the gene(s) into common wheat, we produced three double-monosomic chromosome populations (3A/$3S^s$, 3B/$3S^s$, and 3D/$3S^s$) of wheat–*Ae. searsii* and and two populations of T550 (T$5M^gS$·$5M^g$L-5DL) crossed with *ph1b* mutant and Lakin, and then applied integrated molecular and cytogenetic approaches to develop wheat–alien recombinants conferring stem resistance. Three wheat–*Ae. searsii* compensating, Robertsonian translocations (T$3S^sS$·3AL, T$3S^sS$·3BL and T$3S^sS$·3DL) and three wheat–*Ae. geniculata* translocation lines with shortened $5M^g$L were selected and confirmed on the basis of genomic in situ hybridization and analysis of $3S^sS$ and $5M^g$ using homoelogous wheat chromosome-specific SSR/STS–PCR markers. These translocation lines were highly or moderately resistant to stem rust race RKQQ. Evaluation of Ug99 resistance and agronomic characterization of the recombinants are currently in progress; efforts to reduce potential linkage drag associated with $3S^sS$ of *Ae. searsii* also is underway.

Poster 10. Reactive oxygen species are involved in plant defense against a gall midge.

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Reactive oxygen species (ROS) play a major role in plant defense against pathogens, but evidence for their role in defense against insects is still preliminary and inconsistent. In this study, we examined the potential role of ROS in defense of wheat and rice against Hessian fly (*Mayetiola destructor*) larvae. Rapid and prolonged accumulation of H_2O_2 was detected in wheat plants at the attack site during incompatible interactions. Increased accumulation of both H_2O_2 and superoxide was detected in rice plants during nonhost interactions with the larvae. No increase in accumulation of either H_2O_2 or superoxide was observed in wheat plants during compatible interactions. A global analysis revealed changes in the abundances of 250 wheat transcripts and 320 rice transcripts encoding proteins potentially involved in ROS homeostasis. A large number of transcripts encoded class-III peroxidases that increased in abundance during both incompatible and nonhost interactions, whereas the levels of these transcripts decreased in susceptible wheat during compatible interactions. The higher levels of class-III peroxidase transcripts were associated with elevated enzymatic activity of peroxidases at the attack site in plants during incompatible and nonhost interactions. Overall, our data indicate that class-III peroxidases may play a role in ROS generation in resistant wheat and nonhost rice plants during response to Hessian fly attacks.

Poster 11. Use of barley stripe mosaic virus for virus-induced gene silencing and gene expression in various wheat tissues.

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Barley stripe mosaic virus (BSMV)-induced gene silencing (VIGS) has shown to be an effective strategy for rapid functional analysis of genes in the leaf tissues of barley and wheat. To extend the potential of VIGS in wheat, we investigated gene silencing in roots and reproductive tissues, compared severity of VIGS in 12 bread wheat cultivars, and demonstrated the transmission of silencing in three selfed generations of inoculated plants. Out of the 12 bread wheat cultivars, Zak and Eltan were most responsive to the silencing of *phytoene desaturase* (*PDS*), and a range from 53–85% suppression of *PDS* transcripts was observed in various wheat cultivars. Incidence of *PDS* gene silencing ranged from 8–11% in the progeny of pγ.PDSas-inoculated plants, from 53 to 72% in the first selfed generation, and 90–100% in the second selfed generation. Spread of the VIGS vector, monitored using green fluorescent protein, was observed in inoculated leaf tissues, phloem, and root cortex at 10 and 17 days-post-inoculation but was absent in apical meristems and reproductive tissues. An antisense construct of the wheat *coronatine insensitive1* (*TaCOI1*) showed suppression of *TaCOI1* transcripts by 50–70% in the roots and 63–68% in the foliage. Similarly, successful silencing of *seed-specific granule bound starch synthase* (*GBSS*) with antisense and hairpin constructs resulted in up to 81% reduction in amylose content, and silencing of the wheat homologue of disrupted meiosis cDNA1 (*TaDMC1*) resulted in 75–80% suppression of the *TaDMC1* transcripts in pollen mother cells.

Poster 12. Characterizing the lignocellulose pathway in wheat by TILLING Triticum monococcum subsp. monococcum.

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Cellulosic biofuel crops are poised to become a major source of energy in the United States, necessitating the understanding the basic biology underlying the traits that control the utility of wheat biomass as an energy source. Mutagenesis is an important tool in crop improvement and is free of the regulatory restrictions imposed on genetically modified organisms. We are developing 'TILL monococcum' a resource for discovery of chemically induced mutants in the diploid wheat ancestor (*T. monococcum* subsp. *monococcum*) to better understand basic wheat biology. A TILLING population of 2,700 single M_2s was developed in *T. monococcum* subsp. *monococcum* using EMS mutagenesis (0.24% EMS). Pools of four M_2 plants were used to screen for lignocellulose pathway mutants in the TILLING population using Cel-I endonuclease. In our preliminary experiments with RT- PCR, 16 ESTs (homologous with annotated genes for lignin precursors in rice) showed a significant developmental regulatory pattern and were in close agreement with total lignin content. Primers were designed from all 16 ESTs for screening the TILLING population. One mutant each was identified for the *PAL 6* and *HCT* locus from the first 716 M_2s screened. The genomic constitution of the selected mutants was determined by Cel-I digestion of the M_3 progeny. Phenotypic validation for the total lignin content of the mutants will be done at maturity.

Poster 13. Unraveling a meiotic gene complex on wheat chromosome arm 5BL.

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The *Ph1* (*pairing homoeologous 1*) locus has been at the heart of wheat research since its discovery in early 1950s. From that time, much speculation and hypotheses have been proposed to explain its mode of action but the identify of the underlying gene(s) remained illusive. Building upon its localization to chromosome arm 5BL, we first localized the locus to a ~3-Mb segment bracketed by the deletion breakpoints of 5BL-1 (FL 0.55) and *ph1c* on chromosome 5B (*Ph1* gene region). Additional mapping of 238 wheat group-5 specific markers assigned nine loci to the *Ph1* gene region. A consensus genetic-linkage map of the whole region also was constructed to determine the order of markers within the region. Extensive blastn/tblastn comparisons of the *Ph1* gene region marker sequences with the rice genomic DNA sequences allowed identification of a 450-kb orthologous region on the rice chromosome 9. This wheat–rice comparison not only allowed alignment of the *Ph1* gene region to the BAC scaffold of rice R9 but also with the BAC scaffold of wheat chromosome 5B. To determine the location of the deletion break points of 5BL-1 and *ph1c* (delimiting the *Ph1* gene regions) on the BAC scaffold of bread wheat, we designed primers from six selected genes and used additional deletions spanning the region. The analysis allowed demarcation of the *Ph1* gene region to a very small fraction of the 2.5-Mb wheat BAC scaffold, carrying only 12 genes. To identify gene responsible for the *Ph*-like phenotype, we undertook virus-induced gene silencing (VIGS) of three candidate genes and nine other genes flanking the region of interest (including *TaDMC1*, *TaASY1*, and *TaCDC2-4*). The candidate genes were short-listed on the basis of domain/motif searches. Silencing of the *TaDMC1* via VIGS showed univalents, whereas *TaASY1* showed multivalents. When VIGS was performed on the *Ph1* gene candidates mapping in the *Ph1* gene region, one of the candidates (*TaWSU-1*) showed formation of quadrivalents/higher order pairing upon silencing, which is a characteristic phenotype of the *ph1* gene mutants. Another candidate (*TaH51L*) showed an average of four univalents and 19 bivalents. These findings suggest that one of the candidate genes, *TaWSU-1*, represents a novel meiotic gene that influences diploid like pairing behavior of hexaploid wheat and also suggests the role of other genes in chromosome just apposition and synapsis at meiotic prophase I.

Poster 14. Virus-induced gene silencing for durable Russian wheat aphid resistance in wheat.

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Russian wheat aphid (RWA), *Diuraphis noxia* (Kurdjumov), is an important insect pest of wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) in the western United States. The most effective control strategy is the development of resistant cultivars, but a gene-for-gene relationship between RWA virulence effectors and R genes results in biotype-specific resistance. Therefore, identifying more durable resistance, effective against all RWA biotypes, would be a significant advantage. Our objective was to test whether silencing a candidate gene, with suspected involvement in compatible interactions between the aphid and wheat, would confer resistance to a susceptible wheat cultivar. Several genes have been identified as being up-regulated in the susceptible cultivar Gamtoos-S (GS) or down-regulated in the near-isogenic resistant line Gamtoos-R (GR; carrying *Dn7*), in a transcript profiling study. Virus-induced gene silencing (VIGS), using the barley stripe mosaic virus, was used to test whether a candidate gene identified from the microarray experiment is involved in the susceptible reaction of GS. Controlled infestation with RWA2, the most virulent biotype to date, was used to estimate aphid fecundity and aphid prenymphopositional period (PNP) and to assess symptom development. No variation in PNP was observed among the treatments. However, silenced plants did show significantly lower aphid fecundity compared to GS and the viral control and similar fecundity to GR. At 14 days-post-infestation, chlorosis scores for the silenced treatment were not significantly different from GR. There also was a significant correlation between the average aphid counts and expression of the candidate gene across treatments. These results indicate that this gene may play an important role in susceptibility and could be exploited for breeding broad-spectrum resistance.

Poster 15. Association analysis of wheat resistance to stem rust in U.S. winter wheat.

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, has become a new threat for wheat production in the U.S. after the emergence and quick spread of race TTKSK from East Africa to other countries. To evaluate the current status of U.S. winter wheat resistance to stem rust, validate markers associated with known genes, and identify new loci effective against the disease, an association mapping population was assembled with 174 U.S. winter wheat cultivars and breeding lines from the 2008 regional nurseries. A total of 267 genome-wide, simple sequence repeat (SSR) markers, including those linked to reported major stem rust resistance gene/QTL, were used to genotype this population. The population was evaluated for seedling resistance to race TTKSK and both seedling and adult-plant resistance to a bulk of U.S. races. About 40% of accessions showed resistance or moderate resistance to the U.S. races in the seedling or adult stage, but only 11.5% of seedlings were resistant to the race TTKSK with an infection type (IT) of 2 or lower. The accessions carrying *Sr36* showed a high level of resistance to both U.S. races and TTKSK in the seedling stage and appeared to confer the best resistance to TTKSK in the population. *Sr38* and *Sr24* conferred a high level of resistance to the U.S. races at the adult stage, with severities lower than 10% and at least moderate resistance. *Sr24* also showed seedling resistance to TTKSK with ITs of ;2 to 2. Accessions with *Sr31* or the new SSR allele, *Xgwm334-123* on chromosome 6A, showed resistance to U.S. races in seedling and adult stages but not to TTKSK. Three additional marker alleles were associated with a low IT (2 or lower) to TTKSK and *Sr* genes linked to these alleles need further investigation. However, the frequency of all these resistance alleles for TTKSK was low in the population studied. Introducing new *Sr* genes and increasing the frequency of known effective resistance genes should be the focus of research to improve wheat resistance to stem rust.

Poster 16. A gut transcriptome of the Hessian fly (Mayetiola destructor), a member of the gall midges.

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Hessian fly, *Mayetiola destructor*, is a serious pest of wheat and an experimental organism for the study of gall midge-plant interactions. In addition to food digestion and detoxification, the gut of Hessian fly larvae also is an important interface for insect–host interactions. Analysis of the genes expressed in the Hessian fly larval gut will enhance our understanding of the overall gut physiology and may also lead to the identification of critical molecules for Hessian fly–host-plant interactions. Over 10,000 expressed sequence tags (ESTs) were generated and assembled into 2,007 clusters. The most striking feature of the Hessian fly larval transcriptome is the existence of a large number of transcripts coding for so-called small secretory proteins (SSP) with amino acids less than 250. Eleven of the 30 largest clusters were SSP transcripts with the largest cluster containing 11.3% of total ESTs. Micorarray and qPCR analyses of representative SSP transcripts revealed that most of them were predominantly present in the gut tissue and the transcript levels of many SSP were affected by plant genotypes on which larvae feed. Transcripts coding for diverse digestive enzymes and detoxification and metabolic proteins also were identified. The putative digestive enzymes included serine proteinases (trypsins and chymotrypsins), cysteine proteases, aspartic protease, endo-oligopeptidase, aminopeptidases, carboxypeptidases, and α-amylases. Putative detoxification proteins included cytochrome P450s, glutathione S-transferases, peroxidases, ferritins, a catalase, and peroxiredoxins. This study represents the first global analysis of gut transcripts from a gall midge. The identification of a large number of SSP transcripts in the Hessian fly larval gut provides a foundation for future study on the functions of these genes.

Poster 17. Two homoeologous wheat genes confer sensitivity to a single, host-selective toxin and susceptibility to Stagonospora nodorum blotch.

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The pathogen *Stagonospora nodorum* produces multiple host-selective toxins that interact with corresponding wheat sensitivity genes in an inverse gene-for-gene manner to cause the disease Stagonospora nodorum blotch (SNB) in wheat. We screened accessions of *Aegilops tauschii*, the D-genome donor of common hexaploid wheat (*Triticum aestivum*), with culture filtrate derived from isolate Sn4. One sensitive (TA2377) and one insensitive (AL8/78) accession were selected to develop an F_2 population. Bulked-segregant analysis and molecular mapping indicated that the new toxin sensitivity gene, temporarily designated *Snn5DS*, mapped to chromosome arm 5DS. Inoculation of the population with spores from Sn4 indicated that a compatible host–toxin interaction explained 100% of the variation in SNB development. In related research, *SnTox3*, which interacts with the *Snn3* gene on wheat chromosome arm 5BS, was isolated. Further evaluation of the F_2 population indicated that the toxin interacting with *Snn5DS* was SnTox3. Comparative mapping revealed that *Snn3* and *Snn5DS* are homoeologous and, thus, derived from a common ancestor. Further characterization indicated that, as opposed to most host–toxin interactions in the wheat–*S. nodorum* pathosystem, the *Snn3*/*Snn5DS*-SnTox3 interaction is not dependent on light, which suggests that a different host metabolic pathway is exploited to cause disease. Saturation and high-resolution mapping delineated the *Snn5DS* locus to a 1.4-cM interval, and analysis of colinearity indicated the *Snn5DS* region is well conserved between wheat, rice and *Brachypodium*, which will aid in the map-based cloning of *Snn5DS*.

SPEAKER AND POSTER ABSTRACTS HARD WINTER WHEAT WORKERS WORKSHOP

7–9 MARCH, 2010
UNIVERSITY OF NEBRASKA–LINCOLN

SESSION I: ADVENTURES IN WHEAT BREEDING

The ghosts of wheat breeding – past, present, and future.

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Most public wheat breeding programs have a long and storied history in the Great Plains. They usually predate commercial programs, although farmer breeders made substantial contributions to early wheat improvement. Large companies often have a shorter history in wheat breeding but have invested considerable resources and have made, and continue to make, significant contributions to wheat improvement. Currently, wheat breeding is undergoing a resurgence of private investment and, as a community, we may need to develop new models for how we interact and how public breeders can be successful in the future. Globally, privatization has occurred in most developed countries. An obvious question is 'What have we learned from our past and the experience of other countries?" First, private investment is a good thing, and the wheat community benefits from greater investment. Hence, private involvement should be embraced and supported. Second, as a wheat community, we will need to decide the future we want to create and how we will determine success (we define ourselves). Clearly, both the public and private sector will evolve. Lessons that we should remember from the first major wave of private investment (when hybrid wheat became an objective and PVP extended intellectual protection to self-pollinated crops) are that 1. we remain a community, 2. we benefit from our collective efforts, and 3. public investment can harm or benefit private investment and vice versa. Retrospectively, a major flaw with our public efforts was that we did not embrace hybrid wheat breeding as an intellectual and practical concept. Only Karl Lucken in the public sector worked diligently on this effort. Private companies invested heavily, but the tools were insufficient and the corporate patience lacking to make this effort successful. Concurrently, public researchers in rice worked for years in the 'wilderness' and eventually created the hybrid rice industry that is now grown on millions of hectares. Accepting the advantages of transgenic traits has similarly limited wheat improvement. On a personal note, every program I have worked with (USDA–ARS, Monsanto, and now the University of Nebraska) has evolved based upon their unique needs and opportunities. Some of the things that I have learned over my career are: 1. Plant breeding is at its core a question driven science, 2. Plant breeding requires logistical and personal skills, and 3. You determine how its impact will shape your program. I also learned that to be successful, it is first important to find a job you love, because you will never work a day in your life (Confucius). Second, be an optimist. Most people prefer to work around happy people. Also, be generous with your time, and when you accept a request, never give it anything less than your best effort. Others count on you and do not let them down. Finally, learn from others as they will teach you what and what not to do, and both are valuable.

2010, A Wheat Odyssey (reflections on private wheat breeding in the Southern Plains).

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Most private wheat breeding programs have, over time, attempted a number of different avenues to differentiate themselves and generate a profit outside traditional breeding focuses. These have included hybrid wheat, special end use quality coupled with identity preservation, and in the future, transgenic wheat. Although conceptually successful, hybrid wheat was hampered by breeding bottlenecks and high production costs. Identity preserved, end use quality has had niches of success but has failed to materialize as a major contributor to wheat production due to low seed margins, less than hoped for 'value added' opportunities, storage problems, and inconsistent variety performance. In the past 25 years, there has been an increase in the number of biotic and abiotic factors, which have become significant hindrances to the rate of progress that breeders have envisioned. As biotechnology has developed and been implemented into competing crops such as corn, soybeans, canola, and cotton, resources have withdrawn from wheat into these more 'private friendly' crops. As we begin a new decade, the wheat industry seems poised to embrace transgenic wheat, and there is an anticipated return of significant investment into wheat research both at the public and private level. Public and private breeding programs have existed in a synergistic relationship that contrasts significantly to other major breeding crops. This relationship will be a key focus on the introduction and acceptance of transgenic wheat.

The search for broad adaptation and genetic diversity: the experience of an international breeding program.

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The International Winter Wheat Improvement Program (IWWIP) was established 25 years ago as a joint program between Turkey, CIMMYT, and ICARDA. The IWWIP aims to develop winter/facultative germplasm for the region of Central and West Asia. It operates multilocational breeding network in Turkey utilizing its natural diversity of wheat production environments. The program also plays a very important role in facilitating the global winter wheat germplasm exchange among its 100+ coöperators in more than 50 countries. The IWWIP develops germplasm for both irrigated and semi-arid areas combining adaptation with the resistance to prevailing pathogens (yellow, leaf, and stem rusts) and bread-making quality. Advanced lines developed by the program, along with the selected introduced germplasm, are annually distributed through international nurseries to cooperators for evaluation, selection, and utilization in their breeding programs. The success in broad adaptation and cultivation of CIMMYT spring wheat varieties was one of the driving forces to establish a breeding program in Turkey, which would replicate similar success for winter wheat. However, despite identification of the broadly adapted winter wheat lines, none of the varieties developed so far was adopted on areas similar to that of spring wheat. The regional diversity of winter wheat production environments might be one of the reasons for specific adaptation playing a relatively important role. Genetic diversity is an aspiration of many breeding programs to assure that new varieties are not vulnerable to biotic and abiotic stresses. The IWWIP, being an 'engine' of global winter wheat germplasm exchange, has access to tremendous genetic diversity represented by modern germplasm from all major breeding programs. Utilization of this diversity by the IWWIP proved beneficial for adaptation, abiotic stresses, and new emerging threats such as stem rust Ug99 or the cereal cyst nematode. The IWWIP traditionally has maintained close linkages and cooperation with the U.S. winter wheat breeding community. Possible avenues to enhance this collaboration for priority research topics (drought tolerance, rust resistance, and winterhardiness) are presented.

SESSION II: WHEAT QUALITY

Association analysis of hard white wheat high- and low-molecular-weight glutenin subunits and their relationship to end-use functionality.

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Allelic variation at the glutenin loci is known to contribute to end-use qualities in wheat (*Triticum aestivum* L.). The *Glu-A1*, *Glu-B1*, and *Glu-D1* loci, which encode high-molecular-weight glutenin subunits (HMW-GS), and the *Glu-A3*, *Glu-B3*, and *Glu-D3* loci, which encode low-molecular-weight glutenin subunits (LMW-GS), are highly polymorphic and many combinations of alleles exist in different breeding programs. However, the effect of different glutenin alleles at all six loci on dough and bread-making properties is poorly characterized, particularly in U.S. breeding programs. In this study, a set of advanced breeding lines and cultivars from the USDA–ARS Hard Winter Wheat Regional Performance Nursery (RPN) was used to determine the effects of glutenin alleles and 1RS translocation on mixograph peak time (MPT) (adjusted for protein content) and loaf volume (LV). Association analysis was implemented using the MIXED model procedure to reduce spurious associations. The ANOVA results demonstrate that both *Glu-B1* and *Glu-D1* loci had a significant effect ($P < 0.0005$) on MPT, with *Glu-B1al*, *Glu-D1d*, and *Glu-B1f* alleles associated with longer MPT, whereas the *Glu-B1e* and *Glu-D1a* alleles were associated with reduced MPT. The *Glu-D3* locus had a significant influence ($P < 0.05$) on LV, with the *Glu-D3f* allele generally associated with increased LV compared to other alleles at that locus. Although the presence of the 1RS translocation did not have a significant effect on MPT, it was significantly correlated with LV ($P < 0.005$), with the T1BL·1RS translocation associated with decreased LV.

A new viscoelastic test for assessing wheat gluten strength.

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Buyers of U.S. wheat have long been asking for functional quality information. Through a meeting with a broad group of wheat researchers, GIPSA has identified gluten strength as a key intrinsic property that may provide this information. A shipload is made up of different wheat cultivars grown in diverse regions; therefore, it is likely that there will be varied functional characteristics within and between shipments. As the industrial processing capabilities of wheat buyers become more automated, varied consistency within and between shipments presents serious challenges. Since the 1930s, over one dozen dough functional test methods came into being, and generally, they are burdensome and empirical in nature. All of these methods, in one way or another, assess dough or gluten rheological characteristics; however, few if any of them are rapid enough for use in the field to test and blend wheat to meet buyers' needs. On the other hand, provided with a rapid test, the sophisticated grain handling systems in the U.S. are fully capable of tailor-making wheat lots to meet the needs of processors. Therefore, GIPSA is engaged in the development of a scientifically sound, rapid test for assessing wheat functionality. This test could be used to assess gluten strength from the breeder to the processor, eventually leading to a standardized method that could be used throughout the wheat marketing chain. With this goal in mind, a workgroup has been formed to test new concepts and develop a fundamentally sound, yet rapid, viscoelastic test for assessing gluten strength. The results of exploratory work using novel instrument prototypes, which have shown promise, will be presented.

Induction of wheat antioxidants.

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Producers of whole wheat products are interested in using high antioxidant (AOX) wheat in their products and marketing the recognized nutritional benefits but need assurance that they can access wheat with consistent, significant AOX levels. Research is now emerging that shows AOX to be the plant's defensive response to stress, particularly, insect or fungal attack. Recognition of insect feeding induces wheat plants to produce stress signals that activate peroxidases. Peroxidases, in turn, then mediate the production of phenolic compounds, which have been shown to act as chemical defenses, as well as lignin, which has been shown to act as a structural defense in wheat against feeding damage by the Hessian fly and several species of aphids. Previous work in our labs has enabled identification of wheat varieties with genetic potential to generate high AOX levels. The purpose of this research, sponsored by the Kansas Wheat Commission, is to determine the effect of specific stress factors that may be responsible for plant expression of higher AOX levels as a defensive response to the stress. Initial results will be shown.

SESSION III: ABIOTIC STRESSES

Improving drought stress tolerance in wheat: A grand challenge for the 21st century.

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Increasing global demand for food and predictions of a drier climate in many regions mean that crops will have to be more productive with less water. Although crop management offers some scope for increased productivity, enhanced crop genetics certainly will play a major role in dealing with more frequent and severe episodes of drought. But what are the best strategies for improving such a complex, multi-faceted trait as drought tolerance of wheat? One approach for improving yields under moisture stress is to select for yield potential or correlated traits under more favorable conditions, with the expectation that part of that yield benefit will be carried over to lower yielding, moderately stressed environments. For more severe stress, selection for specific drought adaptation traits may be beneficial, as long as those traits do not reduce yield under higher moisture conditions. Depending on the environment, selection for traits such as seedling root architecture, early vigor, leaf waxy layer, preflowering assimilate translocation, stem soluble carbohydrates, biomass through the Normalized Difference Vegetation Index (NDVI), or transpiration and plant water status through thermal imagery and near infrared spectroscopy may be of value. Useful sources of variability for drought adaptation include existing elite germplasm, landraces, and wild wheat (*Triticum turgidum* subsp. *dicoccoides* or *Aegilops tauschii*) in the form of synthetic hexaploids. Quantitative trait locus analysis and association analysis are gene discovery methods that will benefit from the development of a SNP marker platform, which is currently underway. Transgenes are another potential source of improved stress tolerance. Although the field performance of transgenic wheat designed for drought tolerance has not been encouraging, efforts in this arena are continuing and may bear fruit. We will present examples of drought tolerance research at Colorado State University and elsewhere and discuss some of the opportunities and challenges for achieving greater levels of drought tolerance for our region.

Mid-season determinations of nitrogen need to maximize yield and optimize inputs.

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The annual variability of yields in winter wheat production creates a conundrum when the ultimate goal is the production of maximum yields while minimizing inputs. The optimization of nitrogen (N) inputs becomes absolutely necessary due to the current market volatility and concentration on environmental stewardship. In 1971, a long-term, winter wheat fertility study was established in north-central Oklahoma. The 38-yr maximum yield ranged from 1,422 kg/ha to 5,935 kg/ha with an average of 3,011 kg/ha and standard deviation of 1,016.56 kg/ha. The average optimum N rate over the 38 years was 59 kg/ha. However, the optimum annual rate ranged from a minimum of 0 kg/ha to a maximum of 160 kg/ha with a standard deviation of 48 kg/ha. Yield goals and traditions lead the area producers N rate recommendation tools. For this region, total precipitation and the distribution of the events is the greatest yield determining factor. Many producers decide total N applications before the seed is sown, which lends to excessive N application in most years and a loss of yields in others. The technique of using optical sensor to determine midseason N rates has been implemented to account for the temporal and spatial variability experienced by every producer. Utilizing crop canopy reflectance measures (NDVI) and growing degree day units, yield potential can be determined prior to Feekes' growth stage 6. Yield potential combined with a measurement of N response (reference strips and the response index) a fertilizer N rate can be determined. This technique has been developed over many environments and varieties. Studies show on average a benefit of $20/ha in winter wheat through the use of these technologies. The sensor and reference strip approach also allows for the ability to account for varietal differences in nitrogen need and use efficiency.

Wheat tolerance to aluminum toxicity in Asian and U.S. wheat.

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Aluminum (Al) toxicity is a major constraint for wheat production in acidic soils worldwide and especially in the southern Great Plains. Growing Al-tolerant cultivars is one of the most effective approaches to reduce Al damage. Malate release from root tips is considered a major mechanism for Al tolerance. Recently, citrate efflux has been suggested as an additional mechanism. A major quantitative trait locus (QTL) for Al tolerance has been mapped on chromosome 4DL and an Al-activated malate transporter, *ALMT1*, was cloned from this QTL region. Several markers developed from both the gene coding and promoter regions of *ALMT1* have been used for marker-assisted selection (MAS). However, markers fully diagnostic for the QTL have not been found. To evaluate the effectiveness of previously reported markers in MAS and identify new QTL for Al tolerance, an association mapping population with 94 Asian cultivars and landraces and 211 U.S. elite winter wheat breeding lines was evaluated for Al tolerance in laboratory and field experiments and genotyped with 270 genome-wide markers, including all previously reported markers for Al tolerance. Association analysis was conducted separately in both Asian and U.S. groups as suggested from structure analysis. Hematoxylin staining identified 33% of the accessions as highly resistant in each group. Among these accessions, 93% amplified a large fragment (≥720 bp) of UPS4, a part of the *ALMT1* promoter. All highly susceptible accessions amplified a smaller fragment (438 or 469 bp). However, only 33% of the highly resistant Asian accessions amplified the large fragments of UPS4, and most Al-tolerant accessions and all Al-sensitive accessions amplified either of the smaller fragments. Sequence analysis indicated that some accessions in the Asian group carrying an identical allele at *ALMT1* differed widely in Al tolerance. Besides UPS4, one marker on 3BL and two new markers on 4A and 7A were associated with Al tolerance in the U.S. and Asian groups, respectively. Linkage mapping to validate the putative new QTL from the Asian source is in progress. Therefore, the QTL on 4DL is the major source of Al tolerance in U.S. germplasm, and UPS4 is an ideal marker for MAS of the QTL. Further exploring Asian sources of Al tolerance may lead to the discovery of new QTL for Al tolerance.

SESSION IV: WHEAT DISEASE

Exploring plant susceptibility genes in pest management.

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Plants are under constant attack from various pathogens and other types of herbivores. To survive these attacks, plants have evolved layers of defense mechanisms. During the long course of co-evolution, many plant insects and pathogens have gained the ability to suppress plant defense and alter plant metabolic pathways. A typical example is the Hessian fly (*Mayetiola destructor*), one of the most destructive pests of wheat worldwide. In order to survive on wheat, Hessian fly larvae need to suppress wheat basal defense, induce the formation of nutritive cells that act as a nutrient sink, and inhibit wheat growth. Recently, we have identified a gene in wheat that is required for Hessian fly to manipulate wheat seedlings. Because it is essential for wheat susceptibility to Hessian fly attacks, we named this gene *Mayetiola destructor susceptibility gene-1* (*Mds-1*). Knockdown of *Mds-1* can prevent Hessian fly from successful manipulation of wheat seedlings. As a result, plants that are normally susceptible to Hessian fly attack become resistant. On the other hand, elevated expression of *Mds-1* artificially make wheat seedlings, that are normally resistant due to the presence of a major R gene, susceptible. The essentiality of *Mds-1* for wheat seedlings to Hessian fly attacks provides us an opportunity to use it as a target for Hessian fly management.

Integrating genetic resistance and fungicides for Fusarium head blight management.

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Fusarium head blight (FHB) continues to be a serious problem in many wheat-producing regions of the North America. In recent years, portions of Kansas and Nebraska have experience significant yield losses from this disease. The breeding programs within the hard winter wheat production region have been actively pursuing genetic resistance to FHB for nearly a decade. These efforts have resulted in the release of several varieties with elevated resistance to the disease. The current challenge now is to demonstrate the value of these new varieties as part of an integrated approach to reducing the risk of the severe yield loss and deoxynivalenol contamination resulting from FHB. Multi-state research projects are underway to evaluate the potential of value of combining genetic resistance with crop rotation and fungicide application. The results of these trials indicate that genetic resistance to FHB is most important factor influencing disease intensity, but that crop rotation and fungicides can also be used effectively to reduce the risk of yield loss and DON contamination. A disease forecasting system that provides daily estimates of disease risk also is available to help producers evaluate the need for timely fungicide applications. Additional research is needed to evaluate the potential variations of this integrated approach that will maximize the value of each tool to the producer.

Genetic dissection of wheat–necrotrophic fungus interactions: breeder beware !

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Tan spot and Stagonospora nodorum blotch (SNB) are both devastating foliar diseases of wheat caused by the necrotrophic pathogens *Pyrenophora tritici-repentis* and *Stagonospora nodorum*, respectively. Both pathogens produce numerous host-selective toxins (HSTs) that interact with dominant host genes in an inverse gene-for-gene manner to cause disease. However, broad-spectrum, race-nonspecific QTLs conferring resistance to tan spot also have been identified and are current targets for marker-assisted selection (MAS). For SNB, we have developed molecular markers closely linked to five *S. nodorum* HST sensitivity genes. We have used MAS to introgress the race nonspecific tan spot resistance QTLs and to eliminate the *S. nodorum* toxin sensitivity genes from the wheat cultivar Alsen while retaining the *Fhb1* locus. In related, but more basic, research, we are working to characterize these host-toxin interactions at the molecular level. The HST known as ToxA is produced by both *P. tritici-repentis* and *S. nodorum*, and sensitivity to ToxA is governed by the *Tsn1* gene in wheat. The cloning of *Tsn1* revealed that it contains numerous resistance gene signatures, and further characterization of the *Tsn*–ToxA interaction indicates that the mechanisms are much the same as in classic R gene–Avr gene interactions, except that the end result is susceptibility as opposed to resistance. The difference in outcome likely is due to the biology of the pathogen, i.e., necrotrophs have acquired mechanisms to exploit the resistance mechanisms acquired by plants to combat biotrophic pathogens. Therefore, it is possible that breeding for resistance to a biotrophic pathogen could result in the acquisition of susceptibility to a necrotrophic pathogen, or visa versa.

SESSION V: VIRUSES

The status of wheat viruses in the Great Plains.

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Wheat is an economically important crop in the Great Plains of North America. Several viruses infect wheat in this region, causing yield losses ranging from trace to 100% in the most severely affected fields. The major virus infecting wheat in the Great Plains is wheat streak mosaic virus (WSMV). However, in 2006, *Triticum* mosaic virus (TriMV) was discovered in Kansas and was recently (2008) confirmed in Colorado, Nebraska, Oklahoma, South Dakota, Texas, and Wyoming. Both WSMV and TriMV are transmitted by the wheat curl mite (WCM). Co-infection of wheat by both viruses has been confirmed under field conditions, and synergism in symptom expression has been demonstrated in controlled environment studies. Therefore, the potential exists for greater yield loss from co-infection of wheat by WSMV and TriMV. In addition, preliminary work has shown that cultivars with resistance to WSMV appear to be susceptible to TriMV, implying that recent progress in the development of WSMV-resistant cultivars is potentially threatened by the presence of TriMV. Another virus also transmitted by the WCM, and which has been shown to co-infect wheat with WSMV, is wheat mosaic virus (WMoV, formerly High Plains virus). Other viruses of wheat in the Great Plains include wheat soilborne mosaic virus, wheat spindle streak mosaic virus, barley yellow dwarf virus, and cereal yellow dwarf virus. The current status of these viruses in the Great Plains and their implications on wheat production in the region will be discussed.

Characterization of the Triticum mosaic virus genome and interactions between Triticum mosaic virus and wheat streak mosaic virus.

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The complete genome sequence of *Triticum* mosaic virus (TriMV) has been determined to be 10,266 nucleotides encoding a large polyprotein of 3,112 amino acids. The proteins of TriMV possess only 33–44% (with NIb protein) and 15–29% (with P1 protein) amino acid identity with the reported members of Potyviridae. These results suggest that TriMV should be classified in a new genus, and we propose the genus *Poacevirus* in the family Potyviridae with TriMV as the type member.

TriMV and wheat streak mosaic virus (WSMV), distinct potyvirid species, infect wheat naturally in the Great Plains and are transmitted by wheat curl mites. We examined the interaction between WSMV and TriMV in three wheat cultivars at two temperature regimens (19ºC and 20–26ºC). Double infections in wheat cultivars Arapahoe and Tomahawk at both temperature regimens induced disease synergism with severe leaf deformation, bleaching, and stunting with a 2.2- to 7.4-fold increase in accumulation of both viruses over single infections at 14 days post-inoculation (dpi). However, at 28 dpi, in double infections at 20–26ºC, TriMV concentration increased by 1.4- to 1.8-fold in Arapahoe and Tomahawk, but WSMV concentration decreased to 0.5-fold. WSMV and/or TriMV replicated poorly in Mace at 19ºC with no synergistic interaction, whereas both viruses accumulated at moderate levels at 20–26ºC and induced mild to moderate disease synergism in doubly infected Mace when compared to Arapahoe and Tomahawk. Co-infections in Mace at 20–26ºC caused increased TriMV accumulation at 14 dpi and 28 dpi by 2.6- and 1.4-fold, and WSMV accumulated at 0.5- and 1.6-fold over single infections, respectively. Our data suggest that WSMV and TriMV induced cultivar-specific disease synergism in Arapahoe, Tomahawk, and Mace, and these findings could have several implications on management of wheat viruses in the Great Plains.

Biology, phylogenetics, and distribution of wheat curl mite population.

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Wheat streak mosaic has long been recognized as one of the most important diseases of winter wheat in the Great Plains. However, the identification of High Plains virus in the mid 1990s and *Triticum* mosaic in 2008 create a complicated virus complex in wheat. All three of these viruses are vectored by the wheat curl mite, and management of this virus complex is dependent on cultural practices that reduce the probability of mite infestation. Research into aspects of the biology and ecology of the mite has provided valuable insights into the potential for success of various management tactics. The development of resistant wheat varieties has had an impact on the virus but has not resulted in stable control. Distribution of mite biotypes explains the limited success of varietal mite resistance. Mite biotypes have shown differences in the mite's ability to transmit virus but also differences in survival on virus infected plants. Thus, one biotype is better adapted to the presence of these viruses. Recent studies on the movement of the mite also have provided better understanding of virus epidemiology and have improved recommendations for the management of this virus complex.

SESSION VI: RUSTS

Sources of stem rust resistance and potential for strategic deployment.

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Routine deployment of broadly effective, stem rust resistance gene combinations has not been possible, practical, and/or sufficiently emphasized in most wheat breeding programs throughout the world in recent decades. Stem rust races in the Ug99 lineage demand an exhaustive and strategic effort to disrupt this cycle and incline the balance of this ancient battle towards wheat resistance. The current global emphasis and investments in stem rust pathology, germplasm enhancement, dissection of resistance genetics, and breeding will provide the necessary information and materials to adequately address the stem rust threat over the next 20+ years of wheat breeding and on-farm production. The exploitation of perfect markers for durable resistance loci, nonhost resistance mechanisms, and/or novel biotech solutions will most likely predominate in the long term. The most obvious limitations to achieving durable stem rust resistance in the short to medium term are 1) the pace of variety development and replacement in winter wheat breeding and 2) insufficient community coordination and commitment to gene deployment.

In addition to 'new' genes resulting from ongoing discovery and germplasm enhancement efforts, seedling resistance genes *Sr22*, *Sr25*, *Sr26*, *Sr32*, *Sr35*, *Sr39*, *Sr40*, *Sr42*, *Sr1A·1R*, *SrTmp*, *SrA*, *SrB*, *SrC*, *SrACCadillac*, and *SrR* should be on the radar of hard winter wheat breeders. The durable resistance locus *Sr2* should be considered in every gene-deployment strategy/pyramiding effort. Durable rust resistance locus *Lr34*/*Yr18* also is associated with stem rust adult-plant resistance, at least in the Thatcher background, and represents another likely component of gene pyramids. Introgression of uncharacterized adult-plant resistance in hard winter wheat is underway, and molecular markers should enable this effort, in spite of screening limitations in East Africa.

Stripe rust resistance in hard winter wheat.

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Stripe rust resistance data for the 2009 hard winter wheat Regional Germplasm Observation Nursery (RGON, n = 261) were reported by researchers in Manhattan, KS, and Raleigh, NC, from field nurseries or greenhouse seedling tests. Adult-stage field infection type (IT) and percent severity data from KS and NC were well correlated within and between sites ($r = 0.65$-0.88, $P < 0.0001$). The distribution of mean field adult-stage infection type (0–9 scale) over both locations was strongly skewed toward resistance. The percentages of resistant (IT = 0–3), intermediate (IT = 4–6), and susceptible (IT = 7–9) lines were 70%, 20%, and 10%, respectively. On the other hand, greenhouse seedling ITs were strongly skewed toward susceptibility. The percentages of resistant, intermediate, and susceptible lines at the seedling stage were 2%, 25%, and 73%, respectively. Therefore, the majority of effective resistance in the RGON lines is adult-plant resistance (APR). Some lines had an intermediate ITs but high disease severity, which was associated with a necrotic stripe reaction. For the 2009 Northern and Southern Regional Performance Nurseries (NRPN, n = 25; SRPN, n = 46), field and greenhouse data were available from KS, NC, and three locations in WA. Data for the NRPN and SRPN were combined for analysis. Adult-stage IT and severity data were again well correlated within and between KS and NC ($r = 0.50$–0.75, $P < 0.0001$). IT and severity data from KS and NC were correlated with severity, but not IT from Pullman, WA ($r = 0.35$-0.47, $P < 0.01$), but were practically uncorrelated with data from Mt. Vernon or Walla Walla, WA. The percentage resistance in the NRPN+SRPN based on mean adult-stage infection type over three locations was 61% resistant, 31% intermediate, and 8% susceptible. At the seedling stage, 0% were resistant, 25% intermediate, and 75% susceptible, thus again showing the prevalence of APR. Thirty-eight percent of lines were positive for the VENTRIUP-LN2 marker for the *Ae. ventricosa* chromosome segment carrying *Yr17*. Lines with the marker had average adult-stage field severities of 10%, whereas lines without the marker had average severities of 33%.

Virulence in Puccina triticina and leaf rust resistance in hard red winter wheat.

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Leaf rust, caused by *Puccinia triticina*, is a common disease of hard red winter wheat in the Great Plains region of the U.S. In 2008, 52 races of leaf rust were described in the U.S. Races TDBGH (virulence to *Lr24*), MLDSD (virulence to *Lr39*/*Lr41*, and *Lr17*), TDBJH (virulence to *Lr24*) were among the most common races in the Great Plains region. Two major groups of *P. triticina,* based on simple sequence repeat (SSR) genotypes, are present in the Great Plains region. Isolates avirulent to *LrB*, *Lr17*, and *Lr3bg* are in one SSR group and are long established in North America. Isolates with virulence to *LrB*, *Lr17*, and *Lr3bg* are in a different SSR group and were likely introduced to the Great Plains region in the mid 1990s and increased with the widespread cultivation of Jagger with *Lr17*. Races with virulence to *Lr24*, *Lr26*, and *Lr39*/*Lr41* are found in both groups of SSR genotypes. Leaf rust resistance genes *Lr24*, *Lr17*, *Lr14a*, and *Lr39*/*Lr41* are very common in the hard red winter wheat cultivars. Genes *Lr16* and *Lr26* are present in fewer cultivars. Leaf rust races with virulence to these genes have been found in the hard red winter wheat area, thus none of these genes condition resistance to all leaf rust races. The adult-plant gene *Lr34* also is present in hard red winter wheat, however many cultivars derived from Jagger have an inactive allele at this locus. Preliminary results of genetic analysis of leaf rust resistance in the cultivar Duster indicated the presence of *Lr11*, an additional seedling-resistance gene, plus a functional allele of *Lr34* and an additional adult-plant resistance gene. The cultivar Santa Fe likely has the seedling resistance genes *Lr3* and *Lr17*, plus at least one adult-plant resistance gene that is likely not *Lr34*.

POSTER SESSION ABSTRACTS

Poster 1. Identification of quantitative trait loci associated with maintenance of bread-making quality under heat stress in wheat (Triticum aestivum).

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High temperature during reproductive development is a major factor limiting wheat production and end-use quality in the Southern Great Plains as well as in many other environments worldwide. We have initiated multiple projects integrating both genotypic and phenotypic data to identify quantitative trait loci (QTL) controlling reproductive stage heat tolerance in wheat, defined here as the maintenance of yield and end-use quality during reproductive-stage heat stress. In this study, we have focused on the mapping of QTL associated with end-use quality due to their importance and known sensitivity to heat stress. QTL mapping was carried out based on morphological, yield, and quality data from recombinant inbred lines (RILs) grown in controlled environments. The RILs were derived from the cross between Halberd, a heat-tolerant Australian line, and Cutter, an advanced line selected for its high score in yield and other agronomically important traits. RILs were phenotyped using the sodium dodecyl sulfate sedimentation (SDSS) test of grain harvested from heat-treatment greenhouse trials. Four QTL were identified: two associated with variation in SDSS levels under control conditions, one associated with variation in SDSS levels under heat stress conditions, and one associated with the maintenance of SDSS score between heat stress and control conditions. Identified QTL were confirmed in a population of advanced lines grown in field trials at three Texas nurseries. In addition, data from the advanced line trials was used to further analyze the identified QTL for their relation to yield and quality characteristics. An improved understanding of the correlation between end-use quality maintenance and yield stability QTL during reproductive stage heat stress will aid both in the breeding of plants possessing each attribute using marker-assisted selection and in basic research aimed at defining the molecular basis of heat tolerance.

Poster 2. A comparative study of clump vs. row planting geometry on dryland maize yield and harvest index.

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Water for dryland grain production in the Texas Panhandle is limited. Agronomic practices such as reduction in plant population and change in sowing time help increase yield potential. Tiller formation leads to more vegetative growth and less yield. I hypothesized that clump planting maize (*Zea mays* L.) under dryland would reduce environmental stress, tillering, and vegetative growth and increase grain yield and harvest index by moisture conservation. Clump plantings were studied during 2008 at Bushland, TX. Treatments were two plant populations (30,000 and 40,000 pl/ha) and three geometries 3 PPC (plants/clump), 4 PPC, and ESP (equally spaced plants). All treatments were replicated three times in rows 75 cm apart. Precipitation during the growing season was 209 mm. Harvest index, 200-seed mass, and number of harvested ears were significantly greater and leaf area index (LAI) is lower in clumps compared to ESP. The treatment with 3 PPC spaced 1.33 m apart (40,000 pl/ha) had the greatest harvest index of 0.46 due to more productive ears. The number of unproductive ears in ESP from total number of ears produced was 25,100/ha, which was 87% of the total ears (54,100/ha). The leaf area index was significantly greater (17%) in ESP compared to 3 PPC. Grain yield and aboveground biomass were not significant. Lower populations had greater harvest index and seed mass values than did greater populations. Thus, although grain yields were not greater in clumps in 2008, increased seed mass, harvest index, number of harvested ears, and decreased LAI values suggest clump geometry may be a good strategy for conserving water under dryland conditions.

Poster 3. Mapping of QTL associated with leaf cuticular waxes in wheat (Triticum aestivum L.).

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Leaf cuticular waxes in plants provide a protective barrier to biotic and abiotic stresses. The objective of this study was to identify quantitative trait loci (QTL) associated with leaf waxes in wheat. We utilized a 120 recombinant inbred line (RIL) population derived from the cross of 'Halberd' and 'Karl 92' for mapping leaf cuticular waxes. Plants were grown in the greenhouse at 25°C/20°C day/night temperature regime. Leaf wax content was estimated at 10 days after pollination (DAP) from the flag leaf. The flag leaf temperature and leaf width was measured in the greenhouse. The RIL population also was evaluated for yield and yield components. A variation in leaf wax content was observed between the parent lines with 'Halberd' having higher wax content. We have 190 SSR markers polymorphic between the parent lines. Preliminary QTL analysis identified QTL associated with leaf wax on chromosomes 3B, 4A, and 5D. A nonwaxy locus was identified in chromosome 1B that corresponds to a previously identified spike non-glaucousness locus.

Poster 4. Water availability and winter wheat yield in eastern Colorado.

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The yield of winter wheat in eastern Colorado is constrained by water availability during the growing season. Water shortage may occur at anytime throughout the growing season but may have the greatest impact at three growth stages. In the autumn, lack of water may decrease seed germination and plant stand. In early spring, the wheat plant is coming out of cold dry winters and may suffer from drought until spring rains come. Later in the season, especially around flowering and during grain filling, temperatures increase and precipitation may not meet the ET requirements. In order to determine when water shortage has a more dramatic impact on winter wheat yield, 24 winter wheat genotypes (experimental lines and cultivars) adapted to the High Plains were planted under five water treatments, ranging from full irrigation to dryland. Three intermediate treatments targeted two main wheat developmental stages, jointing and anthesis. The ANOVA of yield and yield components showed that there were strong genotype and water-treatment effects and 'genotype x water treatment' interaction for yield. Correlations across water treatments between yield and yield components showed that yield was mostly related to the number of grains per unit area, which in turn was related to the number of spikes per unit area and the number of grains per spike. The 'genotype x water treatment' interaction was analyzed in terms of differences of yield formation of the different cultivars grown in different water treatments. From our results, we can conclude that the number and size of spikes (in terms of number of spikelets per spike) are important traits for winter wheat yield in eastern Colorado across a range of water availabilities.

Poster 5. Introgression and characterization of stem rust resistance from Aegilops tauschii Coss.

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An evaluation of a diverse set of 454 accessions of *Ae. tauschii* with six races of the stem rust pathogen *Puccinia graminis* f. sp. *tritici* Pers. identified 198 lines with seedling resistance. Of the accessions with resistance, 14 with resistance to nearly all races were targeted for introgression of stem rust resistance genes into hexaploid wheat, *Triticum aestivum* L., by direct crossing of the *Ae. tauschii* accession (2n=2x=14) with hexaploid wheat (2n=6x=42). A hard white winter wheat, KS05HW14, previously identified as having high crossability, and the spring wheat WL711 were used as females with the *Ae. tauschii* accessions as males. Embryos were rescued between 14 and 18 days-after-pollination. Embryo maturity was highly variable depending on the *Ae. tauschii* genotype. Upon the production of shoots, plantlets were transferred to a modified MSE medium until the full development of roots and then placed in vernalization. Currently, dihaploid F_1 plants (ABDD) have been generated for nine *Ae. tauschii* genotypes. One *Ae. tauschii* genotype produced few embryos for rescue but was present in a synthetic from which F_1 seed was produced with the KS05HW14 parent as a female. The sterile F_1 plants will be backcrossed as females to the hexaploid parent to restore fertility. A bulked-segregant analysis of the BC_1F_2 or BC_2F_1 genotypes with SSR markers will identify loci linked to stem rust resistance genes and determine the chromosome location of the genes for subsequent linkage analysis.

In a separate evaluation of stem rust resistance in *Ae. tauschii*, accessions CDL4424 and CDL4366 were identified as having seedling resistance to stem rust. These accessions were crossed directly to KS05HW14 and WL711. A bulked-segregant analysis of a BC_2F_1 population from CDL4424 revealed two SSR loci polymorphic between resistant and susceptible bulks, *Xwmc222* and *Xbarc119*, on chromosome 1DS, which is the same chromosome location as the previously described genes from *Ae. tauschii*, *Sr33* and *Sr45*. Allelism test crosses will be made between CDL4424 and the diploid accessions carrying *Sr33* (TA1600) and *Sr45* (TA1599).

Poster 6. Study of low-molecular-weight subunits of glutenin proteins in durum wheat.

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Glutenins and gliadins are two important endosperm proteins in wheat seed. Gluteins are composed of low-molecular-weight (LMW-GS) and high-molecular-weight (HMW-GS) subunits. The LMW-GS are encoded by the *Glu-A3*, *Glu-B3*, and *Glu-D3* loci on the group-1 chromosomes. These subunits are important in durum wheat mostly because of its role in pasta quality. In this study, ten different lines of Iranian 'Omid-Baksh' were studied by SDS–PAGE in order to evaluation of allelic variety of the LMW-GS. Pasta-making quality and some other important parameters in pasta making (protein content, SDS precipitation height, Zeleni number, and seed hardness) also were analyzed in these lines. The results showed a similarity in the protein profiles and allelic distribution among the ten lines. Due to the presence of the LMW-2 subunit (according to Payne et al. 1984 and Pogne et al. 1988), these lines are categorized as high-quality wheats. These lines also are good candidates for pasta making because of *Glu-A3* (allele 6), *Glu-B3* (alleles 2+4+15+19), and *Glu-B2* (allele 12) (Neito-Taladriz 1997). These lines did not show broad differences in pasta quality properties. According to our results, line number 10 is better than the others for having more appropriate parameters for pasta making and also the appropriate distribution of the *Glu-3* allele.

Poster 7. The comparison between morphological and pasta-quality traits among some durum wheat lines in Iran.

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In order to assess pasta quality and determine the effects of morphological traits on quality, ten lines of Iranian durum wheat were examined. Traits related to pasta quality (such as 1,000-kernel weight, wet gluten percent, and Zeleny sedimentation volume) and morphological traits of the lines including growing (such as plant length, length of spike, length of flag leaf, and, number of leaves) and generative traits (such as number of spikelets and number of fertile and infertile florets) were analyzed for two different years.

Data collected through sampling were analyzed statistically based on a randomized complete block design. The variance analysis (ANOVA) of the quantitative traits showed that the difference between some traits, such as length of flag leaf, number of leaves, number of nodes, and number of fertile and infertile florets, and internode distance and number of spikelets per spike, were significant ($P = 0.05$). No significant differences were observed among the other traits. ANOVA of the morphological traits showed that all morphological traits among the lines were significant ($P = 0.05$). Means of test traits were checked against the means of control group using LSD method. Mean comparison indicated that some lines had significant increases, others had significant decreases, and others were indifferent according to the control group. Altogether, some morphological traits, such as length of spike, the number of fertile florets, and the number of spikelets showed a positive correlation to some quality traits such as 1,000-kernel weight and wet-gluten percent, especially among lines 1 and 8.

Poster 8. Statistical analysis on pasta quality traits among durum wheat lines in Iran.

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Pasta quality is related to some traits that can be measured and quantified. Of the nearly 20 traits are related to pasta, we analyzed nine among ten durum wheat lines. The traits were moisture content, protein percent, hardness index, 1,000-kernel weight, SDS sedimentation volume, wet gluten, dry gluten, Zeleny sedimentation volume, and disc pressure test according to international criteria. Among the ten durum wheat lines under study, moisture content was highest in lines 1 and 4; protein percent in line 8, hardness index in lines 6 and 7, 1,000-kernel weight in line 1, SDS sedimentation volume in lines 1 and 5, wet gluten in line 8, Zeleny sedimentation volume in line 8, and the disc pressure test in lines 5 and 6. Lines 1 and 8, which have the highest value for three traits, are the best cultivated lines for pasta making.

ITEMS FROM ARGENTINA

CÓRDOBA NATIONAL UNIVERSITY
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Harvest index. The alter ego of grain yield under terminal drought stress.

Matias Lamarca, Jeremias Brusa, Agustina Pividori, and Ricardo Maich.

In a plant-breeding program, gene effects, genotypic variability, and the selection environment are factors that influence the heritability of the improved character. Concerning the biological determinants and as selection and gene recombination cycles elapse, the allelic variability tends to decrease. In the selection environment, low heritability estimates usually are obtained under stress conditions, consequently the response to selection is less than that obtained in nonstress conditions. However, a particular environment can be a stress for one attribute or character and not stress another. Our objective was to measure the response to divergent selection for grain yield in wheat and triticale grown under terminal drought. The study was conducted at the Experimental Farm of the College of Agriculture (Córdoba National University) Córdoba, Argentina. Crops were grown under rain-fed conditions, stored soil moisture, and direct seeding. The experimental material consisted of S_0 progenies of wheat and triticale derived from two recurrent selection programs.

During 2008, the C_9S_0 (wheat) and C_6S_0 (triticale) progenies were evaluated and divergently selected with respect to grain yield/plot according to a selection intensity of 1.554. The experimental units were one-row plots without replications, 1.3 m in length, spaced at 0.20 m, and with a seeding rate of 100 kernels/m^2. Systematic controls were used in order to adjust for environmental heterogeneity. In addition to grain yield, aerial biomass, harvest index, and spike number/plot also were measured. During 2009, the 20 S_1-derived families for each species (ten per each high and low group) were evaluated using 5-m, one-row plots spaced 0.20 m apart at seeding rate of 250 kernels/m^2. Completed randomized designs with two replications were used. The S_1-derived family traits measured on a plot basis were grain and biological yield (g/m^2), spike number (n/m^2), 1,000-kernel weight (g), harvest index (%), and grain number (n/m^2). An S_1 evaluation of available soil-water content to a depth of 2.0 m was measured gravimetrically. Soil samples were taken at seeding (DC 0.0), flag leaf sheath extending (DC 4.1), physiological maturity (DC 9.5), and harvest maturity. The amount of rainfall during the crop cycle was 52 mm (26 mm of effective precipitation). Correlations were computed between grain yield and the other agronomic traits measured during the S_0 and S_1 evaluations. The DGC test was used for comparing the mean differences between the high and low groups of the S_1-derived families.

Significant and positive associations in the wheat germ plasm were found between grain yield and harvest index (S_0 r = 0.49; S_1 r = 0.48), grain yield and aerial biomass (S_0 r = 0.97; S_1 r = 0.74), grain yield and spike number (S_0 r = 0.90; S_1 r = 0.65), and aerial biomass and spike number (S_0 r = 0.92; S_1 r = 0.73). For triticale, the analyzed variables also showed positive and significant relationships between grain yield and harvest index (S_0 r = 0.55; S_1 r = 0.68), grain yield and aerial biomass (S_0 r = 0.91; S_1 r = 0.89), grain yield and spike number (S_0 r = 0.92; S_1 r = 0.53), and aerial biomass and spike number (S_0 r = 0.83; S_1 r = 0.61). Significant differences between the high and low group mean values were observed for harvest index in both species. The amount of available soil water varied from 268.4 mm (81% of field capacity or FC) at DC 0.0; 90.0 mm (27% of FC) in wheat, and 59.0 mm (17.8% of FC) in triticale at DC 4.1; 7.1 mm (2.1% of FC) in wheat and 12.2 mm (3.8% of FC) in triticale at DC 9.5; and 3.6 mm (1% of FC) in wheat and 0.0 mm (0% of FC) in triticale at harvest maturity. Both species extracted soil water below the -1,500 kPa (wilting point or WP), with evapotranspired water amounts of 21.7 mm and 17.6 mm in wheat and triticale, respectively. As physiologically expected, a nonsignificant, direct response to selection for grain yield was balanced by a significant response for harvest index, one its physiological components. In both SR programs, harvest index was the only grain yield component that showed significant response and heritability estimates along the last four cycles in wheat (C_6 to C_9) and two cycles in triticale (C_5 and C_6). Independent of the cycles of SR elapsed, harvest index showed enough genetic variability for further genetic improvement. The 78% of available water depletion at the beginning of the critical period and the terminal drought stress in both cereals did not affect with the same intensity the phenotypic expression of the analyzed traits. In

summary, an taking into account previous results, harvest index shows us an alternative way to interpret grain yield improvement under marginal conditions of cultivation.

Straw production and water use under direct seeding.

Ricardo Maich, Facundo Ripoll, Silvana Garcia, María Belén Tell, and Verónica Herrera.

The monsoon regime of the central region of Argentina is the main constraint for the wheat production in this area, where winter crops grow and develop with scarce amount of precipitation and depend on stored soil moisture at sowing. Effective use of water implies maximum soil moisture for transpiration, which also involves reduced nonstomatal transpiration and minimal water loss by soil evaporation. The presence of straw mulch has a positive impact on suppressing evaporation and, consequently, greater carbon sequestering is a priority. The objectives of this study were to evaluate the influence of seeding date on straw production and quantify the corresponding water use. Three commercial cultivars and three experimental lines were grown under rainfed and direct seeding conditions at Córdoba (Argentina) in 2009. The late-flowering genotypes were sown on 1 May, intermediate on 12 May, and early on 21 May. The different sowing dates were used in order to diminish the risk of frost damage after spike emergence. Completely randomized blocks designs with three replications were used. Plot size was '1.0 m x 5.0 m' with a row spacing of 0.2 m. A seeding rate of 250 seed/m^2 was used. A gravimetrical method was used in order to quantify (0–200 cm) the available soil water content. At sowing, the available stored soil moisture was 233 mm (late genotypes), 239 mm (intermediate genotypes) and 223 mm (early genotypes). Grain and straw yield, harvest index, water-use (WU), water-use efficiency for grain (WUEg) and straw (WUEs) production, intercepted radiation in flowering (Ei), and percentage soil water at harvest for every 0.2-m depth interval were determined. Data was analyzed with the INFOSTAT statistical package.

The late-flowering genotypes showed the highest mean value for straw production (7,189.7 kg DM/ha) with significant differences for the intermediate and early genotypes (5,854.7 kg DM/ha and 5,654.3 kg DM/ha, respectively). Higher straw production was associated to a significant and increased WU (283.6 mm in the late genotypes versus 258.6 mm in the early genotypes) and WUEs (25.35 kg DM/mm in the late genotypes versus 20.85 kg DM/mm and 21.87 kg DM/mm for the intermediate and early genotypes, respectively). For grain yield, nonsignificant differences were noted between materials with different biological cycles. The straw of the late, experimental genotypes had a higher C:N ratio and lignin percentage than those for the corresponding intermediate and early genotypes. The percentage of soil moisture content at harvest differed significantly between commercial (9.2%) and experimental (9.41%) genotypes and late (8.98%), intermediate (9.32%), and early (9.61%) flowering materials. Significant statistical differences also were observed between the 0–40 cm (8.70–8.83%), 40–180 cm (9.18–9.63%), and 180–200 cm (9.92%) soil profiles. In all cases, the wheat crop used water below -1,500 kPa of suction (10.3–13.5%). For intercepted radiation at flowering, the Ei of the early genotypes (83.95%) was significantly higher than those measured for the late (75.33%) and intermediate (68.30%) genotypes.

In conclusion, the use of late-flowering genotypes sequestered more carbon in terms of straw production, captured more water, and used it most efficiently. In addition, under rainfed conditions, with crops grown on stored soil moisture and the use of no-till practices such as direct seeding, water uptake by wheat surpassed the physical estimate of the permanent wilting point.

ITEMS FROM BRAZIL

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

Wheat in Brazil – the 2009 crop year.

Eduardo Caierão and Flávio Martins Santana.

Brazilian wheat production was about 5 x 10^6 tons (Conab 2009) in the 2009 crop year, which is enough to supply 50% of the domestic demand (Table 1). The deficit in production makes Brazil the largest wheat importer. The south region, comprised of the states of Rio Grande do Sul, Santa Catarina, and Paraná, accounts for 90% of the national production. Nonetheless, due to the characteristics of the cultivation system utilized, average grain yield is not the highest in the country.

Table 1. Cultivated area, total production and grain yield of wheat in Brazil in 2009 (Source: CONAB, 2010).

Region	Area (ha x 1,000)	Production (t x 1,000)	Grain yield (kg/ha)
North	—	—	—
Northeast	—	—	—
Central-west	67.5	171.8	2,546.0
Southeast	84.1	225.0	2,675.0
South	2,276,4	4,629.4	2,034.0
Brazil	2,428.0	5,026.0	2,070.0

The wheat area planted in 2009 was similar to that in 2008. However, the total production and average grain yield/hectare achieved in 2009 were about 16.7% and 16.8% smaller than those of 2008, respectively. In the state of Rio Grande do Sul (south region), high rainfall conditions observed in October and November (harvest months) affected the grain quality for milling industries. In the state of Paraná, the high incidence of wheat blast and Fusarium head blight in the north of the state reduced dramatically the average grain yield in some fields.

In 2010, there is no evidence that the Brazilian wheat area will increase or remain the same.

Reference.

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

ITEMS FROM THE PEOPLES REPUBLIC OF CHINA

UNIVERSITY OF ELECTRONIC SCEINCE AND TECHNOLOGY OF CHINA
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The genomic evolution of the Thinopyrum and Dasypyrum: Evidence from α-gliadin sequences.

G.R. Li, C. Liu, T. Zhang, J. Zhou, and Z. Yang.

The genus *Thinopyrum* represents a vast reservoir of useful agronomic traits for wheat and forage improvement. Wide hybridization and chromosomal engineering enabled the incorporation of alien genetic material from *Thinopyrum* into common wheat in the last four decades (Chen et al. 2005; Li and Wang 2009). Chen et al. (1998) analyzed *Thinopyrum*

species in detail with genomic *in situ* hybridization using an S^t-genomic DNA probe, which can detect detail in the physical organization of the DNA sequences of *Thinopyrum* chromosomes. The basic genomes of the *Thinopyrum* species are J, J^s, and S^t, where J is closely related to *Th. bessarabicum* and J^s is a modified version of the J genome with the signal of the S^t genome (Wang et al. 1994). Kishii et al. (2005), using the *Daypyrum* genomic DNA to hybridize with *Th. intermedium*, considered that the genomic formula of *Th. intermedium* can be tentatively redesignated as $S^tS^tJ^sJ^s$(V-J-R)^s(V-J-R)^s. Recently, Liu et al. (2009) distinguished the J^s genome from *Th. intermedium* using FISH of the Sabrina-like LTR sequences. The hybridization pattern of the J^s genome was similar to that of the V genome of *Dasypyrum*, implying that the constitution of J^s genome in *Th. intermedium* may have the V genome. In this study, we investigated a number of α-gliadin sequences, which represent a evolutionariyy fast gene family of seed-storage proteins, in order to provide evidence to the relationship between *Thinopyrum*, in particular *Th. intermedium* with *Dasypyrum* species.

Materials and Methods. The *Dasypyrum villosum*, *Th. intermedium*, *Lophopyrum elongatum*, *Th. bessarabicum*, and *Pseduoroengeria spicata* lines were kindly provided by Dr. Harold Bockelman, National Plant Germplasm System, USDA–ARS, Aberdeen, Idaho, USA. Diploid *D. breviaristatum* was obtained from Dr. Shoji Ohta, Department of Bioscience, Fukui Prefectural University, Matsuoka, Yoshida, Fukui, Japan. The PCR amplification, cloning, and sequence analysis of α-gliadin genes were according to Li et al. (2009).

Results and Discussion. A Total of 137 unique clones were sequenced from the six species (Table 1). The nucleotide comparison of these entire sequences showed a high degree of homology with other α-gliadin sequences in wheat. On the basis of the deduced amino acid sequence of the α- gliadin genes, 58 sequences included complete ORFs, whereas 79 sequences were pseudogenes, because they contained a typical in-frame premature stop codon. Among the species, different frequencies of pseudogenes were observed, including 19 of 21 *Th. bessarabicum* α-gliadin sequences and 6 of 16 *D. villosum* α-gliadin sequences. The general structure of the α-gliadin protein consists of a short N-terminal signal peptide (S) followed by a repetitive domain (R) and a longer nonrepetitive domain (NR1 and NR2), separated by two polyglutamine repeats (Q1 and Q2). In the first glutamine repeat (Q1), the *L. elongatum* α-gliadin sequences contained 6–24 (average 18) glutamine residues. In the second glutamine repeat (Q2) region, *D. villosum* had 12–24 (average 18.6)

Table 1. The α-gliadin sequences from six species. Q1 and Q2 are polyglutamine repeats.

Species	Genomic formula	Putative full-ORF	Pseudogenes	Length of ORF	Length of Q1	Length of Q2	Glia-α
D. breviaristatum	V^b	13	14	810–954	8 (3–14)	6 (2–11)	3
D. villosum	V	10	6	846–897	14 (8–10)	18 (12–24)	10
L. elongatum	E	15	10	855–884	18 (6–24)	8 (7–9)	11
Ps. spicata	S^t	10	18	812–1,073	6 (3–8)	13 (6–28)	5
Th. intermedium	JJ^sS^t	8	12	831–861	5 (3–8)	5 (3–10)	6
Th. bessarabicum	J	2	19	855–872	8 (7–9)	5 (3–7)	2

The reported T cell stimulatory epitopes Glia-α (QGSFQPSQQ), Glia-α-2 (PQPQLYPQ), Glia-α-9 (PFPQPQLPY), and Glia-α-20 (FRPQQPYPQ) have their own conserved position in the wheat α-gliadin protein (van Herpen et al. 2006). All the α-gliadin sequences from six species lacked Glia-α-2, Glia-α-9, and Glia-α-20, which were all found in the first repetitive (R) domain. The Glia-α in the second nonrepetitive (NR2) domain was found in all species with different frequency. Only 3 of 13 full-ORF of *D. breviaristatum* sequences contained epitope Glia-α, whereas all 10 *D. villosum* ORFs possessed epitope Glia-α (Table 1).

Sequence comparisons were performed among the α-gliadin genes to understand the relatedness and the divergent time by construction of phylogenetic trees. In addition to the α-gliadin nucleotide sequence, two γ-gliadin sequences from wheat were used as an outgroup. The phylogenetic tree indicated that the sequences from *D. breviaristatum* were clearly separated from other groups, indicating the earlt divergence of the *D. breviaristatum* α-gliadins (Fig. 1, p. 43). Genes from *L. elongatum* and *Ps. spicata* were clustered into two different groups, suggesting that the α-gliadin genes in the two species exhibit higher diversity than those in *D. villosum* and *Th. intermedium*. The sequences from *D. villosum*, *L. elongatum*, *Th. bessarabicum*, and *Ps. spicata* were clustered in one subgroup. These results suggested that the J, S^t, E, and V genomes are closely related to the *Th. intermedum* genome. Because only a part of the *L. elongatum* and *Ps. spicata* α-gliadin sequences were closely clustered to *Th. intermedium*, *Th. intermedium* may have lost diversity after polyploidization.

Based on the calculation of the evolutionary rates of the α-gliadin sequences, *D. breviaristatum* possibly evolved 15–20 MYA, the separation of genomes J, S^t, E, and V occurred at 8–13 MYA, and the *Th. intermedum* genome generated 7–8 MYA.

We speculate that the *Dasypyrum* species are relatively close to *Thinopyrum* and its putative ancestry species *L. elongatum*, *Th. bessarabicum*, and *Ps. spicata*. *Dasypyrum villosum*, not *D. breviaristatum*, most likely joint the *Th. intermedium* evolution. The relationship between *Dasypyrum* and *Thinopyrum* also is supported by the phylogenetic studies from several chloroplast and nuclear single-copy genes. We also expect to develop the molecular markers to help trace the transfer of both *Dasypyrum* and *Thinopyrum* chromatin to wheat (Liu et al. 2009).

Acknowledgement. We are thankful to the National Natural Science Foundation of China (No. 30671288, 30871518), and Young Scholars Foundation from the Science and Technology Committee of Sichuan, China (2008-31-371), for financial support.

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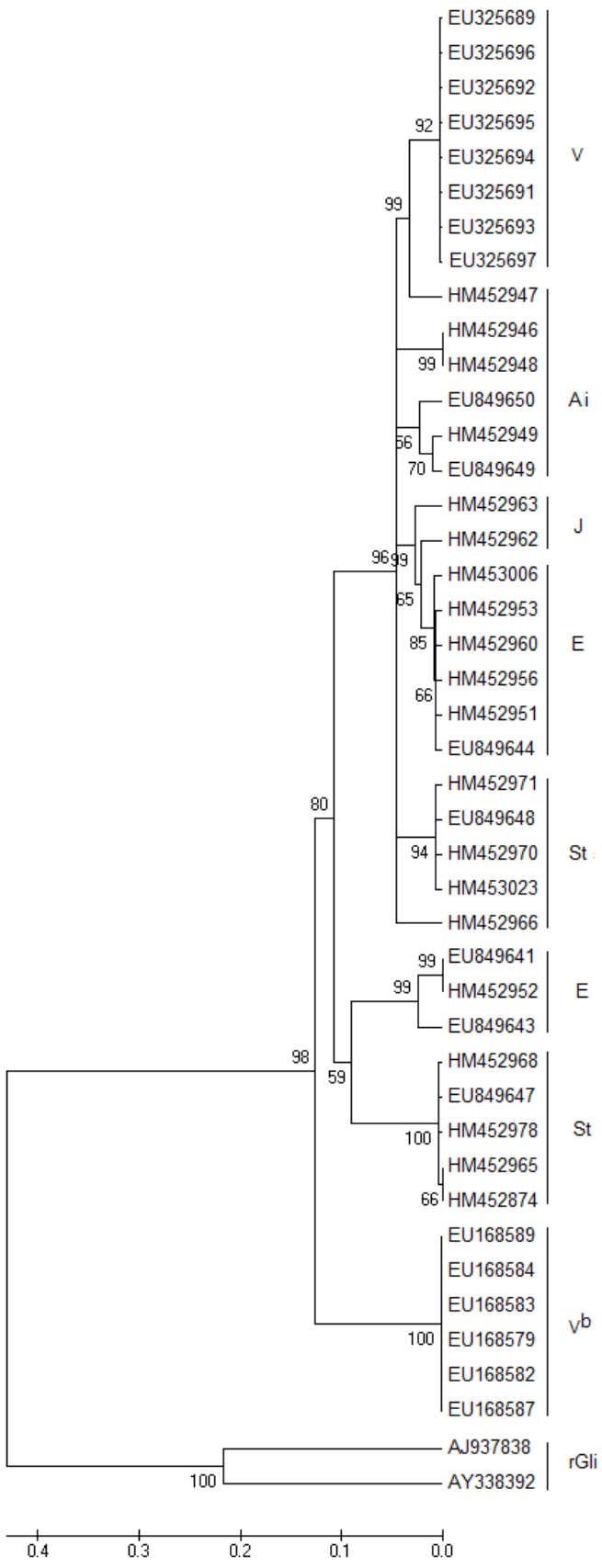

Fig. 1. A phylogenetic tree was developed with NJ and MP analyses using the MEGA4 with 1,000 iterations.

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ITEMS FROM CROATIA

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A study of the technological traits of high-quality, Bc wheat cultivars in different environments.

The technological traits of the Bc winter cultivars Mihelca and Zdenka, which are widely grown in Croatia, Slovenia, and Bosnia and Herzegovina, as well as the newly registered cultivars Bc Mira and Bc Renata, were analyzed. Samples were taken partly from small-scale trials at locations in Botinec, Lovas, Rugvica, and Osijek (Table 1) and partly from wheat production fields throughout Croatia (Table 2, p. 45). Over a three-year period, each sample was tested for dough rheological traits using a farinograph and an extensograph. Preliminary results showed a high and stable quality for cultivars Mihelca, Zdenka, Bc Mira, and Bc Renata and during the following years it was confirmed in wide produc-

Table 1. Test results of bread-making quality for BC Institute wheat cultivars from small-scale trials at locations in Botinec, Lovas, Rugvica, and Osijek, Croatia.

Location	Farinogram							Extensogram			
	Water absorance (%)	Dough develop time (min)	Stability (min)	Resist-ance (min)	Degree of softening (FJ)	Quality number	Quality group	Energy (cm^2)	Extensi-bility (mm)	Resist ance (EJ)	R/E
Zdenka (2006–07)											
Botinec	66.5	8.5	6.5	15.0	0	100.0	A1	135.3	190	313	1.65
Rugvica	65.8	2.0	1.7	3.7	24	77.7	A2	141.8	176	388	2.20
Lovas	65.9	7.0	2.7	9.7	16	88.0	A1	120.4	202	270	1.34
Osijek	65.1	2.1	1.9	4.0	65	61.5	B1	133.7	178	370	2.08
Zdenka (2007–08)											
Botinec	66.2	2.3	1.3	3.6	65	62.0	B1	130.9	178	360	2.02
Mihelca (2006–07)											
Botinec	57.9	6.8	8.2	15.0	0	100.0	A1	130.1	178	350	1.97
Rugvica	58.6	10.3	3.0	13.3	3	92.1	A1	125,.7	185	308	1.66
Lovas	57.4	7.2	7.5	14.7	3	94.5	A1	106.5	190	260	1.37
Osijek	56.0	1.8	0.6	2.4	65	56.2	B1	136.3	180	350	1.94
Mihelca (2007–08)											
Botinec	57.2	1.6	0.7	2.3	70	57.7	B1	100.5	172	290	1.69

Table 2. Test results of bread-making quality for BC Institute wheat cultivars from wheat production fields throughout Croatia.

Location/ Company	Farinogram							Extensogram			
	Water absorance (%)	Dough develop time (min)	Stability (min)	Resist-ance (min)	Degree of softening (FJ)	Quality number	Quality group	Energy (cm^2)	Extensi-bility (mm)	Resist ance (EJ)	R/E
Zdenka (2007–08)											
Žito	62.6	3.0	6.5	9.5	30	88.0	A1	80.0	190	215	1.10
Novi Agrar	67.9	2.5	1.0	3.5	95	56.4	B1	84.6	178	245	1.38
Zdenka (2008–09)											
Županja	64.6	2.2	0.9	3.1	80	55.6	B1	126.2	173	360	2.08
Bc Mira (2007–08)											
Agrome-đimurje	61.9	9.5	5.5	15.0	0	100.0	A1	91.0	192	235	1.2
Bc Institut	61.2	3.5	4.0	7.5	51	74.6	A2	78.0	170	255	1.5
Bc Mira (2008–09)											
Županja	63.0	2.0	2.8	4.8	90	58.7	B1	53.8	178	160	0.9
Bc Renata (2007–08)											
Lovas	61.5	3.5	3.0	6.5	50	68.8	B1	95.0	214	220	1.03
Bc Renata (2008–09)											
Županja	62.2	2.7	0.9	3.6	75	61.0	B1	96.4	203	230	1.13
Dora (2008–09)											
Županja	64.7	2.2	0.5	2.7	80	53.2	B1	46.1	143	190	1.33
Marina (2008–09)											
Županja	59.4	2.0	0.7	2.7	85	56.0	B1	72.0	170	225	1.32

tion. We concluded from these analyses that the tested cultivars possess very good bread-making quality. Quality is our advantage, i.e., Zdenka, Mihelca, Bc Mira, Bc Renata, Dora and Marina are cultivars of very good bread-making quality. These cultivars possess divergent genetic parameters for the most important quality components. These results confirm that the Bc Institute possesses high-quality, winter wheat cultivars that can fully meet the requirements of the modern milling and baking industries.

The yield potential of Bc winter wheat cultivars.

The Bc Institute conducted in large-scale trials at Županja and Lovas of winter wheat cultivars during the 2008–09 growing season (Table 3, p. 46). Large-scale trials also were conducted by companies at Belje, Orahovica, and Kutjevo (Table 4, p. 46) in which other cultivar present in the Croatian market also were included. Apart from the yield results in these large-scale trials, yield also is monitored from trials conducted at family farms (Fig., 1; Table 5, p. 46). This investigation tested the yield of the Bc cultivars in several trials.

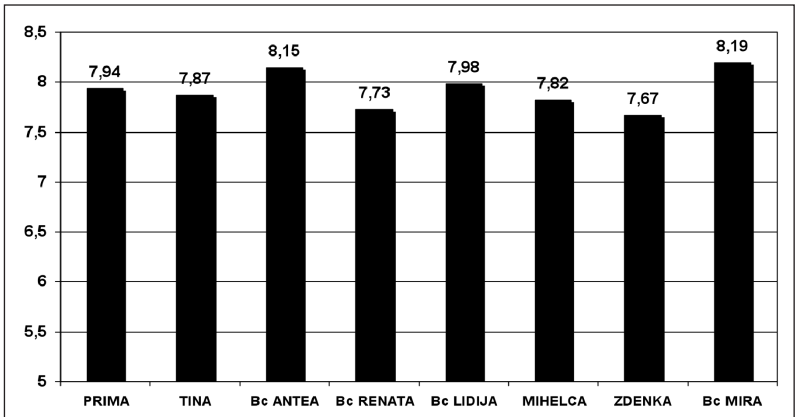

Fig 1. Yield results (t/ha) of Bc winter wheat cultivars in large-scale trials, 2009.

Table 3. Yield results (t/ha) of 14 Bc winter wheat cultivars in large-scale trials at locations in Županja and Lovas, Croatia, in 2009.

Cultivar	Županja	Lovas	Average
Prime	8.53	7.60	8.06
Mihelca	7.69	7.80	7.74
Sana	8.40	8.32	8.36
Marija	9.13	8.37	8.75
Zdenka	8.09	8.13	8.11
Tina	8.58	8.25	8.41
Adriana	7.33	8.26	7.79
Bc Antea	8.74	8.22	8.48
Bc Elvira	7.67	6.73	7.20
Bc Renata	8.44	8.33	8.38
Bc Mira	8.93	9.47	9.20
Bc Lidija	8.82	7.54	8.18
Dora	8,14	9.22	8.68
Marina	8.48	9.17	8.82
Average	8.36	8.24	

Table 4. Yield results (t/ha) of Bc winter wheat cultivars in large-scale trials at locations Belje, Kutjevo and Orahovica, Croatia, in 2009.

Cultivar	Belje	Kutjevo	Orahovica
Prima	7.71	7.72	8.16
Tina	7.98	7.47	7.05
Bc Antea	8.44	7.92	7.43
Bc Renata	7.62	7.11	7.15
Bc Lidija	8.48	7.02	8.04
Mihelca	8.22	7.64	7.74
Zdenka	8.14	7.15	6.86
Bc Mira	7.07	7.64	7.85
Average	7.72	7.25	7.92
Number of cultivars in trial	51	40	20

The highest yielding ability was expressed by cultivars Bc Mira (8.19 t/ha), Bc Antea (8.15 t/ha), Bc Lidija (7.98 t/ha), and Prima (7.94 t/ha) (Fig. 1, p. 45). The average yield per location was considerably higher in trials conducted by the Bc Institute at locations Županja and Lovas in comparison with other locations. In the trial at Lovas, Bc Mira produced 9.47 t/ha.

Table 5. Yield results (t/ha) of Bc winter wheat cultivars in trials conducted on family farms in east Croatia, 2009.

Cultivar	Prakaturović Privlaka	Đurić Đeletovci	Cerin Korođ	Čosić Vrbanja	Average
Prima	7.76	7.01	8.93	7.39	7.77
Tina	7.35	6.14	8.20	7.82	7.38
Bc Antea	7.04	6.91	8.54	6.68	7.29

The result of breeding winter wheat in the Bc Institute is six new cultivars: Bc Mira, Bc Renata, Dora, Marina, Bc Lidija, and Bc Lira. These cultivars represent genetically different material and are a breakthrough for some important agronomical traits. These cultivars guarantee high yielding ability, production stability and excellent quality.

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Tomasović S, Mlinar R, Ikić I, and Ivanušić I. 2010. Yield potential and quality of Bc winter wheat varieties. *In:* Proc 45th Croatian and 5th Internat Symp on Agriculture, Opatija, Croatia, 15-19 February. Book of Abstracts, p. 111-112, Plenary Lectures (in Croatian with English Summary).

ITEMS FROM GERMANY

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Association mapping of agronomic traits exploiting historical field data in winter wheat.

Association-based trait mapping is an innovative methodology in detecting genes and is based on linkage disequilibrium in a collection of unrelated plant material. Studies especially in wheat are rare. We exploited historical field data of a winter wheat collection, using a genome-wide assay with diversity array technology (DArT) markers. In total, 520 polymorphic markers were genetically mapped. Two subpopulations were identified by examining the population structure. The collection was field trailed and phenotyped for agronomic traits in up to eight different years. The associations and the extent of LD in the collection and the two subgroups were calculated with the Tassel 2.1 program using two different models for calculating the associations. The general linear model (GLM) corrects for population structure incorporating the Q-Matrix for the two subgroups while a newer approach is additionally including the Kinship-Matrix in a mixed linear model (MLM), which should further reduce the number of false-positive associations. These two approaches are compared for the trait flowering time. A number of 99 significant marker-trait associations was detected with the GLM, whereas with the MLM, only 14 associations were significant. One association was only significant with the MLM, whereas the others were detected with the GLM as well. The 13 coincident associations are located on chromosomes 1B, 1D, 2B, 2D, 4B, 5B, 5D, 6A, 6B, and 7A.

A genetic linkage map of durum wheat.

Based on a cross between two durum wheat cultivars, 'Omrabi5/Belikh2', a genetic linkage map is being constructed using segregation data from a set of 114 recombinant inbred lines. The parents are known to posses tolerance to several traits associated with drought, heat, and salt stress. Additionally, they carry resistance to main rust races (yellow rust and leaf rust) and *Septoria tritici* but also have good processing quality and yellow pigmentation. The parents were screened with 1,072 GWM, BARC, and WMC SSR markers. A total of 275 polymorphic markers consisting of 161 GWM, 64 BARC, and 50 WMC markers, amplifying 292 loci, were utilized for map construction. Phenotyping for drought- and salt-adaptive traits are being carried out by ICARDA/CIMMYT and will be used to identify and characterize the genomic regions associated with those traits. The linkage map also will prove to be useful for marker-assisted improvement and/or developing tolerant cultivars for drought, heat, and salt stress.

Identification of QTL determining post-anthesis drought tolerance and other agronomic traits in bread wheat.

QTL mapping analysis was applied on a new mapping population (HTRI 11712/HTRI 105), which was developed at IPK, Gatersleben, and contained 133 $F_{2:3}$ families. The genetic linkage map contained 285 SSR loci forming 19 linkage groups. Chromosomes 6D and 4D failed to have proper genetic maps. Population phenotyping on both control and for post-anthesis drought stress was conducted four times, including two greenhouse experiments in 2004 and 2007 and two field experiments in 2004 and 2005. Drought stress was imposed in three experiments using chemical desiccation by spraying with potassium iodide and in one greenhouse experiment by water stress. In both methods, stress was applied from two weeks after anthesis for each $F_{2:3}$ familiy separately. The linear mixed model analysis of variance on

the control and stress condition showed highly significant differences among the $F_{2:3}$ families for the all traits, such as 1,000-kernel weight, seed size, days-to-flowering, number of seeds/spike, weight of seeds/spike, spike length, and plant height, and justified the QTL mapping analysis.

Composite interval mapping analysis revealed 64 and 51 QTL in control and stress condition, respectively. Thirty-seven QTL were repeated either in different experiments or under different stress conditions. The QTL are distributed over all linkage groups except 6A, 6B, and 3D. The number of QTL on the linkage groups were not equal and showed a range from one on chromosomes 1D and 3B to 15 on chromosome 7D. For 1,000-kernel weight, chromosomes 1B and 4B had QTL under control condition, whereas chromosomes 7D and 7A carry the QTL under stress. Both parents contributed increasing alleles for all the traits including thousand-grain weight under stress condition.

Mapping of QTL for terminal heat tolerance in bread wheat.

Post-anthesis high temperature (>30°C) at the time of grain filling is a major cause of yield reduction in wheat in many environments of the world. Hence, finding QTL for heat tolerance is an important objective for future food security.

A QTL analysis of the recombinant inbred population 'NW1014 (tolerant)/HUW468 (susceptible)', segregating for heat tolerance in hexaploid wheat, was completed by applying composite interval mapping. The QTL were detected on chromosomes 2B, 7B, and 7D using three different parameters for heat tolerance: heat susceptibility index of 1,000-kernel weight (HSITGW), heat susceptibility index of grain-filling duration (HSIGFD), and canopy temperature depression (CTD). The QTL for HSITGW were detected on chromosomes 2BL, 7BL, and 7DS in all three environments. The QTL for HSIGFD were detected on the same genomic region of the chromosome 2BL where the QTL for HSITGW was identified. Other co-localized QTL controlling HSITGW and CTD were detected on the long arm of chromosome 7B. One more QTL for HSITGW was detected on the short arm of chromosome 7D.

Microsatellite mapping of a leaf rust resistance gene transferred to bread wheat from Triticum timopheevii subsp. timopheevii.

A leaf rust-resistance gene transferred from the tetraploid wheat *T. timopheevii* subsp. *timopheevii* (genomic composition A^tA^tGG) into common wheat *T. aestivum* subsp. *aestivum* conditioned resistance at the seedling and adult-plant stages in the introgression line 842-2. To determine chromosome location and map the resistance gene, an F_2 population from a cross between line 842-2 and the susceptible wheat cultivar Skala was developed and screened against leaf rust pathotype 77. Microsatellite markers detected introgressions of the *T. timopheevii* subsp. *timopheevii* genome on chromosomes 1A, 2A, 2B, 5B, and 6B of line 842-2. Linkage analysis revealed an association between leaf rust resistance and microsatellite markers located on chromosome 5B. The markers *Xgwm880* and *Xgwm1257* were closely linked to the resistance gene with genetic distances of 7.7 cM and 10.4 cM, respectively. Infection-type tests with three leaf rust isolates resulted in different patterns of infection types of line 842-2 and a Thatcher NIL with the *Lr18* gene on chromosome 5B. The data corroborated the hypothesis of the diversity of the resistance coming from *T. timopheevii* subsp. *timopheevii* The resistance gene of the introgression line 842-2 seems to be different than *Lr18* and, therefore, was designated *LrTt2*.

Leaf rust and powdery mildew resistance derived from Aegilops markgrafii.

A complex crossing program was initiated to detect the number and location of powdery mildew-resistance genes in introgression lines carrying the resistance coming from *Ae. markgrafii* accession S740-69. In addition, the location of a leaf rust-resistance gene originating from the same *Ae. markgrafii* accession and also introgressed in a wheat background should be combined with the powdery mildew resistance mentioned above in one genotype. The results of the segregation analyses at seedling and adult-plant stage were described in 2009 (Ann Wheat Newslet 55:54).

For detailed investigations with microsatellite markers, F_2 generations with resistance to both diseases and for powdery mildew resistance only were selected. The leaf rust-resistance gene in both double-resistant progenies was located on 2AS. The powdery mildew resistance originating from two different introgression lines was identified on chromosomes 7AL for one progeny and 1AS for the other. The same markers that were suitable for the identification of

powdery mildew-resistance genes in the crosses of resistant introgression lines with the susceptible wheat parent Kanzler could also be successfully employed for the identification of the powdery mildew resistance in the double-resistant progenies.

Genetic mapping of ent-kaurenoic acid oxidase genes in bread wheat.

Ent-kaurenoic acid oxidase (KAO) catalysis three steps in the gibberellin biosynthesis pathway, which yields a large hormone family affecting plant growth and development. We performed partial gene cloning and DNA polymorphism-based mapping of three KAO genes in bread wheat. The KAO loci mapped to the distal ends of the chromosome arms 7AS, 4AL, and 7DS, corresponding to the 7BS/4AL translocation region. Co-linearity of the chromosomal regions carrying the KAO genes was shown, suggesting that the KAO genes represent a homoeoloci set. Following the rules of wheat homoeologous gene designation, the KAO genes were designated *Kao-A1* (chromosome 7AS), *Kao-B1* (4AL), and *Kao-D1* (7DS).

Functional allelic diversity at the Rc (red coleoptile) gene in bread wheat.

The wheat *Rc* genes are thought to be regulatory genes in the anthocyanin biosynthesis pathway (ABP), determining specific expression of the ABP structural genes in coleoptiles. The presence of anthocyanin pigmentation in coleoptiles of Russian bread wheat cultivar Saratovskaya 29 (S29) and the standard cytogenetic disomic substitution stock Chinese Spring (Hope 7A) (DS CS–H 7A) is determined by the same gene *Rc-A1* mapped to chromosome 7AS. The *Rc-A1* alleles of S29 and DS CS–H 7A differ from each other phenotypically; S29 has light red coleoptiles, whereas the coleoptiles of DS CS–H 7A are dark red, suggesting that *Rc-A1* may have different transcriptional activity in these two genotypes. The wheat *Rc* genes have not been isolated and sequenced thus far, hindering direct analysis of their expression profiles. However, their activity may be accessed indirectly by analysis of expression patterns of their target genes. Expression of the *F3h-1* gene, encoding one of the key ABP enzymes, flavanone 3-hydroxylase, is activated by the *Rc-1* genes in wheat coleoptiles. In green coleoptiles, *F3h-1* is not active, thus, *F3h-1* is an appropriate target gene that may be used for indirect evaluation of *Rc-1* activity. The patterns of *F3h-1* expression in the coleoptiles of S29 and DS CS–H 7A were compared. There was a significant difference, with *F3h-1* expression being lower in S29 than in DS CS–H 7A. The lower level of *F3h-1* expression in S29 compared to DS CS–H 7A was consistent with the pattern of development of coleoptile pigmentation. This result suggested that there may be functional allelic diversity at *Rc-A1*, which affects the transcription of the *F3h-1* genes in colored coleoptiles.

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

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

Seed ageing studies in bread wheat.

The influence of long-term storage (natural aging) and artificial ageing on seed germinability were compared using a bread wheat example. Eight lines of differential germinability, after being in storage at low temperature and low humidity for 35 years in the Genebank of IPK, Gatersleben, were used. The seeds were reproduced in 2008, and the renewed seeds were artificially aged by a 72-h treatment with a combination of high temperature and high humidity. The arti-

ficial ageing reduced the germination percentage to a different degree corresponding to the germination percentage of the long-term stored (naturally aged) material. This reduction was significantly less in lines that had maintained high germinability compared to lines with a considerable decline in germinability. The ability of an artificial-ageing treatment applied to fresh seeds to reveal genotypic differences in seed germination capacity comparable to those exposed by long-term natural ageing at low temperature is of importance for seed vigor and seed longevity assessments in both genetic studies on these traits and genebank seed-management activities.

Seed longevity and dormancy in bread wheat.

A QTL-mapping approach was adopted to discern the genomic regions that impart long life and stability to bread wheat seeds. Seeds of the ITMI mapping population were available from regeneration in 2003. Standard germination tests and artificial aging tests were performed. Initial germination percentage ranged from 59% to 97%. Germination percentage after artificial aging ranged from 28% to 90%. QTL mapping revealed one major QTL on chromosome 2A putatively responsible for the higher percentage of germination after an artificial-aging treatment.

The whole population was regenerated in 2009. Seeds were subjected to standard germination tests, artificial ageing tests, and controlled deterioration tests. Initial germination ranged from 24.5% to 98%. Germination percentages after artificial ageing and controlled deterioration ranged from 0.5% to 92% and 0.5% to 90%, respectively. Artificial aging tests revealed two minor QTL on chromosomes 3B and 7A, whereas the controlled deterioration tests identified one major and one minor QTL were detected on chromosomes 1A and 3D, respectively. These lines also were subjected to dormancy tests to discover the relationship between dormancy and longevity. One major QTL for dormancy was discovered on chromosome 4A indicates that there seems to be no relationship between dormancy and longevity for the population under investigation.

Response of the antioxidant glutathione to ageing of wheat seeds.

Seeds can be stored long-term, but their viability is limited. A variety of intrinsic and extrinsic factors influences the longevity of seeds. The viability of seeds in response to ageing correlates with concentrations of the antioxidant glutathione and its half-cell reduction potential.

Viability and changes in the glutathione/glutathione disulphide couple of 120 wheat samples (13 treatments including long-term storage and artificial ageing at 43°C and 18% and 13% seed moisture content) were assessed using germination tests and HPLC analysis, and half-cell reduction potential was calculated using the Nernst Equation.

With a depletion of total glutathione, the total germination of differently treated wheat accessions decreased ($r = 0.73^{**}$). Oxidized glutathione differs between the treatments naturally aged, artificially aged at 13% seed moisture content, and artificially aged at 18%. Half-cell reduction potential also shows a clear difference between the treatments.

Overall, half-cell reduction potential tends to be a good viability marker in wheat seeds ($r = 0.72^{**}$) and, considering the treatments independently, the correlations improve (long term storage: $r = 0.83^{**}$; artificial aging 18%: $r = 0.88^{**}$; and artificial aging 13%: $r = 0.76^{**}$).

Embryo lethality in wheat-rye hybrids.

In crosses between hexaploid wheat and inbred lines of cereal rye, a small number of rye genotypes produce seeds carrying undifferentiated nonviable embryos. Hybrids between such lines and those not giving this phenotype were used as pollen donors in wide crosses with bread wheat to determine the genetic basis of the embryo failure phenomenon. These showed that a single major gene, named *Eml-R1*, is responsible for the embryo lethality character. A set of molecular markers genotyped in an F_2 population between contrasting rye inbreds was used to determine linkage to embryo lethality among a set of F_5 RILs. *Eml-R1* maps to chromosome 6RL in the region of the two co-segregating microsatellite loci *Xgwm1103* and *Xgwm732*.

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ITEMS FROM HUNGARY

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The wheat season. The third extreme drought in one decade characterized the 2008–09 wheat season. A total lack of rain in April and May accompanied by high temperatures caused early maturing and yield decrease. The national wheat average reached only 3.84 t/ha, which was only slightly better than the 3.6 t/ha harvested in the extra dry year 2007. The quality of wheat harvested was good, with low protein in some regions where fertilizer uptake was prevented by drought.

Breeding.

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

Breeding. Four winter wheat cultivars were registered in Hungary in 2009.

Mv Menüett (Mv 07-05) is an early maturing cultivar with very good quality, selected from the cross 'F1959W1-2/MV22'. Yield level is slightly higher than that of the existing quality wheats. The cultivar has reliable winterhardiness and good lodging resistance. Dough characteristics are favorable, measured both with Farinograph and Alveograph. The HMW-glutenin composition is 2*, 7*+9, 5+10. Mv Menüett is moderately resistant to powdery mildew and leaf rust and resistant to stem rust.

Mv Karizma (Mv 08-07), an early maturing, facultative wheat with winterhardiness, is similar to the medium frost-tolerant winter wheats, which is sufficient under the average Hungarian conditions. Mv Karizma represents a

unique quality type, because it overproduces the Bx7 HWW-glutenin subunit that leads to a very strong dough. The top quality has been inherited from a selected line of the famous wheat cultivars of the 1930s, Bankuti 1201 and the short-strawed cultivar Ukrainka characterized by low protein content but very good dough quality. Mv Karizma has a relatively low protein content and very good baking quality; the dough strength and stability, especially, are excellent. The HMW-glutenin composition is 1, 7*+8, 5+10.

Mv Petrence (Mv 08-06) is a medium-early, dwarf wheat with high yield and good baking quality. Mv Petrence is recommended for intensive production under better than average growing conditions. The short straw and very good lodging resistance allow the use of a high rate of fertilizers thus ensuring yield up to 8–9 t/ha. Mv Petrence is the only awnless Martonvásár wheat.

Mv Kolompos (Mv 10-06) is a midseason cultivar selected from the cross 'Eureka/Mv Vekni'. This wheat belongs to the high protein Martonvásár wheat group characterized by 35–38% wet gluten content, A2–B1 Farinograph quality, high water uptake, and high loaf volume. Mv Kolompos carries the T1B·1R translocation.

Disease resistance studies.

Molecular marker-assisted selection. Molecular MAS is being used to incorporate effective resistance genes (*Lr9*, *Lr24*, *Lr25*, *Lr29*, *Lr35*, *Lr37*, *Pm21*, and *Stb2*) into Martonvásár-bred wheat genotypes. The backcross program has been subsidized by national and international research projects (Bioexploit-EU FP6, NAP-BIO-NEWSEED, and DTR_2007).

Molecular markers were used to detect the presence of the *Lr1* and *Lr10* genes in 72 winter wheat cultivars from Martonvásár (Mv). The *Lr1* gene was found in 15% of the genotypes examined (Mv 17, Mv Irma, Mv Madrigál, Mv Matador, Mv Summa, Mv Magvas, Mv Mezőföld, Mv Tamara, Mv Mazurka, Mv Hombár, and Mv Laura) and the *Lr10* gene in 21% (Mv 13, Mv Matador, Mv Martina, Mv Kucsma, Mv Emese, Mv Palotás, Mv Prizma, Mv Matild, Mv Mambo, Mv Béres, Mv Garmada, Mv Hombár, Mv Gorsium, Mv Kemence, and Mv Laura). Three of the Mv cultivars included in the experiments contained both genes (Mv Matador, Mv Hombár, and Mv Laura). Cultivars carrying the *Lr10* gene proved to be more susceptible than those in which the *Lr1* gene was present. Several wheat cultivars containing the *Lr1* or *Lr10* gene were found to be moderately resistant or moderately susceptible.

Effective *Lr* genes. In an artificially infected nursery, the following *Lr* genes continued to provide effective protection against leaf rust in Martonvásár in 2009: *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr28*, *Lr29*, and *Lr35*; the formerly effective *Lr37* became moderately infected.

Powdery mildew race survey. Powdery mildew isolates collected in the Martonvásár area were used to determine the race composition of the pathogen population, the degree of virulence, and the efficiency of known resistance genes. The races dominant in 2009 (and their frequency) were 76 (55.1%), 51 (28.1%), and 77 (9.7%). The virulence complexity in the pathogen population was calculated as 6.13, which was almost as high than in the previous year.

Abiotic stress resistance studies. In the case of water stress, we found that higher general activities of the antioxidant enzymes might indicate that a genotype had better stress tolerance. More sensitive cultivars had relatively higher increases in the activity due to water withdrawal, but even at their highest levels, the antioxidant enzyme activities were lower than those under normal conditions in genotypes with good resistance. Mv Mambo, which had excellent drought tolerance, had outstandingly high antioxidant enzyme activity levels even under normal soil water conditions.

The size and shape of starch granules developing in the endosperm of wheat grains were altered due to heat stress and drought. Heat stress alone had little effect on the granule size while drought or heat and drought reduced it to a great extent (below 7 μm).

From a group of winter wheats characterized for heat stress tolerance, two cultivars (Mv Magma and Plainsman V) were chosen for creating a biparental mapping population consisting of anther culture derived DH lines and RILs for studying the genetic components of heat stress tolerance. Based on AFLP and SSR polymorphisms, the two parental cultivars proved to be genetically diverse, and they also represent different plant developmental types. The early devel-

opment of Mv Magma is quicker, but this is followed by a significantly longer intensive stem elongation phase leading to later heading, compared to Plainsman V.

The genetic basis of earliness of the winter wheat cultivar Mv Toborzó and its association with the yield components has been studied with the characterization of the F_2 and the F_3 progenies of its various biparental populations segregating for the insensitivity and sensitivity allele of the *PPD-D1* photoperiod response locus. The allele phase of *PPD-D1*, in a population dependent fashion significantly influenced heading date, plant height, the average number of kernels/spike, and the seed yield but had no effect on the number of reproductive tillers and 1,000-kernel weight.

A set of 24 winter wheat cultivars of diverse geographic origins are involved in a series of controlled growth chamber tests for establishing the effects of suboptimal, optimal, and supraoptimal ambient temperature levels on plant developmental patterns with the purpose of studying the extent of plant developmental variability independent of the vernalization requirement and photoperiod sensitivity.

Climate change studies. Wheat plants grown under elevated atmospheric CO_2 level had higher number of spikes and grains per plant, produced more above-ground biomass and grain yield. Due to water deprival, plants had a substantial drop in the grain yield, especially at the ambient CO_2 level, whereas CO_2 enrichment resulted in much more effective biomass accumulation at high CO_2 than that at the ambient concentration despite water stress. The yield decrease due to a water withdrawal for 7 days was attenuated well by the doubled CO_2 level while the effect of longer drought could only be mitigated to a much lesser extent.

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The detection of intergenomic chromosome rearrangements in irradiated *T. aestivum–Ae. biuncialis* amphiploids by multicolor genomic in situ hybridization. The frequency and pattern of irradiation-induced intergenomic chromosome rearrangements were analyzed in the mutagenized (M_0) and the first selfed (M_1) generations of *T. aestivum–Ae. biuncialis* amphiploids (2n = 70, AABBDDU^{b}U^{b}M^{b}M^b) by multicolor genomic in situ hybridization (mcGISH). mcGISH allowed the simultaneous discrimination of individual *Ae. biuncialis* genomes and wheat chromosomes. Dicentric chromosomes, fragments, and terminal translocations were most frequently induced by γ-irradiation, but centric fusions and internal exchanges also were more abundant in the treated plants than in control amphiploids. Rearrangements involving the U^b genome (U^b-type aberrations) were more frequent than those involving the M^b genome (M^b-type aberrations). This irradiation sensitivity of the U^b chromosomes was attributed to their centromeric or near-centromeric regions, because U^b-type centric fusions were significantly more abundant than M^b-type centric fusions at all irradiation doses. Dicentrics completely disappeared, but centric fusions and translocations were well transmitted from the M_0 to M_1. Identification of specific chromosomes involved in some rearrangements was attempted by sequential fluorescence in situ hybridization with a mix of repeated DNA probes and GISH on the same slide. The irradiated amphiploids formed fewer seeds than untreated plants, but normal levels of fertility were recovered in their offspring. The irradiation-induced wheat–*Ae. biuncialis* intergenomic translocations will facilitate the successful introgression of drought tolerance and other alien traits into bread wheat.

Physical mapping of a T7A·7D translocation in the wheat–*Thinopyrum ponticum* partial amphiploid BE-1 using multicolour genomic in situ hybridization and microsatellite marker analysis. The absence of chromosome 7D in the wheat–*Th. ponticum* partial amphiploid BE-1 was detected previously by mcGISH, sequential FISH (fluorescence in situ hybridization) using repetitive DNA probes, and SSR marker analysis. In the present study, the previous cytogenetic and SSR marker analyses were expanded to include 25 other SSR markers assigned to wheat chromosomes 7A and 7D to confirm the presence of a T7A·7D translocation and to specify its composition. An almost complete chromosome 7A and a short chromosome segment derived from the terminal region of 7DL were detected, confirming the presence of a terminal translocation involving the distal regions of 7AL and 7DL. In both cases, the position of the translocation breakpoint was different from that of known deletion lines. The identification of the T7AL·7DL translocation and its breakpoint position provides a new physical landmark for future physical mapping studies, opening up the possibility of more precise localization of genes or molecular markers within the terminal regions of 7DL and 7AL.

Identification of new winter wheat–winter barley addition lines (6HS and 7H) using FISH and the stability of the whole 'Martonvásári 9 kr1–Igri' addition set. A previous paper reported the development of disomic addition lines (2H, 3H, 4H, and 1HS isochromosomic) from hybrids between the winter wheat Martonvásári 9 *kr1* and the two-rowed winter barley cultivar Igri. We isolated two new additions, 7H disomic and 6HS ditelosomic, using FISH with the repetitive DNA probes Afa-family and HvT01. The identification of the barley chromosomes in the wheat genome was confirmed with simple sequence repeat markers. The morphological characterization of the new addition lines is also discussed. Studies of the genetic stability of the whole set (2H, 3H, 4H, 7H, 1HS iso, and 6HS) of 'Martonvásári 9 *kr1*–Igri' additions revealed that the most stable disomic additions are 2H and 3H and the most unstable line is the 1HS isochromosomic addition.

Detection of the 1RS chromosome arm in Martonvásár wheat genotypes containing T1BL·1RS or T1AL·1RS translocations using SSR and STS markers. Several molecular markers have been reported for the detection of the 1RS chromosome arm. Our aim was to study the reliability and reproducibility of six molecular markers specific to the 1RS rye chromosome (GPI, Bmac213, 5S, IAG95, SCM9, and RMS13) in distinguishing between wheat genotypes with and without the T1BL·1RS or T1AL·1RS translocations. In the course of the analysis, PCR products of the expected size were obtained with all the markers, which were found to give a reliable indication of the presence of the 1RS chromosome arm in the wheat genome.

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Genetic and Physiological Studies.

G. Kocsy, A. Szűcs, I. Vashegyi, and G. Galiba.

Involvement of free amino acids and polyamines in the stress response. The involvement of free amino acids and polyamines in the cold acclimation was studied by comparison of wheat genotypes with different freezing tolerance. The increase in proline content correlated with the level of freezing tolerance. Cold acclimation affected the free amino acid composition and resulted in great changes in the ratio of the amino acids belonging to the aspartate and glutamate family, respectively. Among the polyamines, putrescine and spermidine concentrations exhibited a great cold-induced increase. The effect of cold on free amino acid and polyamine levels is probably not mediated by abscisic acid and is not determined at the transcriptional level. The cold-induced increase in amino acid and polyamine contents may improve stress tolerance due to the direct protection of macromolecules or due to the activation of various signal transduction pathways.

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ITEMS FROM INDIA

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Current activities: Genetic improvement for rust resistance and quality traits in Indian wheat.

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

Rust resistance genes, such as *Sr31*/*Lr26*/*Yr9*, *Sr26*, *Sr24*/*Lr24*, and *Lr34*, and specific HMW-glutenin subunits are being recombined with good agronomic traits. Selected lines from several intervarietal crosses are in different generations (F_2–F_5) and are being evaluated. Marker-assisted selection is being used to screen for specific rust resistance genes.

Using induced mutations, some early flowering mutants in the cultivars C-306 and MP-3054 were isolated and are being further evaluated. The early mutants were crossed with HW-2004 (C-306 + *Sr24*/*Lr24*) to recombine earliness and rust resistance. With the aim of isolating mutants resistant to rust diseases, the cultivars PBW343 and NI917 were mutagenized with gamma rays and populations from the M_1 generation were grown.

Marker-assisted backcrossing is being used to improve the rust resistance and dough strength of HD2189 wheat by incorporating the *Lr24*/*Lr24* and *Glu-D1d* genes. Eighteen BC_4F_1 plants were grown, and DNA from leaves of four-week old individual plants was extracted and screened using SCAR markers for these two genes. In the winter of 2009–10, five plants carrying both markers were identified. Backcrosses were made using the recurrent parent HD2189 and carriers of both the markers.

Marker-assisted selection to combine rust resistance genes (*Sr24* and *Sr26*) and *Glu-D1d* (coding for HMW-glutenin subunits 5+10) is being carried out in a cross between FLW-2 and Kite. In the F_2 generation, ~220 plants were analyzed using SCAR markers. Plants carrying markers for rust resistance genes *Sr24* and *Sr26* and *Glu-D1d* were selected and will be evaluated for their field performance.

Validation of a SCAR marker (Sr26#43) for stem rust resistance gene Sr26 in Indian wheat genotypes and segregating populations.

B.K. Das, Ruchi Rai, and S.G. Bhagwat.

Stem rust is a potential threat to the wheat crop and causes significant losses worldwide. Ug99, a race of black stem rust detected in Uganda, shows virulence to a great majority of wheat cultivars. The stem rust resistance gene *Sr26* is translocated to wheat from *Thinopyrum elongatum* and no virulence towards the *Sr26* gene has been reported. A SCAR marker, Sr26#43, was reported for this gene by Mago et al. (2005). To validate this marker in Indian wheat genotypes, 49 wheat genotypes were screened using SCAR marker Sr26#43. Analysis of these genotypes showed that the SCAR marker was present in all the genotypes carrying *Sr26*, except HW2090, which was reported to carry *Sr26* gene. The marker was absent in the genotype that lacked *Sr26* or carried any other stem rust resistance genes.

Two F_2 populations from crosses involving susceptible (Kalyansona (-*Sr26*) and resistant (Kite (+*Sr26*) and Takari (+*Sr26*) genotypes were used for validation. The phenotypic rust reaction data and marker data matched one-to-one, indicating that this marker can be used in early generations to selecte for the *Sr26* gene. Incorporating this gene is recommended to prevent stem rust epidemics caused by Ug99. The validated marker Sr26#43 will facilitate incorporating this gene in new breeding lines. The durability of *Sr26* can be enhanced by pyramiding it with other rust resistance genes. Multiplex PCR for the simultaneous screening of *Sr26* and *Sr24* is in progress.

The help of the DWR Regional Station, Flowerdale, Shimla, for phenotypic screening of some F_3 lines is acknowledged. The genotypes carrying *Sr26* were provided by DWRRS, Shimla, and IARIRS, Wellington. During this period, Shri. K. Arun participated in some of the experiments as project trainee.

Analysis of semidwarfing genes and polymorphisms at the Xgwm261 locus in a recombinant inbred population of bread wheat.

Suman Bakshi and S.G. Bhagwat.

Recombinant inbred lines (RILs) derived from a cross between cultivars Sonalika and Kalyansona in the F_9 generation were grown in the winter season of 2009–10. Leaves of one individual from each line were harvested and used for DNA extraction. The parental cultivars and the RILs were analyzed for the presence of *RhtB1b* and *RhtD1b* using perfect markers (Ellis et al. 2002). Variation at the microsatellite locus *Xgwm261* was studied. The parent cultivar Kalyansona had a 192-bp allele; the other parent Sonalika had a 165-bp allele. The RILs showed a 1:1 ratio for the presence of these alleles. Culm height was recorded on the RILs by measuring the culm of the main tiller of five plants when the plants were near maturity. The results showed that the RILs carrying *Rhtb1a* and *RhtD1a* were the tallest, followed by those with *RhtB1b* and *RhtD1b*. Plants with both semidwarfing genes were shortest. The RILs with a given a *Rht* gene composition were further classified according to the presence of *Xgwm261*. The results indicate that there was no reduction in culm height associated with the presence of the 192-bp allele. Further analysis is in progress.

Canopy temperature depression studies in bread wheat.

Heat stress is one of the most important stresses in subtropical, wheat-growing areas of the world and results in grain yield losses. The stage at which the wheat crop faces heat stress varies with the location and cropping season. In some areas, the stress is experienced at either at the seedling stage or at the grain-filling stage, in other cases the stress is felt through out the life of the plant. Heat stress affects the crop by altering many traits. Wheat cultivars differ in their canopy architecture, and this may result in differences in canopy temperature. Canopy temperature depression, the difference between air temperature and canopy temperature, can be measured. An experiment was carried out at the experimental field in Trombay in the winter of 2009–10. Seventeen wheat cultivars, which included both heat stress tolerant and susceptible cultivars, were grown in a replicated experiment. Canopy temperature was measured with an infrared thermometer. Measurements were made around 12:00 PM from tillering to flag leaf senescence at weekly intervals. At harvest, data on agronomic parameters were recorded using five plants from each replicate of each cultivar. Canopy temperature values appeared to vary across cultivars and growth stages. Data are being analyzed.

Threshability in recombinant inbred lines of bread wheat.

S.G. Bhagwat.

In wheat, threshability is an important trait. Very soft glumes and loose attachment to the rachis results in deciduous glumes that fall off if the spikes are not harvested in a timely fashion resulting in some grain loss. Thick glumes, with a strong attachment to rachis, make threshing hard. Tough glumes are associated with a brittle rachis, which is know as the nonfreethreshing habit.

Studies on the genetics of tough glumes and brittle rachis have been reported. Using interspecific crosses, QTL for threshability have been identified. Crosses between semi-wild and common wheat indicated that the fragile rachis and nonfreethreshing character of semi-wild wheat are dominant to the tough rachis and freethreshing character of common wheat. Rachis fragility and glume tenacity of semi-wild wheat were each controlled by a single gene (Cao et al. 1997). In hexaploid wheat, the glume tenacity gene *Tg* and *Q* locus control threshability. The *Tg* gene was mapped on 2DS of *T. aestivum* in the distal region (Sood et al. 2009). RILs evaluated for kernel shattering, glume strength, glume-pair angle, open-floret percentage, spike density, and plant height in different environments showed that glume strength consistently correlated with kernel shattering in all test environments, but their correlation was moderate. One QTL for glume strength was identified in the genomic regions containing the kernel-shattering QTL, suggesting that glume

strength is not the only genetic factor that determines kernel shattering. These results indicate that glume pair angle and open floret percentage might be the direct causes of kernel shattering (Zhang et al. 2009).

We are developing RILs from a cross between the cultivars Sonalika and Kalyansona, and RILs in the F_9 generation were grown in field. Single spikes were harvested at maturity, threshed by hand, and classified according to their ease or difficulty in threshing. Kalyansona was easier to thresh than Sonalika. The RILs varied for the trait. Lines easier to thresh than Kalyansona and harder to thresh Sonalika were observed. Each line was given a major category rating as follows: 1, deciduous glumes or very soft threshing; 2, similar to cultivar Kalyansona; 3, similar to cultivar Sonalika; 4, tougher glumes and hard to thresh; and 5, tough glumes very hard to thresh. Data were taken on 138 RILs in 2009–10. Based on the hand feel, the RILs were given scores in between the major categories mentioned above (Table 1).

Table 1. Scoring of glume and threshing traits in field-grown, F_9 RILs between the cultivars Sonalike (tough threshing) and Kalyansona (freethreshing).

Description	Rating	Frequency
Very soft and deciduous	1.0	00
Intermediate	1.5	09
Kalyansona type	2.0	31
Intermediate	2.5	12
Sonalika type	3.0	40
Intermediate	3.5	22
Tougher glumes, hard threshing	4.0	14
Intermediate	4.5	05
Tough glumes, very hard threshing	5.0	05

The data showed transgressive segregation for the trait. Observations also were taken in the F_7 and F_8 generations in 2007–08 and 2008–09, respectively, however the RILs were not rated as in 2009–10. Of the 18 RILs that were rated 4.0 or above in 2009–10, 14 were rated as hard or medium hard to thresh in 2007–08 and 12 were rated as hard or medium hard to thresh in 2008–09. Five lines were rated as soft in 2007–08 and four in 2008–09. Of the 40 lines that were rated from 1.0 to 2.0 in 2009–10, data on 26 were available from 2008–09; 24 were rated soft and two were rated as hard or medium hard. In 2007–08, 37 were rated as soft threshing, and three were rated hard or medium hard. These results indicate that some consistency between years. The disagreement could be due to error in judgment, environmental variation, or segregation.

Rachis breaking on 138 RILs was recorded in 2009–10. Fragile rachis was observed in 19 lines, the rachis remained intact in 98 cases, and was intermediate in 21. Of the 19 lines rated as fragile, 13 rate 4.0–5.0, indicating that the fragile rachis was largely accompanied by tougher glumes and hard threshing. Two lines with fragile rachis were rated 1.0, 3.0, and 3.5.

The RILs and parents were classified according to number of spikelets/cm of spike length. This value indicated whether the spike was compact or lax. Kalyansona showed a more compact spike with 2.47spikelets/cm; Sonalika had 1.72 spikelets/cm. RILs with lax spikes were more frequent than those with denser spikes. Fifty-six percent of the RILs were in the category of less than or equal to the Sonalika parent. More compact spikes (with 2.0 or more spikelets/cm) were observed in 30% of the RILs.

The RILs with denser spikes were classified according to their threshability rating. Of the 43 RILs, 18 were easy to thresh (rating 2.0 or lower), 21 were in the medium range (rating 2.5 to 3.5), and four were in the hard threshing range (rating 4.0 or more). The rachis remained intact in 31 of the 43 RILs, was intermediate in seven, and fragile in five. These results showed that there was an incomplete association between high spike density and easy threshability or nonfragile rachis. These RILs originated from intervarietal crosses and could be useful in identifying loci governing threshability trait in bread wheat.

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Deployment of molecular markers for the improvement of some important quality traits in bread wheat.

Construction of framework linkage map(s) using trait-specific, intervarietal RIL populations. Three framework linkage maps using three mapping populations have been prepared in our laboratory for QTL interval mapping of various agronomically important traits. These three mapping populations were originally developed for the following three traits by Dr. H.S. Dhaliwal and his coworkers at Punjab Agricultural University (PAU), Ludhiana, India: (i) grain protein content (GPC); (ii) preharvest sprouting tolerance (PHST), and (iii) grain weight (GW).

QTL analyses for 11 yield and yield-related traits. The GPC and ITMI populations were used to identify QTL for nine yield traits including plot yield and its components, plant height, and peduncle length. For this purpose, single-locus (using QTL Cartographer) and two-locus (using QTLNetwork) QTL analyses were conducted. For all 11 traits, a total of 80 putative M-QTL on 19 chromosomes in the GPC population and 140 putative M-QTL on 20 chromosomes in ITMI population were detected. QTLNetwork identified a total of 113 and 190 QTL that included QTL with significant main effect and/or significant interaction effect (epistatic QTL or QTL involved in interaction with the environment). An important genomic region harboring important major co-localized QTL for each of the six yield traits was identified on chromosome arm 2DS in both the GPC and ITMI populations. In the ITMI population, this QTL influenced 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, the QTL influenced 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 genomic region with the above QTL was physically located in the distal bin (2DS5-0.47-1.00) covering 53% region of 2DS. Comparative mapping revealed that the genomic region harboring the QTL in wheat spans a distance of 11.51 Mb on rice chromosome 7 (R7). This information may prove useful for high-resolution mapping leading to map-based cloning of the above major QTL.

Marker-assisted selection for GPC and leaf rust resistance. In bread wheat, high grain protein content (HGPC) determines nutritional value, processing properties, and quality of the end-product. In view of this, marker-assisted selection (MAS) was used to introgress a major gene for high GPC (*Gpc-B1*) into six wheat genotypes. These six wheat genotypes included (i) three elite Indian bread wheat cultivars and (ii) three advanced lines derived from the cultivar PBW343 (each containing the leaf rust resistant gene *Lr*24). During backcrossing, foreground selection was exercised using tightly linked markers. Background selection was performed using SSR markers evenly distributed throughout the genome. As a result, 14 BC_3F_4 lines carrying *Gpc-B1* were developed and evaluated for GPC and grain yield. Ten of

these lines, homozygous for *Gpc-B1*, had significantly higher GPC, the increment ranging from 0.42% to 2.50% of the GPC (increment on the original concentration was ~4% to 25%). One of the derived lines with enhanced GPC also had significantly higher grain yield (others were equal with their recipient genotypes). No negative correlation was observed between grain yield and GPC (%), suggesting no yield penalty with improved GPC. The results presented in this study suggest that introgression of *Gpc-B1* gene through MAS, in combination with phenotypic selection, is a useful strategy for development of wheat genotypes combining high GPC with higher grain yield.

Marker-assisted selection for preharvest sprouting tolerance and leaf rust resistance. Preharvest sprouting and susceptibility to leaf rust are two major problems in wheat that lead to the degradation of grain quality and significant losses in yield. Development of PHST and leaf rust resistant wheat genotypes was undertaken in our laboratory using MAS. A major QTL (*QPhs.ccsu-3A.1*) for PHST, which we had earlier identified, was introgressed into HD2329, an elite but PHS-susceptible cultivar that has two *Lr* genes (*Lr24* + *Lr28*) earlier introgressed at IARI by Dr. K.V. Prabhu and coworkers using MAS. In each backcross generation, foreground selection for the PHS QTL was exercised using flanking markers (*Xgwm155* and *Xwmc153*), and background selection was performed using 61 simple sequence repeat markers mapped at loci spread over the whole genome. During backcrossing, desirable alleles of *Lr24* and *Lr28*, also were tracked using linked SCAR markers. Seven BC_3F_3 progenies having both the desirable PHST QTL and *Lr* genes and showing up to 93.44% genetic similarity with the recipient parent were selected. These lines exhibited a high level of PHST (PHS score 2–4) and resistance against leaf rust under artificial conditions. The study demonstrated successful application of MAS for targeted pyramiding of QTL/genes for more than one trait into an improved wheat cultivar (Kumar et al. 2009).

Introgression of QTL for grain weight using MAS. Crosses involving 10 elite Indian bread wheat genotypes as recipient parents and the genotype Rye Selection111 as a donor parent were attempted during the off-season of 2005–06 in a Phytotron Facility at IARI, New Delhi, and the F_1 seed collected. These F_1s were raised during the rabi season 2006–07 and backcrossed with their respective recurrent parents to obtain the BC_1F_1 seed. A total of 470 BC_1F_1 seeds belonging to five crosses (RS111/HD2329, PBW343 (*Lr9*)/RS111, HI977/RS111, K9107/RS111, and RAJ3765/RS111) were obtained. Using this seed material, ~259 BC_1F_1 plants were raised during rabi 2007–08. Following foreground selection, 27 positive plants for markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for grain weight on chromosome 1A), 127 positive plants for the marker *Xwmc24* and 57 positive plants for the marker *Xwmc59* were selected. The selected BC_1F_1 plants were backcrossed with their respective recurrent parents and BC_2F_1 seeds was obtained, which were used to raise BC_2F_1 progenies in the field during the rabi season 2008–09. Following foreground selection, three positive plants for markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for grain weight on chromosome 1A) involving the recipient genotype PBW343 (*Lr9*); 142 positive plants for the marker *Xwmc24* only involving recipient genotypes PBW343 (*Lr9*), K9107, and Raj3765; and 18 positive plants for the marker *Xwmc59* involving recipient genotype PBW343 (*Lr9*) were selected. The selected plants were backcrossed with their respective recurrent parents to obtain BC_3F_1 seed, which was used to raise the BC_3F_1 progenies during the rabi season 2009–10. The selfed seed (BC_3F_2 seed) of the corresponding progenies was harvested and phenotypic data on 1,000-kernel weight is being recorded. The BC_3F_2 seed will be used to raise the BC_3F_2 progenies during the rabi season 2010–11, and both foreground and background selections (for progenies possessing the desired QTL) will be undertaken to identify desirable plants for raising the BC_3F_3 progenies.

Genetic dissection of grain weight in bread wheat through QTL analysis. For the genome-wide genetic dissection of GW in bread wheat, both QTL interval mapping and regional association mapping were undertaken. QTL interval mapping involved preparation of framework linkage map with 294 loci (194 SSRs, 86 AFLP, and 14 SAMPL) using a biparental RIL mapping population derived from the cross 'Rye Selection111/Chinese Spring'. Using the genotypic data and data on GW of RILs collected over six environments (3 locations × 2 years), genome-wide single-locus QTL analysis (using inclusive composite interval mapping, ICIM) and two-locus QTL analysis (using QTLNetwork) were conducted to identify main effect QTL (M-QTL) and epistatic QTL (E-QTL). Single-locus QTL analysis identified 10 QTL (including four major and three stable QTL), contributing >20% phenotypic variation for GW. Two-locus QTL analysis resolved a total of 24 QTL, which included three M-QTL (also detected by single-locus analysis) and 21 E-QTL, the later involved in 12 digenic Q × Q interactions; no Q × E and Q × Q × E interactions were detected. The total PV due to all the M-QTL was 28.11%, whereas the PV due to all the E-QTL was 43.36%, which suggested that nearly three quarters (71.47%) of PV for GW was fixable. This study was further supplemented with association mapping, which allowed validation of seven QTL (including above two QTL) and helped to identify two new markers in the genomic regions that were not reported to contain QTL for GW in earlier studies. The validated markers linked with QTL for high grain weight may prove useful in marker-assisted selection for the development of cultivars with high GW in bread wheat.

Genetic diversity and population structure analysis among Indian bread wheat cultivars. As a first step towards association mapping in wheat, we analyzed genetic diversity and structure in a collection of 263 Indian bread wheat cultivars (45 developed during pre-Green Revolution period and 218 developed during post-Green Revolution period) that were released over a period of ~100 years (1910 to 2006). For this purpose, we used a set of 42 unlinked neutral SSRs and 48 SSRs (60 loci) from the genomic regions reported to have QTL for GW. The 42 SSRs detected a total of 295 alleles (mean 7.02; range 2-14/SSR), which is more than a total of 273 alleles (mean 4.55; range 2–9 alleles/SSR) detected by 60 SSR loci subjected to selection. The average number of alleles/locus (5.91 vs. 5.74) and the estimates of genetic diversity (0.65 vs. 0.61) in the pre- and post-Green Revolution period cultivars did not differ significantly indicating that the Green Revolution did not lead to any loss of genetic diversity. However, to better understand the scenario, decadal diversity also was studied, which indicated gradual loss in diversity during three decades (1970s-2000s). This loss in diversity is alarming and, therefore, needs attention of breeders. The model-based *Structure* analysis identified a total of 14 subpopulations including two subpopulations largely comprising cultivars from pre-Green Revolution period and the 12 subpopulations mostly comprising cultivars from post-Green Revolution period. These results suggest that modern wheat-breeding practices in India are slowly decreasing genetic diversity and, therefore, this issue need to be addressed by involving diverse/synthetic wheat germ plasm in Indian wheat-breeding programs.

Association analysis for grain weight, grain protein content, and preharvest sprouting tolerance. We attempted association analyses for the grain-quality traits GW, PHST, and GPC. For this purpose, only 230/263 of the above cultivars were used, because for the remaining 33 cultivars, either phenotypic data was not available, they had similar pedigrees, or they flowered/matured too early or very late making them unsuitable for study. The model-based *Structure* analysis identified a total of 13 subpopulations. These included two subpopulations largely containing pre-Green Revolution cultivars and the remaining 11 subpopulations containing post-Green Revolution cultivars.

The *Structure* analysis was used to make marker-trait associations for GW and GPC using a set of 48 SSR markers mapped in the genomic regions harboring QTL for GW. The association mapping allowed identification of nine and four markers ($P < 0.05$) having significant association for GW and GPC, respectively. The study validated two markers on chromosome 1A that earlier were reported to be associated with QTL for GW (through QTL analysis), and also helped in identification of two new markers for GW in the genomic regions that were not reported to contain QTL for GW in earlier studies. Five new markers also were identified in the genomic regions previously reported to have QTL for GW, so that relatively more closely linked markers with the QTL were identified in these cases.

Marker-assisted pyramiding of quality traits and leaf rust resistance in the background of PBW343. Pyramiding the QTL/genes for quality traits and leaf rust resistance in the background of PBW343 also was undertaken using the genetic stocks developed through MAS by us at our research farm and Punjab Agricultural University (PAU), Ludhiana, India. We decided to develop the following two single cross hybrids (i) PBW343 (*Lr24+GPC-B1*) / PBW343 (PHST) developed by us and (ii) PBW343 (*Lr24+Lr28*+GW) / PBW343 (*GluAx-Ay*) developed by PAU. F_1 seeds of these two hybrids were distributed between each institute (CCSU and PAU) for producing double cross hybrids for carrying out MAS for pyramiding the genes/QTL for leaf rust resistance, PHST, GW, and *GluAx-Ay*.

The above two hybrids were raised at CCSU and PAU in an off-season (2009) nursery at Keylong (a research station for raising off-season nurseries) for preparing the double cross hybrid seed. The two hybrids were intercrossed, and double cross hybrid seed (F_1 seed) was obtained. The double cross population comprising a set of ~192 plants were grown at CCSU during 2009–10 and foreground selection was undertaken using a set of six SSR/SCAR markers linked to corresponding gene/QTL for GPC, PHST, GW, and leaf rust resistance. Following foreground selection, four plants containing all the above genes/QTL in homozygous condition were selected and bagged to allow them self pollinate. An additional two plants containing all the above genes but showing heterozygosity for markers associated with GW or GPC loci also were selected and allowed to self pollinate. To increase the frequency of plants possessing all the important genes, we selected ~15 plants possessing either four or more than four genes and intercrossed them in different combinations and F_1 seeds were obtained.

Molecular marker-assisted transfer and pyramiding of one or more of the QTL/genes for quality traits.
To mobilize or pyramid one or more QTL/genes for grain quality into high-yielding wheat cultivars to develop genotypes/cultivars combining improved, five institutions from India, including CCSU, will focus on developing wheat cultivars combining grain quality traits (high GW, high PC, PHST, grain hardness, and flour quality) with leaf rust resistance and high grain yield using molecular MAS.

Analysis of host-pathogen interaction in leaf rust-infected bread wheat: wet-lab approach. To understand the host-pathogen interaction in detail, it is essential not only to study temporal and spatial expression of a particular gene, but also those of other genes that may be similarly co-regulated, at both seedling and adult-plant stage. The well known, classical method cDNA–AFLP analysis is most suitable for the above purposes, because it covers the whole transcriptome. For the study of seedling resistance provided by the gene *Lr28*, total RNA was isolated from seven-day-old seedlings of each of the resistant (HD2329 + *Lr28*) and susceptible (HD2329) wheat stocks (a) before inoculation, i.e., at 0 h; (b) at 48 h, 96 h, and 168 h after inoculation with leaf rust pathogen race 77-5; and (c) at 168 h after mock inoculation. Using the above RNA samples, high-quality cDNA samples were obtained. These cDNA samples were utilized to study the transcript derived fragments (TDFs) following cDNA–AFLP analysis using 17 *Eco*RI+3/*Mse*I+3 γP32 labeled primer combinations. Highly reproducible, single banded, and over-expressed, 37 TDFs in the resistant and susceptible hosts following pathogen inoculation were isolated, cloned, and sequenced. Analysis of the sequences showed that 29 TDFs had significant similarity with known nucleotide or protein sequences in the database, including a number of wheat BAC clones and known proteins. To gain more information regarding expression of the above TDFs across different treatments, quantitative RT-PCR analysis is being conducted.

For the study of adult-plant resistance provided by the gene *Lr48*, total RNA was isolated from leaves of a 120-day-old, leaf rust inoculated and mock inoculated APR resistant wheat stock CSP44 + *Lr48* at (a) 0 h, (b) 24 h, (c) 48 h, (d) 72 h, and (e) 168 h. Using the above derived 10 purified RNA samples, 10 high quality cDNA samples were synthesized followed by cDNA-AFLP analysis using 16 *Eco*RI+3/*Mse*I+3 γP32 labeled primer combinations. A total of 483 differentially expressed TDFs were identified, and 52 TDFs (out of 483) were eluted from the gels. A total of 48 TDFs were cloned and sequenced successfully. Some of these TDFs showed similarity with known genes which include genes expressed in leaf rust and stripe rust infected bread wheat plants and other stress responsive genes. A few TDFs did not match with nucleotide or protein sequences in the database and were considered new. One TDF showed similarity with a genomic sequence of *P. triticina* and was considered to be of pathogen origin. Primers for quantitative RT-PCR were designed using software primer express.

Analysis of host–pathogen interaction in leaf rust-infected bread wheat: *in-silico* approach. The availability of wheat UniGenes and ESTs from cDNA libraries of leaf rust infected susceptible and resistant wheat plant stocks in UniGene and the dbEST database of the NCBI are powerful resources to identify differentially expressed wheat genes expressed during resistance reaction . Using these transcriptomic resources, and with the help of the data-mining tool Digital Differential Display (DDD), three pair-wise comparisons were performed on three cDNA libraries, each derived from leaf rust inoculated susceptible wheat stock (i) Thatcher, leaf rust inoculated resistant wheat stock, (ii) Thatcher + *Lr10* and leaf rust inoculated resistant wheat stock, and (iii) Thatcher + *Lr1* . A total of 68 differentially expressed UniGenes were identified. Using the Cluster 3.0 program, the differentially expressed UniGenes were clustered in five major clusters based on correlated expression pattern . In this exercise, resistance specific up- and down-regulated genes were identified for both genes *Lr10* and *Lr1* in the cultivar Thatcher. Some of the differentially expressed UniGenes encode for proteins similar to DNAJ heat shock family protein, thiol-disulfide exchange intermediate (*A. thaliana*), Triticain gamma (CTSH), membrane-binding proteins, and many known and unknown but novel gene sequences. Further tissue-based cluster analysis of the differentially expressed UniGenes was performed and revealed that all the identified UniGenes are highly expressed in leaves, have moderate expression in the sheath, stem, and inflorescence, and have low expression in the seed, root, flower, crown, callus, and cell culture. The present study will be followed by wet-lab experiments to identify differentially expressed genes in leaf rust infected wheat.

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Behavior of spring wheat genotypes under late and very late situations in northwestern India.

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Summary. A field experiment conducted during the winter seasons in 2000–01 to 2001–02 at the Directorate of Wheat Research, Karnal, evaluated new, promising genotypes under late and very late sowing situations. The mean of 2 years data revealed reductions of 16.96% and 17.15% in biomass and yield, respectively, when sowing was delayed from late to very late. This decline was due to 8.38% and 11.77% reductions in 1,000-kernel weight and grains/spike, respectively, and a more than 10 days less grain-filling period between late to very late sowings. Cultivar differences were observed for yield and yield-attributing parameters. For mean basis, cultivar HD 2643 produced the maximum biomass (106.95 q/ha) followed by Raj 3765 (106.77 q/ha); the lowest was by genotype WR 251 (94. 72 q/ha). Similarly, genotype PBW 435 recorded the maximum grain yield (42.86 q/ha) and lowest by UP 2425 (37.37 q/ha). Differential responses suggested different cultivars were suited for late sown conditions.

Wheat is the second most important crop after rice in India, occupying approximately 28 x 10^6 ha with a production of 78.4 x 10^6 metric tons during 2008–09, the highest level of production since the Green Revolution. Considering environmental and technological adaptation, India is broadly divided in to six wheat-growing regions, the Northern Hill Zone (NHZ; Jammu and Kashmir, Himachal Pradesh, and Uttarakhand), the North Western Plain Zone (NWPZ; Punjab, Haryana, Western Uttar Pradesh, and some parts of Rajasthan), the North Eastern Plain Zone (NEPZ; Eastern Uttar Pradesh, Bihar, West Bengal, Orissa, and Eastern states), the Central Zone (CZ; Madhya Pradesh, Gujrat, Southern Rajasthan, and the Bundel Khand region of Uttar Pradesh), the Peninsular Zone (PZ; Maharashtra and Karnataka), and the Southern Hill Zone (SHZ; Tamil Nadu). The growing period of wheat is variable from one agroclimatic zone to another, which affects vegetative growth and grain-filling duration leading to differences in attainable yield. The maximum wheat growing duration is in the Northern Hills Zone and the mininum is in the Peninsular Zone.

Farmers generally grow wheat in a cropping system that maximizes their total production. In this process, wheat is generally preceded by crops such as rice, cotton, sugarcane, maize, sorghum, potato, toria, and pigeon pea. In this plethora of cropping sequences, some crops, such as basmati rice, cotton, sugarcane, potato, toria, and pigeon pea, delay wheat sowing in different parts of the country. Due to late harvests of sugarcane, potato, and toria, wheat generally is sown in the first week of January. Under late and very late sowing conditions, low temperatures occur during seedling establishment and hot, dry spells prevail during grain-filling. Maturity is accelerated/forced because of high temperature and/or water stress, which reduces grain size and weight.

In India, wheat is sown from November to January, whereas the most appropriate time for sowing is the first two weeks of November. A delay in sowing to late mid-November to first two weeks of December resulted in decreases in yield of 15.5, 32.0, 27.6, 32.9, and 26.8 kg/ha/day in the NHZ, NWPZ, NEPZ, CZ, and PZ, respectively, for timely sown cultivars. Corresponding yield losses were 7.6, 18.5, 17.7, 17.0, and 15.5 %. For late-sown cultivars, a delay in sowing from late to very late, first two weeks of December to first two weeks of January, decreased grain yield by 42.7, 44.8, 51.6, and 44.2 kg/ha/day or 22.8, 27.1, 30.9, and 25.6 % in the NWPZ, NEPZ, CZ, and PZ, respectively (Tripathi et al. 2005). This huge reduction in yield due to delayed sowing prompted us to evaluate late and very late sown genotypes for maximum production. An effort was made to grow advance genotypes/cultivars under late (December sowing) and

very late (January sowing) sowning conditions to evaluate their flowering, maturity, grain filling period, biomass, yield and yield attributes.

Materials and Methods. A field experiment was conducted for two years, from 2000–01 to 2001–02, at the Directorate of Wheat Research, Karnal (Latitude 290°43' N, longitude 760°58' E and altitude 245 m). The experimental soil was sandy clay loam in texture (22% clay), low in organic carbon (0.37%) and available N (145 kg/ha), and medium in available P (17.2 kg/ha) and available K (155 kg/ha) content. The experiment was a split-plot design and replicated three times. The main plots included two sowing times, late sown (9 December in 2000 and 10 December in 2001) and very late sown (22 January in 2001 and 9 January in 2002), and nine genotypes, PBW 435, UP 2425, HD 2643, HP 1744, DL 788-2, WR 251, WR 544, Raj 3765, and PBW 373, were grown as subplot treatments. After the rice forecrop was harvested, the field was prepared by cultivator and disk, and 250 viable seeds were seeded in each subplot. Fertilizer (120 N, 60 P_2O_5, 40 K_2O) was applied to the crop. A one-third dose of nitrogen, in the form of urea, full phosphorous, in the form of di-ammonium phosphate, and potash, in the from of muriate of potash, was applied as before sowing and the remaining nitrogen was top dressed in two splits at the first node stage (DC 31) (Zadoks et al. 1974) and at boot stage (DC 41). Irrigation was applied as needed. Weeds were controlled with the application of isoguard plus (a chemical blend of isoproturon and 2, 4-D (at 0.5 + 0.125 Kg/ha) in 500 liters of water 30 days after sowing. Observations were recorded on biomass, anthesis, maturity, grain-filling period, grain production rate, yield, and yield component characters. Standard statistical methods were were followed for the parameters under study (Gomez and Gomez 1984).

Results and Discussion. Two years of data reveals that during 2000–01 biomass, 1,000-kernel weight, spikes/m^2, and grains/spike were not significant under late and very late sowning condition, whereas during 2001–02, only spikes/m^2 was at not significant. All other parameters under study in late and very late sowning conditions were significant. From the mean of two years, we observed that biomass and yield declined 16.96 and 17.15%, with 8.38% and 11.77% reductions in 1,000-kernel weight and grain/spike and more than 10 days less grain-filling period, from late to very late sowning conditions, respectively (Tables 1 and 2, p. 67). The grain production rate under very late sowning conditions was significantly higher than that under late sowning conditions in both years, probably because of the shorter grain-filling period under very late sowing conditions.

Table 1. The effect of sowing time and genotype on biomass, yield, harvest index, 1,000-kernel weight, and spikes/m^2 for spring wheat genotypes sown at the Directorate of Wheat Research, Karnal, India (NS indicates nonsignificance).

	Biomass (q/ha)		Yield (q/ha)			Harvest index		1,000-kernel weight (g)		Spikes/m^2	
Treatment	2000–01	2001–02	2000–01	2001–02	Mean	2000–01	2001–02	2000–01	2001–02	2000–01	2001–02
Sowing time											
Late	103.31	121.58	40.19	46.55	43.37	0.415	0.384	44.77	42.78	406	406
Very late	97.35	89.38	36.65	35.21	35.93	0.371	0.395	42.65	37.08	424	435
CD at 5 %	NS	8.05	3.55	3.77		0.202	0.04	NS	3.35	NS	NS
Genotype											
PBW 435	93.25	107.04	40.27	45.45	42.86	0.432	0.427	42.93	39.80	396	456
UP 2425	84.25	108.95	34.30	40.44	37.37	0.375	0.376	49.10	44.73	378	363
HD 2643	102.77	111.12	37.32	39.61	38.47	0.370	0.356	46.96	43.27	419	363
HP 1744	108.14	104.83	39.96	40.83	40.40	0.382	0.390	43.15	35.80	415	391
DL 788-2	105.75	107.11	43.31	41.00	42.16	0.412	0.386	42.59	35.87	467	517
WR 251	93.65	95.79	36.17	37.73	36.95	0.417	0.394	47.27	50.27	378	356
WR 544	98.21	96.24	39.17	38.64	38.91	0.408	0.403	39.73	38.00	398	403
Raj 3765	102.77	110.76	39.78	44.32	42.05	0.399	0.402	41.54	36.87	439	442
PBW 373	104.17	107.51	35.53	39.91	37.72	0.342	0.375	40.08	34.80	444	491
CD at 5 %	NS	8.96	6.27	3.93		NS	0.037	3.52	2.39	NS	71

Among the cultivars under study, biomass, harvest index and spikes/m^2 were statistically similar in 2000–01, whereas all other parameters were significant (Table 1). Based on means, the maximum biomass was produced by cultivar HD 2643 (106.95 q/ha) followed by Raj 3765 (106.77 q/ha). In contrast, the lowest biomass was exhibited by genotype WR 251 (94. 72 q/ha). Similarly, genotype PBW 435 recorded the maximum grain yield (42.86 q/ha) but was

Table 2. Effect of sowing time and genotypes on grains/spike, anthesis, maturity, grain-filling period, and grain production rate for spring wheat genotypes grown in the field at the Directorate of Wheat Research, Karnal, India (NS indicates nonsignificance).

	Grain/spike		Anthesis (days)		Maturity (days)		Grain-filling period (days)		Grain production rate (kg/ha/day)	
Treatment	**2000–01**	**2001–02**	**2000–01**	**2001–02**	**2000–01**	**2001–02**	**2000–01**	**2001–02**	**2000–01**	**2001–02**
Sowing time										
Late	22.6	27.5	84	82	112	114	28	33	144.6	144.3
Very late	21.1	23.1	71	62	89	82	18	20	203.6	174.3
CD at 5 %	NS	4.3	0.8	0.3	1	0.4	1	1	16.4	14.9
Genotype										
PBW 435	23.9	25.1	79	71	106	100	28	28	149.4	162.6
UP 2425	18.8	25.5	79	72	108	100	29	28	118.2	148.6
HD 2643	19.2	25.1	82	75	106	100	25	25	152.5	163.5
HP 1744	22.7	29.3	78	72	106	100	28	28	143.5	147.6
DL 788-2	22.2	22.9	77	71	105	100	28	28	157.7	148.7
WR 251	20.9	21.2	71	67	102	94	31	27	120.2	150.3
WR 544	25.5	25.7	71	67	102	94	31	27	128.7	157.0
Raj 3765	22.3	28.4	78	75	107	99	29	24	139.4	187.9
PBW 373	20.8	24.2	83	75	107	100	24	24	145.1	167.1
CD at 5 %	5.11	4.9	2.4	0.6	1.7	0.3	2	0.7	27.1	15.3

followed closely by DL 788-2 (42.16 q/ha) and Raj 3765 (42.05 q/ha). The lowest yield was in UP 2425 (37.37 q/ha). Harvest index ranged from 0.342 to 0.432 and 1,000-kernel weight 34.80 to 50.27 g. The highest mean for grain-filling period (29 days) was recorded in genotype WR 251 and WR 544 due to early anthesis (69 days) whereas lowest grain filling period (24 days) was recorded in cultivar PBW 373 because of delayed anthesis (79 days). From the two-year mean, the maximum grain production rate was observed in Raj 3765 (163.65 kg/ha/day) followed by HD 2643 (158 kg/ha/day) the lowest was in UP 2425 (133.40 kg/ha/day). Under late sowning conditions, cultivars are more sensitive to temperature stress during grain filling, and the critical temperatures required at a specific stage for effective screening can not be repeated in the field (Chatrath at al. 2008).

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Evaluating molecular markers associated with preharvest sprouting resistance in wheat.

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Preharvest sprouting (PHS) refers to the precocious germination of grain in the spike prior to harvest as a result of moist weather conditions at harvest time. The wheat crop grown in the northeastern and far-eastern states of India (West Bengal, Assam, and other eastern hill states) is prone to PHS losses due to pre-monsoon rains and high humidity around maturity. Resistance to PHS is based on seed dormancy, i.e., the ability of the physiologically mature seed to withstand sprouting under conditions otherwise favorable for germination. PHS in wheat represents a major constraint for consistent production of high-quality grain because it causes downgrading of grain, severely limits end-use applications for wheat flour, and results in substantial economic losses to farmers and food processors. A large number of QTL have

been reported and screening of diverse genotypes with the molecular markers associated with PHS resistance will help to identify diverse sources of PHS resistance. In view of this, a set of 216 wheat genotypes was phenotyped for PHS resistance and screened with two markers associated with QTL for PHS resistance on chromosomes 4A and 3B.

Phenotyping for PHS resistance. A set of 216 wheat genotypes was phenotyped for PHS resistance based on germination index (GI). A majority of the genotypes were found susceptible to PHS based on GI. Only 7.8% of the genotypes were resistant to PHS (Table 3). As expected, none of the Indian wheat cultivars were resistant, and only five germ plasm entries were resistant to PHS. However, 22% of the genotypes from the High Rainfall Wheat Yield Trial (HRWYT) and the High Rainfall Wheat Screening Nursery (HRWSN) were resistant and, thus, have potential as donor lines for improving PHS tolerance in future wheat genotypes targeted for cultivation in the regions that are otherwise favorable for PHS. The results also indicated that GI information supports assumption of susceptibility of Indian material as no selection pressure was exerted for this trait. Only one genotype in the hybridization block was found to be resistant to PHS.

Table 3. Germination index of wheat genotypes phenotyped for resistance to preharvest sprouting in various trials in India.

Entries	No. of genotypes	Germination index			
		0.00–0.25	0.26-0.50	0.51–0.75	0.75–1.00
High Rainfall Wheat Yield Trial	23	6	3	8	6
High Rainfall Wheat Screening Nursery	27	5	13	5	4
Indian cultivars	17	—	—	—	17
Germ plasm lines	88	5	7	11	65
Hybridization block	61	1	1	3	56
Total	216	17	24	27	148

Genotyping with markers associated with PHS resistance. Using diverse mapping populations in bread wheat, all chromosomes have been reported to carry QTL/genes for PHS or dormancy. These large numbers of QTL suggest a complex trait controlled by numerous genes that are influenced by environmental conditions and genetic background. However, homoeologous chromosome group 3 and chromosome 4A carry major loci for PHS resistance, which weere revealed in several earlier studies. In the present study, the genotypes were screened with two molecular markers associated with QTL for PHS resistance on chromosome 4A and 3B. One marker, *DuPw004* was mapped in the QTL region on chromosome 4A (Singh et al. 2010) and other marker, *Vp-1B3*, was derived from the vivipary gene on chromosome 3B (Yang et al. 2007). Ninety-nine genotypes amplified the PCR band associated with PHS resistance with *DuPw004*, and the remaining 117 genotypes amplified the PCR band associated with PHS susceptibility. The *Vp-1B3* marker was used in 67 genotypes and amplified three different alleles; 58 genotypes amplified the allele associated with PHS susceptibility.

Eleven out of 17 genotypes having a GI range of 0–0.25 amplified the PCR band with marker *DuPw004* associated with PHS resistance (Fig. 1), whereas, seven out of nine genotypes with a GI range of 0–0.50 amplified the PCR

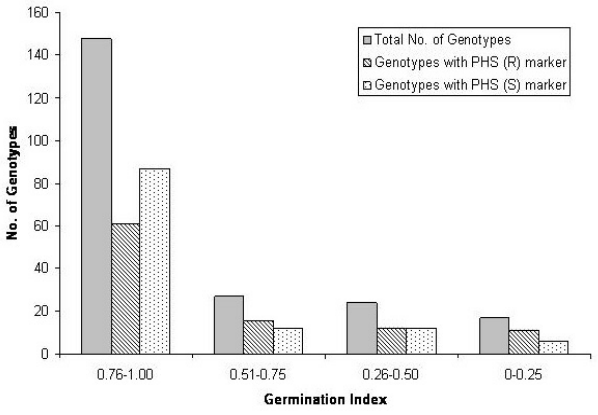

Fig 1. Association between germination index and marker *DuPw004*.

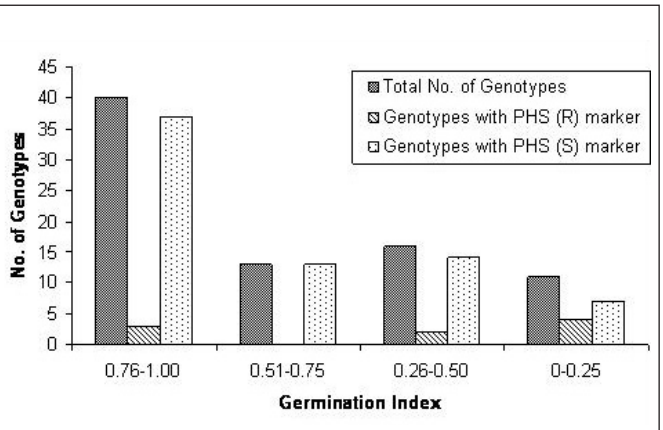

Fig 2. Association between germination index and marker *Vp-1B3*.

band with marker *Vp-1B3* associated with PHS resistance (Fig. 2, p. 68). These results give an indication of the resistance associated with these markers.

One interesting observation to come out of this study is that the combination of *DuPw004* and *Vp-1B3* markers associated with resistance showed a GI range of 0–0.25. However, the results will be confirmed when more resistant type genotypes are included. Three genotypes, lines 203 (FOW1) and 214 (CHIL/CHUM18//ARA90) from the 15th HRWYT and line 2070 (CHAPIO/FRET2) from the 18th HRWSN 2070, showed this combination.

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Gene action for quantitative traits in bread wheat.

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Abstract. An experiment during rabi 2005–06 and 2006–07 estimated gene action in bread wheat. Seven wheat cultivars (DBW 14, HUW 468, HUW 533, GW 273, PBW 443, PBW 502, and DL788-2) were used for five straight crosses (DBW14/HUW468, DL788-2/PBW502, DBW14/HUW533, GW273/HUW468, and PBW443/HUW533) and six generations P_1, P_2, F_1, F_2, BC_1, and BC_2 were obatined for each cross. A generation mean analysis was made on days-to-75% heading, days-to-maturity, plant height, effective tillers/plant, spike length, spikelets/spike, grains/spike, grain weight/spike, seeds/plant, 1,000-kernel weight, grain yield/plant, and at three different stages during Helminthosporium leaf blight infection (dough, soft dough, and hard dough). A majority most of the exhibited significant additive and dominance gene effects in scaling test on different characters in all the crosses indicating the presence of nonallelic interaction.

Joint scaling tests revealed that the simple additive-dominance model was adequate for spike length, grain weight/spike in all five crosses; for days-to-75% heading, days-to-maturity in cross PBW443/HUW533; for spikelets/spike in crosses DBW14/HUW468, DBW14/HUW533, and GW273/HUW468; and for 1,000-kernel weight and grain yield/plant in cross 'PBW443/HUW533'. For the remaining crosses, the model was not adequate. The six-parameter model was used for those crosses where simple additive-dominance model was inadequate. The classification of epistasis revealed the predominance of duplicate type of epistasis in a majority of the crosses for all the traits, whereas complementary type epistasis was present for seeds/plant in crosses 'DBW14/HUW468', 'DBW14/HUW533', and 'PBW443/HUW533'; days-to-maturity and effective tillers/plant in cross 'DBW14/HUW468'; spikelets/spike in cross 'DL788-2/PBW502'; and grains/spike and HLB-3 in cross 'DBW14/HUW533'. Based on the above findings, we concluded that attributes such as spike length and grain weight/spike are controlled by fixable genes and may be improved by adopting simple selection or any other breeding approach that can exploit additive effects. Attributes such as days-to-75% heading, days-to-maturity, plant height, tillers/plant, effective tillers/plant, and other related traits included in the study were controlled by both additive and nonadditive type of gene effects. Therefore, a breeding plan that can exploit both types of gene effects, such as intermating in early segregating generations followed by selection or reciprocal recurrent selection, might be useful. Heterosis breeding might be a useful tool for improvement of grain yield in wheat because it showed a complementary type of epistasis in most of the crosses in this study.

Introduction. Wheat is one of the main food crops of India and contributes significantly to the central pool. The cultivation of wheat in India started very early during prehistoric times and, thus, the origin of wheat is still a matter of speculation. Wheat research for development of high-yielding cultivars and improving management techniques started in India long ago. A large number of valuable cultivars were bred and released for commercial cultivation. These cultivars were tall and mainly suited to low-input management with low yield potential. However, a turning point in the history

of wheat breeding came during mid 1960s with the introduction of semidwarf, photoinsensitive, high-yielding Mexican wheat breeding material developed at CIMMYT with the guidance of Nobel under the All India Coordinated Wheat Improvement Project. Three genotypes, Lerma Roja, S 308, and Sonara-64, that out yielded the old, tall wheat cultivars were released for general cultivation in major wheat-growing areas of India.

The improvement of quantitative traits through selection depends upon the nature and magnitude of the gene effect involved in the inheritance of that particular trait. Generation mean analysis, a first-degree statistic, is a simple but useful technique for characterizing gene effects for quantitative traits (Hayman 1958; Jinks and Jones 1958; Gamble 1962). Generation mean analysis estimates the epistatic effects. Both additive and nonadditive gene effects have been found to be important in wheat (Paroda and Joshi 1970; Singh and Singh 1992), however, both vary with the materials involved. The greatest merit of generation mean analysis lies in the estimate of epistatic gene effects, additive x additive (i), additive x dominance (j), and dominance x dominance (l), which is the most commonly used design. We have estimated the gene effects for yield and yield components using generation mean analysis.

Material and Methods. Seven diverse cultivars of bread wheat, DBW 14, HUW 468, HUW 533, GW 273, PBW 443, PBW 502, and DL788-2, were used in five cross combinations (DBW14/HUW468, DL788-2/PBW502, DBW14/HUW533, GW273/HUW468, and PBW443/HUW533), each with six basic generations P_1, P_2, F_1, F_2, BC_1, and BC_2. The material of five crosses was evaluated in a randomized block design with three replications in a plot size with 2.5-m rows spaced 23 cm apart with a plant-to-plant distance of 10 cm during rabi season 2006–07 at the Research Farm of Janta Vedic College, Baraut Baghpat. Data were recorded on ten randomly selected competitive plants from each replication of parental lines and 30 plants from each of the F_1, F_2, BC_1, and BC_2 populations for 15 characters (days-to-75% heading, days-to-maturity, plant height, effective tillers/plant, spike length, spikelets/spike, grains/spike, grain weight/spike, seeds/plant, 1,000-kernel weight, grain yield/plant, and at three different stages during Helminthosporium leaf blight infection, i.e., HLB-1 (77–80 d, dough stage), HLB-2 (83–86 d, soft dough stage), and HLB-3 (87–89 d, hard dough stage). Mather's scaling test was used to identify the interacting crosses and a joint scaling test was used to test the adequacy of a simple additive dominance model (m, d, h; Mather 1949; Cavalla 1952). The genetic effects in the interacting crosses were estimated using a six-parameter model (m, d, h, i, j, l; Hayman 1958).

Results and Discussion. The mean performance for the different characters of each of the five crosses in different generations are given in Table 1 (pp. 71-72). The F_1 and F_2 populations were higher than the respective parents in cross 'DBW14/HUW468' for all the characters except days-to-maturity, 1,000-kernel weight, and all stages of HLB. Similarly, the high mean value of the $F_1$and F_2 populations from their parents was observed in cross 'DL788-2/PBW502' for plant height, effective tillers/plant, spike length, spikelets/spike, seeds/plant, and grain yield/plant. In cross 'DBW14/HUW533', we observed high mean values in the F_1 and F_2 generations for days-to-maturity, plant height, effective tillers/plant, spike length, spikelets/spike, HLB-2, and HLB-3. High performance of the F_1 and F_2 populations were recorded for effective tillers/plant, spike length, and HLB-1 in cross 'GW273/HUW468'. In cross 'PBW443/HUW533', the higher value of the F_1 and F_2 population to their respective parents was observed for spike length and all three stages of HLB score.

The performance of F_2 generation higher than the F_1 generation was observed for days to 75% heading, plant height, effective tillers/plant, spike length, spikelets/spike, grains/spike, seeds/plant, 1,000-kernel weight, grain yield/plant, HLB-2, and HLB-3 in the cross 'DBW14/HUW468'. Cross 'DL788-2/PBW502' had a higher value in the F_2 population than in the F_1 population for plant height, effective tillers/plant, spike length, spikelets/spike, seeds/plant, and all three HLB stage scores. Higher mean values in the F_2 population over their F_1 were observed for days-to-maturity, plant height, grains/spike, grain weight/spike, seeds/plant, grain yield/plant, and all HLB stages in cross 'DBW14/HUW533'. In the cross 'GW 273/HUW 468', days-to-maturity and all three stages of HLB had higher mean values in the F_2 than in the F_1 population, however, in cross 'PBW443/HUW533', the higher mean values were for plant height, spike length, spikelets/spike, grains/spike, grain weight/spike, HLB-1, HLB-2, and HLB-3. These results revealed no inbreeding depression for 'genotype x environment' interactions or epistasic gene effects; the later effects were invariably noted in the present investigation.

The scaling test parameters (A, B, C, and D) from the data on different traits in all the crosses showed at least one parameter that was significantly different from 0, indicating the presence of a nonallelic interaction (Table 2, p. 73). An additive, dominance model in the analysis of data and the presence of nonallelic interaction (epistasis) in all characters in all crosses were observed. A simple, additive-dominance model was found to be adequate for spike length and grain weight/spike in all five crosses (Table 3, p. 74); for days-to-75% heading and days-to-maturity in cross 'PBW443/HUW533'; for effective tillers/plant in crosses 'DBW14/HUW533', 'GW273/HUW468', and 'PBW443/HUW533';

Table 1. Mean performance of different generations for yield and yield components in five cross combinations of bread wheat (G=generation; D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

Cross	G	D75H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S (g)	S/P	TKW (g)	GY/P (g)	HLB-1	HLB-2	HLB-3
DBW14/HUW 468 (I)	P_1	57.00 ±0.58	117.00 ±0.58	79.33 ±2.73	7.33 ±0.88	9.00 ±0.58	18.00 ±1.15	49.33 ±2.03	1.98 ±0.14	351.00 ±4.10	41.00 ±1.15	13.66 ±0.04	12.33 ±0.33	30.33 ±3.67	45.33 ±0.33
	P_2	80.00 ±20.8	123.00 ±0.58	85.00 ±0.58	7.33 ±0.33	10.00 ±0.58	16.00 ±1.15	44.33 ±1.86	1.71 ±0.05	310.33 ±8.35	39.00 ±2.08	11.60 ±0.50	12.00 ±0.58	27.00 ±4.00	56.33 ±0.33
	F_1	78.67 ±0.88	125.00 ±0.58	83.00 ±1.15	10.00 ±0.58	11.00 ±0.58	19.33 ±1.76	45.00 ±1.15	1.26 ±0.05	447.33 ±4.91	28.00 ±0.58	12.58 ±0.06	12.33 ± 0.33	23.33 ±0.33	38.00 ±3.51
	F_2	81.67 ±1.86	120.67 ±0.88	89.00 ±3.06	11.67 ±0.88	11.33 ±0.67	19.67 ±0.88	47.67 ±0.33	1.24 ±0.03	565.33 ±37.12	31.00 ±0.58	14.19 ±0.53	12.33 ±0.33	45.33 ±0.33	56.33 ±0.33
	BC_1	63.67 ±1.76	116.00 ±1.00	80.67 ±1.33	11.00 ±0.58	11.00 ±0.58	21.00 ±0.58	48.33 ±0.88	1.06 ±0.03	546.00 ±34.43	32.00 ±0.58	13.92 ±0.26	8.67 ±3.33	19.67 ±3.33	38.00 ±3.51
	BC_2	81.33 ±1.76	126.33 ±1.45	82.33 ±0.88	9.67 ±0.33	10.67 ±0.88	20.33 ±0.33	52.67 ±1.76	1.39 ±0.14	519.00 ±29.48	32.33 ±0.88	17.59 ±0.30	5.33 ±3.33	13.00 ±0.00	42.00 ±3.51
DL788-2/PBW 502 (II)	P_1	79.00 ±0.58	124.33 ±1.76	78.33 ±1.45	9.67 ±0.67	9.00 ±0.58	18.00 ±1.15	43.00 ±2.02	1.34 ±0.11	422.67 ±6.17	32.67 ±0.33	13.60 ±0.19	19.33 ±3.67	34.67 ±0.33	59.67 ±3.67
	P_2	84.00 ±0.58	125.00 ±0.58	82.67 ±2.33	9.33 ±0.33	9.00 ±0.58	18.00 ±115	41.00 ±1.53	1.46 ±0.06	386.00 ±6.51	36.00 ±0.58	13.62 ±0.30	5.67 ±3.67	26.33 ±3.84	49.00 ±7.51
	F_1	80.67 ±1.20	128.00 ±1.00	81.00 ±3.21	11.67 ±0.33	11.00 ±0.58	18.00 ±1.15	41.33 ±1.20	1.27 ±0.07	472.33 ±2.40	31.33 ±0.88	14.73 ±0.35	12.33 ±0.33	27.33 ±3.84	52.67 ±3.33
	F_2	76.00 ±0.58	125.00 ±0.58	94.00 ±1.53	14.00 ±0.58	12.00 ±0.58	22.00 ±1.15	35.00 ±1.15	1.00 ±0.01	488.33 ±3.53	28.67 ±0.67	13.70 ±0.12	16.00 ±3.51	56.67 ±6.06	74.00 ±4.00
	BC_1	78.67 ±0.88	131.00 ±0.58	84.00 ±1.53	11.00 ±0.58	10.00 ±0.58	20.00 ±0.58	43.00 ±0.58	1.08 ±0.04	455.33 ±8.84	30.67 ±0.88	11.33 ±0.12	2.00 ±3.51	23.33 ±0.33	53.00 ±7.00
	BC_2	86.33 ± 1.86	126.67 ±0.88	88.00 ±3.61	9.00 ±0.58	11.00 ±0.58	21.33 ±0.67	50.00 ±3.21	1.26 ±0.07	467.20 ±19.61	31.67 ±0.88	11.87 ±0.74	2.00 ±3.52	23.00 ±0.58	45.67 ±6.06
DBW14/HUW 533 (III)	P_1	58.67 ±0.88	117.67 ±0.88	82.00 ±1.73	10.67 ±0.33	9.67 ±0.33	18.33 ±1.45	44.33 ±0.88	1.72 ±0.01	467.33 ±11.62	38.67 ±0.33	18.43 ±0.36	12.00 ±3.51	20.00 ±3.51	34.67 ±6.39
	P_2	84.00 ±1.15	124.67 ±1.20	105.67 ±1.45	10.00 ±0.58	8.00 ±0.58	17.33 ±1.76	40.67 ±0.33	1.24 ±0.09	404.67 ±21.42	29.67 ±0.69	11.34 ±0.88	9.00 ±0.27	27.00 ±3.51	45.67 ±0.33
	F_1	78.33 ±0.88	127.33 ±0.88	99.00 ±1.15	12.00 ±0.58	11.00 ±0.58	20.00 ±1.15	36.67 ±1.20	0.95 ±0.03	428.00 ±6.56	31.67 ±0.33	11.15 ±0.19	5.00 ±3.51	16.33 ±3.33	38.67 ±3.18
	F_2	76.00 ±0.58	128.33 ±0.88	111.33 ±1.20	11.67 ±0.33	10.00 ±0.58	20.00 ±1.15	41.67 ±1.45	1.06 ±0.03	468.33 ±9.35	31.67 ±0.33	11.74 ±0.34	5.33 ±3.33	34.67 ±0.33	56.67 ±0.33
	BC_1	77.33 ±0.88	126.33 ±0.88	95.67 ±1.86	11.00 ±0.58	10.00 ±0.58	20.00 ±0.58	43.67 ±2.40	1.05 ±0.06	464.33 ±8.41	31.00 ±1.00	11.70 ±0.30	1.67 ±0.33	16.00 ±3.00	56.00 ±0.58
	BC_2	87.00 ±0.58	126.00 ±0.58	93.00 ±1.53	12.33 ±1.20	10.00 ±0.33	20.00 ±0.58	38.67 ±4.26	1.07 ±0.12	466.33 ±5.36	32.67 ±1.20	12.36 ±0.10	5.33 ±3.33	16.33 ±3.33	42.67 ±3.84

Table 1 (continued). Mean performance of different generations for yield and yield components in five cross combinations of bread wheat (G=generation; D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

Cross	G	D75H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S (g)	S/P	TKW (g)	GY/P (g)	HLB-1	HLB-2	HLB-3
GW273/HUW 468 (IV)	P_1	80.00 ±2.52	127.33 ±0.88	89.67 ±2.33	9.00 ±0.58	8.33 ±0.88	20.00 ±1.15	38.33 ±0.67	1.05 ±0.06	339.67 ±21.15	27.67 ±1.20	8.91 ±0.21	9.00 ±7.00	30.33 ±7.33	56.33 ±0.67
	P_2	81.33 ±0.88	124.67 ±0.33	86.67 ±0.88	10.33 ±0.33	10.67 ±0.33	17.33 ±0.67	45.00 ±1.53	1.54 ±0.05	464.00 ±4.04	33.67 ±0.33	15.36 ±0.05	5.00 ±3.51	15.67 ±3.67	42.67 ±3.84
	F_1	81.33 ±0.88	124.00 ±0.58	91.00 ±0.58	12.00 ±0.58	12.00 ±0.58	22.00 ±1.15	39.00 ±0.58	1.14 ±0.33	470.33 ±31.42	29.33 ±0.33	13.74 ±0.68	12.33 ±0.33	27.33 ±3.33	56.33 ±0.33
	F_2	76.00 ±0.58	125.33 ±1.20	89.33 ±1.20	11.33 ±0.67	10.67 ±0.33	20.00 ±1.15	38.00 ±1.15	1.08 ±0.03	430.67 ±20.85	29.00 ±0.33	12.17 ±0.40	20.33 ±3.67	49.67 ±3.71	70.33 ±2.85
	BC_1	82.00 ±0.58	126.67 ±0.88	86.67 ±0.88	10.33 ±0.33	11.00 ±0.58	22.00 ±1.15	38.00 ±2.31	0.91 ±0.05	405.00 ±7.51	30.00 ±1.15	9.69 ±0.11	8.33 ±3.67	20.00 ±3.51	56.67 ±6.06
	BC_2	84.33 ±1.20	128.00 ±0.58	85.33 ±1.20	10.00 ±0.58	12.00 ±0.58	22.00 ±1.15	35.33 ±1.76	1.19 ±0.09	338.00 ±3.51	33.67 ±0.88	11.31 ±0.14	2.00 ±0.00	20.00 ±3.51	52.33 ±3.67
PBW443/HUW 533 (V)	P_1	83.00 ±1.53	125.13 ±0.47	79.67 ±1.20	9.67 ±0.33	7.67 ±0.33	17.33 ±1.76	35.33 ±2.60	1.10 ±0.08	349.00 ±16.48	31.00 ±1.00	10.16 ±0.18	12.33 ±6.06	30.67 ±7.17	59.33 ±7.17
	P_2	84.67 ±1.45	125.80 ±1.17	106.00 ±1.53	11.00 ±0.58	8.67 ±0.88	18.00 ±1.15	40.33 ±0.67	1.15 ±0.01	442.33 ±14.50	28.67 ±0.33	12.24 ±0.22	1.33 ±0.33	15.67 ±3.67	45.67 ±6.06
	F_1	84.67 ±0.88	126.20 ±0.81	81.00 ±1.15	10.33 ±0.67	10.67 ±0.88	18.00 ±1.15	36.00 ±2.00	1.05 ±0.07	386.33 ±3.53	29.00 ±0.58	10.89 ±0.11	5.33 ±3.33	34.33 ±0.33	52.67 ±7.17
	F_2	82.33 ±0.88	125.73 ±0.87	94.33 ±2.91	10.00 ±0.58	11.00 ±0.58	20.00 ±1.15	37.00 ±2.08	1.07 ±0.08	361.33 ±12.88	29.33 ±1.33	10.19 ±0.18	16.67 ±3.67	53.33 ±3.67	63.33 ±3.18
	BC_1	83.00 ±1.53	125.20 ±0.53	68.67 ±0.67	10.67 ±0.88	10.00 ±0.58	18.00 ±1.15	31.33 ±1.20	0.97 ±0.04	341.33 ±22.92	30.33 ±0.33	10.18 ±0.64	8.67 ±3.33	37.67 ±7.33	59.67 ±3.67
	BC_2	86.67 ±0.88	125.47 ±0.87	105.33 ±0.88	12.33 ±0.87	10.67 ±0.88	16.00 ±1.15	34.33 ±1.45	0.99 ±0.03	408.00 ±13.11	29.33 ±0.33	11.69 ±0.45	1.67 ±0.33	23.33 ±0.33	49.33 ±3.33

for spikelets/spike in crosses 'DBW14/HUW468', 'DBW14/HUW533', and 'GW273/HUW468'; for 1,000-kernel weight and grain yield/plant in cross 'PBW443/HUW533' (Singh et al. 1998; Dhillon et al. 2002; Shekhawat et al. 2006). The Chi-square (c^2) value was significant for rest of the characters and indicated the complexity of the genetic control of these traits in bread wheat, which may be attributed to epistasis between interacting genes in bread wheat (Singh et al. 1984; Simon et al. 1994; Mostafavi et al. 2005). Differences among the results may be due to differences in the genetic backgrounds. We emphasize that the inferences drawn from the generation mean analysis in crops were specific to the population under study and can not be correlated to other crops.

A six-parameter model was applied to all traits in all crosses (Mohammad et.al. 1991). The m, d, and h components also were estimates that revealed that additive (d) and dominance (h) both components were significant in all five crosses for seeds/plant. For days-to-75% heading in cross 'DBW14/HUW468' and 'DBW14/HUW533'; for days-to- maturity in cross 'DBW14/HUW533'; for plant height in all the crosses except 'DBW14/HUW468'; for grains/spike in crosses 'DBW14/HUW533', 'GW273/HUW468', and 'PBW443/HUW533'; for 1,000-kernel weight in crosses 'DL788-2/PBW502' and 'DBW14/HUW533'; for grain yield/plant in cross 'DBW14/HUW533'; for all the three stages of HLB in crosses 'DBW14/HUW533' and

Table 2. Estimation of scaling tests for testing the adequacy of additive-dominance model for different traits in five crosses of wheat (P=scaling test parameters (A, B, C, and D); D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

Cross	P	D75%H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S	S/P	TKW	GY/P (g)	HLB-1	HLB-2	HLB-3
DBW14/HUW 468 (I)	A	-8.00* ±3.68	-10.00** ±2.20	-1.00 ±3.98	4.66** ±1.56	2.00 ±1.41	4.66 ±2.40	2.33 ±2.92	-1.12** ±0.16	293.33** ±69.15	-5.00** ±1.73	1.59** ±0.53	-7.33 ±6.68	-14.33 ±7.61	-7.33 ±7.85
	B	4.00 ±4.18	4.67 ±3.01	-3.33 ±2.18	2.00* ±0.94	0.33 ±1.94	5.33* ±2.21	16.00** ±4.14	-0.20 ±0.29	280.33** ±59.75	-2.33 ±2.78	10.99** ±0.78	-13.66* ±6.69	-24.33** ±4.01	-10.33 ±7.85
	C	32.33** ±7.93	-7.33 ±3.80	25.67* ±12.74	12.00** ±3.82	4.33 ±3.01	6.00 ±5.24	7.00 ±3.82	-1.24** ±0.21	704.99** ±149.10	-12.00** ±3.51	6.35** ±2.17	0.33 ±1.63	77.33** ±5.62	47.66** ±7.16
	D	18.33** ±4.47	-1.00 ±2.49	15.00* ±6.31	2.66 ±1.88	1.00 ±1.69	-2.00 ±1.88	-5.66** ±2.08	0.04 ±0.15	65.66 ±86.98	-2.33 ±1.56	-3.12** ±1.13	10.66* ±4.76	58.00** ±3.39	32.66** ±5.01
DL788-2/ PBW 502 (II)	A	-2.33 ±2.21	9.66** ±2.33	8.66 ±4.66	0.66 ±1.37	0.00 ±0.00	4.00* ±1.63	1.66 ±2.62	-0.45** ±0.15	15.66 ±18.87	-2.66 ±2.00	-5.67** ±0.46	-21.00* ±7.61	-15.33** ±3.91	-6.33 ±14.85
	B	8.00* ±3.94	0.33 ±2.10	12.33 ±8.23	-3.00* ±1.24	2.00 ±1.41	6.66** ±2.10	17.66* ±6.71	-0.21 ±0.16	76.06 ±39.82	-4.00* ±1.97	-4.62** ±1.54	-14.00** ±3.68	-7.66 ±5.43	-10.33 ±14.64
	C	-20.33** ±3.43	-5.33 ±3.57	53.00** ±9.28	13.66** ±2.51	8.00** ±2.70	16.00** ±5.41	-26.66** ±5.79	-1.32** ±0.19	200.00** ±17.39	-16.66** ±3.21	-1.90* ±0.92	14.33 ±14.98	111.00** ±25.73	82.00** ±19.24
	D	-13.00** ±2.35	-7.66** ±1.56	16.00** ±4.96	8.00** ±1.41	3.00* ±1.41	2.66 ±2.40	-23.00** ±4.00	-0.32** ±0.08	54.13* ±22.63	-5.00** ±1.82	4.19** ±0.78	24.66** ±7.77	67.00** ±12.13	49.33** ±12.23
DBW14/HUW533 (III)	A	17.66** ±2.16	7.66** ±2.16	10.33* ±4.25	-0.66 ±1.33	0.66 ±1.33	1.66 ±2.18	6.33 ±5.03	6.33 ±5.03	33.33 ±21.47	-8.33** ±2.05	-6.18** ±0.72	-6.67 ±5.01	-4.33 ±7.71	38.67* ±7.13
	B	11.66** ±1.85	0.00 ±0.00	-18.66** ±3.57	2.66 ±2.53	1.00 ±0.81	2.66 ±2.40	0.00 ±0.00	0.00 ±8.60	100.00** ±24.83	4.00 ±2.58	2.23** ±0.39	-3.33 ±8.31	-10.66 ±8.23	1.00 ±8.32
	C	4.66 ±3.24	16.33** ±4.21	59.66** ±5.79	2.00 ±1.88	0.33 ±2.66	4.33 ±5.64	8.33 ±6.35	8.33 ±6.35	145.33** ±46.52	-5.00* ±1.76	-5.11** ±1.46	-2.67 ±15.86	59.00** ±8.41	69.00** ±9.11
	D	-12.33** ±1.56	4.33* ±2.05	34.00** ±3.39	0.00 ±1.49	0.00 ±1.29	0.00 ±2.44	1.00 ±5.68	1.00 ±5.68	6.00 ±21.19	-0.33 ±1.69	-0.58 ±0.74	3.67 ±7.46	37.00** ±4.53	14.66 ±3.90
GW273/HUW468 (IV)	A	2.66 ±2.90	2.00 ±2.05	-7.33* ±2.98	-0.33 ±1.05	1.66 ±1.56	2.00 ±2.82	-1.33 ±4.70	6.33 ±5.03	33.33 ±21.47	-8.33** ±2.05	-6.18** ±0.72	-6.67 ±5.01	-4.33 ±7.71	38.67* ±7.13
	B	6.00* ±2.70	7.33** ±1.33	-7.00* ±2.62	-2.33 ±1.33	1.33 ±1.33	4.66 ±2.66	-13.33** ±3.88	0.00 ±8.60	100.00** ±24.83	4.00 ±2.58	2.23** ±0.39	-3.33 ±8.31	-10.66 ±8.23	1.00 ±8.32
	C	-20.00** ±3.94	1.33 ±5.03	-1.00 ±5.53	2.00 ±2.98	-0.33 ±2.00	-1.33 ±5.33	-9.33 ±5.04	8.33 ±6.35	145.33** ±46.52	-5.00* ±1.76	-5.11** ±1.46	-2.67 ±15.86	59.00** ±8.41	69.00** ±9.11
	D	-14.33** ±1.76	-4.00 ±2.62	6.66* ±2.82	2.33 ±1.49	-1.66 ±1.05	-4.00 ±2.82	2.66 ±3.71	1.00 ±5.68	6.00 ±21.19	-0.33 ±1.69	-0.58 ±0.74	3.67 ±7.46	37.00** ±4.53	14.66 ±3.90
PBW443/HUW533 (V)	A	-1.66 ±3.52	-0.93 ±1.41	-23.33** ±2.13	1.33 ±1.91	1.66 ±1.49	0.66 ±3.12	-8.66* ±4.06	-0.21 ±0.14	-53.00 ±48.84	0.67 ±1.33	-0.70 ±1.29	-0.33 ±9.60	10.33 ±16.32	7.33 ±12.51
	B	4.00 ±2.44	-1.06 ±2.24	23.66** ±2.60	3.33 ±1.97	2.00 ±2.16	-4.00 ±2.82	-7.66* ±3.59	-0.21 ±0.10	-12.67 ±30.17	1.00 ±0.94	0.24 ±0.92	-3.33 ±3.41	-3.33 ±3.74	0.33 ±11.51
	C	-7.66 ±4.47	-0.40 ±4.02	29.66* ±12.00	-1.33 ±2.74	6.33* ±3.05	8.66 ±5.57	0.33 ±9.62	-0.07 ±0.37	-119.00* ±56.42	-0.33 ±5.55	-3.43** ±0.80	42.33* ±17.21	98.33** ±16.74	43.00* ±21.34
	D	-5.00* ±2.49	0.80 ±2.00	14.66* ±5.91	-3.00 ±1.69	1.33 ±1.56	6.00* ±2.82	8.33 ±4.57	0.17 ±0.17	-26.67 ±36.88	-1.00 ±2.70	-1.49 ±0.85	23.00* ±8.06	45.67** ±10.37	17.67* ±8.06

Table 3. Estimation of adequacy for simple additive-dominance model in different traits of five crosses of wheat (P=parameter; D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

HLB-3Cross	P	D75%H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S (g)	S/P	TKW	GY/P (g)	HLB_1	HLB-2	HLB-3
DBW14/HUW 468 (I)	m	69.19** ±0.64	119.47** ±0.64	82.66** ±0.64	8.07** ±0.64	9.76** ±0.64	17.76* ±0.64	48.11** ±0.64	1.72** ±0.64	385.31** ±0.64	39.21** ±0.64	13.55** ±0.64	10.94** ±0.64	28.66** ±0.64	51.19** ±0.64
	d	-12.73** ±0.63	-4.46 ±0.63	-2.60** ±0.63	0.26 ±0.63	-0.33 ±0.63	0.93 ±0.63	1.13 ±0.63	0.04 ±0.63	21.80** ±0.63	0.73 ±0.63	0.09 ±0.63	0.79 0.63	2.66** ±0.63	-5.20** ±0.63
	h	10.86** ±1.18	4.47** ±1.18	1.33 ±1.18	3.41** ±1.18	1.76 ±1.18	3.09* ±1.18	-0.54 ±1.18	-0.69 ±1.18	170.98** ±1.19	-12.78** ±1.19	0.88 ±1.18	-1.05 ±1.18	-5.33** ±1.19	-12.47** ±1.18
	c^2	76.720**	24.854**	40.877**	8.188*	**1.238**	**7.338**	42.723**	**0.232**	34,374.200**	8.590*	20.198**	39.994**	570.667**	180.243**
DL788-2/PBW 502 (II)	m	81.23** ±0.64	125.09** ±0.64	83.29** ±0.64	9.76** ±0.64	9.35** ±0.64	19.09** ±0.64	42.35** ±0.64	1.32* ±0.64	415.61** ±0.64	33.45** ±0.64	12.95** ± 0.64	10.86** ±0.64	32.41** ±0.64	55.76** ±0.64
	d	-3.53** ±0.63	0.60 ±0.63	-2.53** ±0.63	0.53 ±0.63	-0.20 ±0.63	-0.20 ±0.63	-0.60 ±0.63	0.085 ±0.63	12.29** ±0.63	-1.53* ±0.63	-0.114 ±0.63	6.13** ±0.63	3.40** ±0.63	5.73** ±0.63
	h	-1.09 ±1.18	3.76** ±1.18	3.29** ±1.18	2.43* ±1.18	2.35 ±1.18	1.09 ±1.18	-0.31 ±1.18	-0.21 ±1.19	79.27** ±1.18	-3.88** ±1.19	0.458 ±1.18	-1.80 ±1.19	-1.25 ±1.18	-0.23 ±1.18
	c^2	39.638**	20.616**	132.491**	12.805*	**3.311**	15.560*	115.178**	**0.093**	2,294.853**	13.167*	8.000*	136.687**	795.466**	430.449**
DBW14/HUW533 (III)	m	73.19** ±0.64	122.09** ±0.64	95.09** ±0.64	10.50** ±0.64	8.86** ±0.64	18.21** ±0.64	43.11** ±0.64	1.42** ±0.64	448.11** ±0.64	33.76** ±0.64	14.50** ±0.64	6.33** ±0.64	24.35** ±0.64	44.52** ±0.64
	d	-12.06** ±0.63	-2.73** ±0.63	-8.93** ±0.63	0.019 ±0.63	0.66 ±0.63	0.40 ±0.63	2.46** ±0.63	0.18 ±0.63	24.66** ±0.63	3.26** ±0.63	2.70** ±0.63	-2.33** ±0.63	-2.86** ±0.62	-1.73** ±0.63
	h	8.86** ±1.18	7.09** ±1.18	6.43** ±1.18	1.84 ±1.18	2.19 ±1.18	2.54* ±1.18	-5.21** ±1.18	-0.59 ±1.18	4.117** ±1.19	-2.90** ±1.19	-4.12** ±1.20	-2.67** ±1.18	-6.31** ±1.120	2.86** ±1.19
	c^2	68.276**	18.838**	294.894**	**1.464**	**0.287**	**1.756**	8.501*	**0.061**	2,114.602**	17.060**	8.794*	8.388*	240.422**	393.443**
GW273/HUW468 (IV)	m	80.58** ±0.64	126.58** ±0.64	87.29** ±0.64	9.56** ±0.64	9.66** ±0.64	19.01** ±0.64	40.52** ±0.64	1.23* ±0.64	385.99** ±0.64	30.98** ±0.64	11.46** ±0.64	7.16** ±0.65	24.67** ±0.64	51.92** ±0.64
	d	-1.00* ±0.63	0.80 ±0.63	1.46* ±0.63	-0.46 ±0.63	-1.13* ±0.63	1.06* ±0.63	-2.13** ±0.63	-0.23 ±0.63	-36.33** ±0.63	-3.13** ±0.63	-2.90** ±0.63	2.86** ±0.62	5.86** ±0.63	6.33** ±0.63
	h	0.58 ±1.20	-1.41 ±1.19	1.96* ±1.19	2.23 ±1.20	2.66** ±1.18	3.68** ±1.19	-3.80** ±1.19	-0.19 ±1.19	52.67** ±1.19	-1.02 ±1.20	0.94 ±1.18	5.52** ±1.20	6.00** ±1.19	9.25** ±1.20
	c^2	35.421**	9.432*	16.047**	**1.416**	**0.788**	**4.789**	30.243**	**0.034**	11,848.610**	6.645*	7.909*	161.298**	639.733**	236.088**
PBW443/HUW533 (V)	m	83.74** ±0.64	125.34** ±0.64	93.72** ±0.64	10.56** ±0.64	8.56** ±0.64	17.72** ±0.64	36.88** ±0.64	1.09* ±0.64	388.47** ±0.64	29.92** ±0.65	11.07** ±0.64	7.86** ±0.65	26.47** ±0.65	54.21** ±0.65
	d	-1.39* ±0.63	-0.32 ±0.63	-17.86** ±0.63	-0.86 ±0.63	-0.53 ±0.63	0.13 ±0.63	-2.60** ±0.63	-0.025 ±0.63	-50.53** ±0.63	1.13* ±0.63	-1.13* ±0.62	5.80** ±0.63	8.86** ±0.63	7.53** ±0.63
	h	0.74 ±1.18	0.60 ±1.19	-10.94** ±1.18	0.23 ±1.18	2.90** ±1.21	0.39 ±1.19	-2.78** ±1.19	-0.099 ±1.18	-16.86** ±1.18	-0.74 ±1.18	-0.43 ±1.19	-0.47 ±1.18	14.47** ±1.19	1.82* ±1.18
	c^2	7.466	0.298	265.772**	2.527	2.138	8.216*	21.923**	**0.0138**	895.576**	**0.266**	**0.644**	101.076**	489.965**	90.279**

'GW273/HUW468'; and for HLB-2 and HLB-3 in crosses 'DBW14/HUW468' and 'PBW443/HUW533'. Additive (d) components were significant for days-to-75% heading in 'DL788-2/PBW502', 'GW273/HUW468', and 'PBW443/HUW533'; for 1,000-kernel weight in crosses 'GW273/HUW468' and 'PBW443/HUW533'; for grain yield/plant in crosses 'GW273/HUW468' and 'PBW443/HUW533'; for HLB-1, HLB-2, and HLB-3 in cross 'DL788-2/PBW502'; and HLB-1 in cross 'PBW443/HUW533'. Dominance (h) components were important for days-to-maturity and effective tillers/plant in crosses 'DBW14/HUW468' and 'DL788-2/PBW502' and for 1,000-kernel weight in cross 'DBW14/HUW 468'. Both main ef-

fects d and h are important in the inheritance of these traits in wheat (Vimal et al. 1999; Sharma et al. 2003).

The analysis of gene effects revealed that interactions played a major role in the inheritance of grain yield and its related components (Table 4, p. 75-76). Additive gene effects were observed for days-to-75% heading in all the crosses except 'PBW443/HUW533'; for days-to-maturity in crosses 'DBW14/HUW468' and 'DL788-2/PBW502'; for plant height in cross 'PBW443/HUW533'; for effective tillers/plant in crosses 'DBW14/HUW468' and 'DL788-2/PBW502; for grains/spike in crosses 'DBW14/HUW468' and 'DL788-2/PBW502'; and for seeds/plant in crosses 'GW 273/HUW468' and 'PBW443/HUW533'. Dominance effects were significant for days-to-75% heading in all crosses except 'PBW443/HUW533'; for days-to-maturity in cross 'DL788-2/PBW502'; for plant height in all crosses except 'DBW14/HUW468'; for effective tillers/plant in cross 'DL788-2/PBW502'; for spikelets/spike in cross 'PBW443/HUW533'; for grains/spike in crosses 'DBW14/HUW468', 'DL788-2/PBW502', and 'PBW443/HUW533'; for seeds per plant in

Table 4. Estimation of the components of generation mean analysis using six-parameter model of Hayman (1958) for16 traits in five crosses of bread wheat (m = mean effect, d = additive effect, h = dominance effect, i = 'additive x additive' interaction, j = 'additive x dominant' interaction, l = 'dominant x dominant' interaction; * and ** equal significance at 5% and 1%, respectively; D = duplicate and C = complimentary).

Cross/ character	Gene effect						Type of epistasis
	m	d	h	i	j	l	
DBW14/HUW 468 (I)							
Days-to-75% heading	81.66**±1.85	-17.66 **± 2.49	-26.49**±9.05	-36.66**±8.94	-6.16*±2.71	40.99**±12.74	D
Days-to-maturity	120.66**±0.88	-10.33**±1.76	7.00±5.03	2.00±4.98	-7.33**±1.81	3.33±8.01	C
Plant height (cm)	89.00**±3.05	-1.67±1.59	-29.16±12.76	-30.00*±12.63	1.16±2.12	34.33*±14.25	D
Effective tillers/plant	11.67**±0.88	1.33*±0.67	-2.67±3.84	-5.33±3.77	1.33±0.81	-1.33±4.67	C
Grains/spike	47.67**±0.33	-4.33*±1.97	9.49*±4.53	11.33**±4.16	-6.83**±2.40	-29.67**±8.76	D
Seeds/plant	56.53**±37.12	27.00±45.32	-14.83±174.10	-131.33±173.97	6.50±45.56	-442.33**±234.74	C
1,000-kernel weight (gm)	31.00**±0.58	-0.33±1.05	-7.33*±3.39	4.67±3.12	-1.33±1.58	2.67±5.48	D
Grain yield/plant (gm)	14.19**±0.53	-3.67**±0.40	6.19**±2.27	6.24**±2.26	-4.69**±0.47	-18.83**±2.70	D
HLB -1	12.33**±0.33	3.33±4.71	-21.16*±9.53	-21.33*±9.52	3.16±4.72	42.33*±18.92	D
HLB -2	45.33**±0.33	6.67*±3.33	-121.33**±7.32	-116.00**±6.79	4.99±4.29	154.67**±14.47	D
HLB -3	56.33**±0.33	-4.00±4.96	-78.17**±10.62	-65.33**±10.02	1.50±4.97	82.99**±21.12	D
DL788-2/PBW502 (II)							
Days-to-75% heading	76.00**±0.57	-7.67**±2.05	25.17**±4.88	26.00**±4.71	-5.17*±2.09	-31.67**±8.90	D
Days-to-maturity	125.00**±0.58	4.33**±1.05	18.67**±3.41	15.33**±3.12	4.67**±1.40	-25.33**±5.53	D
Plant height (cm)	94.00**±1.52	-4.00±3.91	-31.50**±10.53	-32.00**±9.93	-1.83±4.14	11.00±18.20	D
Effective tillers/plant	14.00**±0.58	2.00*±0.82	-13.83**±2.87	-16.00**±2.82	1.83*±0.89	18.33**±4.12	D
Grains/spike	22.00**±1.15	-1.33±0.67	-5.33±5.01	-5.33±4.81	-1.33±1.05	-5.33±6.03	C
Spikelets/spike	35.00**±1.15	-7.00*±3.26	45.33**±8.18	46.00**±8.00	-8.00**±3.50	-65.33**±14.29	D
Seeds/plant	488.33**±3.52	-11.87±21.51	-40.27±45.56	-108.27*±45.27	-30.19±21.97	16.53±87.78	D
1,000-kernel weight (gm)	28.66**±0.67	-1.00±1.24	7.00±3.76	10.00**±3.65	0.67±1.25	-3.33±5.93	D
Grain yield/plant (gm)	13.69**±0.12	-0.53±0.74	-7.27**±1.61	-8.38**±1.56	-0.52±0.76	18.68**±3.12	D
HLB -1	16.00**±3.51	3.33±3.33	-49.50**±15.76	-49.33**±15.54	-3.50±4.22	84.33**±20.06	D
HLB -2	56.67**±6.06	0.33±0.33	-137.17**±24.64	-134.00**±24.26	-3.83*±1.95	157.00**±25.77	D
HLB -3	74.00**±4.00	7.33±9.26	-100.33**±25.05	-98.67**±24.47	1.99±10.15	115.33**±41.74	D
DBW14/HUW 533 (III)							
Days-to-75% heading	76.00**±0.57	-9.67**±1.05	31.67**±3.32	24.67**±3.12	3.00*±1.28	-54.00**±5.32	D
Days-to-maturity	128.33**±0.88	0.33 ±1.05	-2.50±4.26	-8.67*±4.10	3.83**±1.29	0.99±5.96	D
Plant height (cm)	111.33**±1.20	2.67±2.40	-62.83**±6.98	-68.00**±6.79	14.50**±2.65	76.33**±11.22	D
Grains/spike	41.66**±1.45	5.00±4.88	-7.83±11.44	-2.00±11.37	3.17±4.91	-4.33±20.55	C
Seeds/plant	468.33**±9.35	-2.00±9.97	-20.00**±44.59	-12.00±42.39	-33.33*±15.74	-121.33*±61.30	C
1,000-kernel weight (gm)	31.66**±0.33	-1.67±1.56	-1.83±3.44	0.67±3.39	-6.17**±1.63	3.67±6.49	D
Grain yield/plant (gm)	11.74**±0.34	-0.67*±0.31	-2.59±1.51	1.15±1.48	-4.21**±0.38	2.80±1.93	D
HLB -1	5.33**±3.33	-3.67±3.34	-9.33±15.52	-7.33±14.92	-1.67±4.16	17.33±20.76	D
HLB -2	34.67**±0.33	-0.33±4.48	-81.17**±9.97	-74.00**±9.06	3.16±5.12	89.00**±19.81	D
HLB -3	56.67**±0.33	13.33**±3.84	-30.83**±9.01	-29.33**±7.80	18.83**±5.00	-10.33±17.87	C

crosses 'DBW14/HUW533' and 'GW273/HUW468'; for HLB-1 in all the crosses except 'DBW14/HUW533'; and for HLB-2and HLB-3 in all five crosses.

The digenic interactions 'additive x additive' (i) and 'dominant x dominant' (l) had an important role in controlling the inheritance of yield and its related components. 'Additive x additive', 'additive x dominant', and 'dominant x dominant' interactions were significant for days-to-75% heading in the 'DBW14/HUW468', 'DL788-2/PBW502', and 'DBW14/HUW533' crosses; whereas, 'additive x additive'and 'dominant x dominant' components were significant for days-to-75% heading in the 'GW273/HUW468' cross. The 'dominant x dominant' component was predominant for days-to-75% heading in all crosses except 'PBW443/HUW533'. For days-to-maturity, 'additive x dominant' effects were significant in crosses 'DBW14/HUW468', 'DL788-2/PBW502', and 'DBW14/HUW533'; however, 'additive x additive' effects were more important in crosses 'DL788-2/PBW502' and 'DBW14/HUW533' and a 'dominant x dominant' gene interaction was significant in crosses 'DL788-2/PBW502' and 'GW273/HUW468'. For plant height, all types of gene effects were found significant in cross 'DBW14/HUW533', 'additive x additive' and 'dominant x dominant' effects were noticed in crosses 'DBW14/HUW468' and 'GW273/HUW468', and an 'additive x additive' gene interaction was found significant in cross DL788-2/PBW502 (Amawate et al. 1995). Effective tillers/plant had all types of gene effects were found significant only in cross 'DL788-2/PBW502' and 'dominant x dominant' predominanted in cross 'DL788-2/PBW502'. Spikelets/spike were nonsignificant for all types of gene effect in all the crosses except 'PBW443/HUW533'. For grains/spike, 'additive x additive', 'additive x dominant' and dominant components were significant in crosses 'DBW14/HUW468' and 'DL788-2/PBW502', 'additive x dominant' and 'dominant x dominant' effects were significant in cross 'GW273/HUW468', 'additive x additive' and 'dominant x dominant' components were significant in cross PBW443/HUW533, and a 'dominant x dominant' component was predominant in all other crosses except 'DBW14/HUW533'. All types of epistasis were significant for seeds/plant in cross 'GW273/HUW468' and 'additive x additive' and 'dominant x dominant' components were predominant in crosses 'DBW14/HUW468', 'DBW14/HUW533', and 'GW273/HUW468'. For 1,000-kernel weight, the 'additive x additive' components was significant in crosses 'DL788-2/

Table 4 (continued). Estimation of the components of generation mean analysis using six-parameter model of Hayman (1958) for16 traits in five crosses of bread wheat (m = mean effect, d = additive effect, h = dominance effect, i = 'additive x additive' interaction, j = 'additive x dominant' interaction, l = 'dominant x dominant' interaction; * and ** equal significance at 5% and 1%, respectively; D = duplicate and C = complimentary).

Cross/ character	Gene effect						Type of epistasis
	m	d	h	i	j	l	
GW273/HUW 468 (IV)							
Days-to-75% heading	76.0**±0.58	-2.33*±1.33	29.33**±3.87	28.67**±3.52	-1.67±1.88	-37.33**±6.63	D
Days-to-maturity	125.33**±1.20	-1.33±1.05	5.99±5.30	7.99±5.24	-2.67±1.15	-17.33**±6.56	D
Plant height (cm)	89.33**±1.20	1.33±1.49	-10.50*±5.28	-13.33*±5.65	-0.16±1.94	27.67**±8.13	D
Grains/spike	38.00**±1.15	2.67±2.90	-8.00±7.49	-5.33±7.42	6.00*±3.02	20.00*±12.67	D
Seeds/plant	430.67**±20.85	67.00**±8.28	-168.17**±91.29	-236.67**±85.03		495.00**±111.67	D
1,000-kernel weight (gm)	29.00**±0.33	-3.67**±1.45	10.00**±2.99	11.33**±2.90	-0.67±1.58	-18.67**±5.98	D
Grain yield/plant (gm)	12.16**± 0.40	-1.62**±0.17	-5.06**±1.77	-6.67**±1.64	1.61**±0.20	16.43**±2.21	D
HLB -1	20.33**±3.67	6.33±3.67	-55.33**±16.86	-60.67**±16.39	4.33±5.36	78.67**±22.18	D
HLB -2	49.67**±3.71	0.00±4.96	-114.33**±18.62	-118.67±17.86	-7.33±6.43	139.33**±26.95	D
HLB -3	70.33**±2.84	4.33±7.08	-56.50**±18.29	-63.33**±18.18	-2.50±7.35	57.00*±30.80	D
PBW443/HUW 533 (V)							
Plant height (cm)	94.33**±2.90	-36.67**±1.10	-41.17**±11.92	-29.33**±11.83	-23.50**±1.47	29.00**±12.79	D
Spikelets/spike	20.00**±1.15	2.00±1.63	-11.67*±5.86	-12.00**±5.65	2.33±1.94	15.33*±8.58	D
Grains/spike	37.00**±2.08	-2.99±1.88	-18.50*±9.45	-16.67*±9.14	-0.50±2.31	33.00**±12.22	D
Seeds/plant	361.33**±12.87	-67.66**±26.41	43.83±74.67	53.33±73.77	-20.17±28.59	12.33±119.76	C
HLB -1	16.67**±3.67	7.00*±3.34	-47.50**±16.74	-46.00**±16.12	1.50±4.52	49.67**±21.81	D
HLB -2	53.33**±3.67	14.33*±7.34	-80.17**±21.14	-91.33**±20.75	6.83±8.37	84.33**±33.80	D
HLB -3	63.33**±3.17	10.33*±4.95	-35.16*±18.26	-35.33*±16.12	3.50±6.82	27.68±29.13	D

PBW502' and 'GW273/HUW468' and 'additive x dominant' and 'dominant x dominant' interactions were more important in crosses 'DBW14/HUW533' and 'GW273/HUW468', respectively. Grain yield/plant in crosses 'DBW14/HUW468' and 'GW273/HUW468' had significance for all gene interactions, whereas 'additive x additive' and 'dominant x dominant' components were significant in 'DL788-2/PBW502', and 'additive x dominant' effects were important in all crosses except 'DBW14/HUW533'. For HLB-1 and HLB-2, 'additive x additive' and 'dominant x dominant' were more important in all crosses except 'DBW14/HUW533', which had a nonsignificant interaction, but 'additive x additive' and 'dominant x dominant' effects were significant for HLB-2 in crosses 'DBW14/HUW533' and 'GW273/HUW468', and an 'additive x dominant' effect was significant in cross 'DL788-2/PBW502'. HLB-3 had significant 'additive x additive' and 'dominant x dominant' gene effects in crosses 'DBW14/HUW468', 'DL788-2/PBW502', and 'GW273/HUW468', but only an 'additive x additive' effect were significant in cross 'PBW443/HUW533', and 'additive x additive' and dominant components were important in the 'DBW14/HUW533' cross.

Dominant (h) and 'dominant x dominant' (l), for their negative and positive gene effects, revealed a preponderance of duplicate types of epistasis, which will hinder improvement of populations where dominant-type gene actions also exist; thus, heterosis can not be exploited in such a situation. The complementary type of epistasis, which is more favorable for genotype improvement, was present in cross I for days-to-maturity, effective tillers/plant, and seed/plant; in cross II for spikelets/spike; in cross III for grains/spike, seed/plant, and HLB-3; and in cross V only for seed/plant. Cross IV had duplicate-type gene interactions for all the characters (Yadav et al. 1997). The results suggest that the nature and magnitude of gene effects vary within the different crosses for different characters, necessitating specific breeding strategys need to be adopted for particular crosses to obtain improvement (Kaur et al. 2004). Characters that were predominantly additive gene effects can use simple selection procedures efficiently, however, dominant and epistasic effects for most of the character in some crosses would slow progress. In such a situation, exploiting additive, dominant, and nonadditive gene effects simultaneously would be benificial.

For characteristics that are controlled by fixable genes, simple selection or any other breeding methodology that can exploit additive effects might be adopted. For characteristicss that are controlled by both additive and dominant gene effects, a breeding plan that exploits both gene effects, such as intermating in early segregating generations followed by selection or reciprocal recurrent selection, might be useful for improvment. For characteristics with complementary-type epistasis in crosses, heterosis breeding may be useful. We observed that a generation mean analysis for most of the characteristics conform with those of previous workers (Luthara et al. 1991, 1996; Singh et al. 1998; Ghannadha et al. 1999; Mehla et al. 2000; Satyavart et al. 2000; Shekhawat et al. 2000; Hamada 2003; Sharma et al. 2001, 2002, 2003, 2004).

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Detection of heat shock protein in bread wheat through ELISA.

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Introduction. High temperature stress is an important abiotic factor that reduces drastically wheat yields in the arid and semi-arid tropics. Howard (1924) reported that for every one degree rise of mean temperature over the range of 12.2–27.53°C, the crop yield is reduced by 4%. To overcome the limits created by higher-temperature stress, a major impetus is on the use of suitable screening techniques to identify heat-tolerant genotypes. Under natural conditions, abiotic stress is usually encountered gradually. Plants, therefore, are exposed to a sublethal stress before being subjected to severe stress. Several studies have shown that plants develop the ability to withstand lethal temperatures upon exposure to sublethal temperatures (known as induction stress). This phenomenon has been termed 'acquired thermo-tolerance' (Hahn and Li 1990). During the induction stress, many stress-inducible genes are triggered ,which alters several physiological and biochemical processes relevant for stress tolerance. Heat shock proteins (HSP) have been known to play a role in cell protection, survival, and recovery in several species (Vierling 1991; Nguyen et al. 1992). Mild heat treatment induces a so-called heat shock response leading to the immediate induction of a set of new proteins or the over-expression of already existing HSPs that persist over time at high temperature. The 90-kDa HSPs are the second most predominantly

expressed HSPs after the 70-kDa family. These proteins appear to impart thermotolerance, because mutant cells with an impaired capacity to make HSP 90 are incapable of growing at higher temperatures (Borkovich et al. 1989).

Materials and Methods. Twelve wheat genotypes/cultivars were used for the present investigation (Table 1). The experiment was conducted on two sowing dates, 18 November and 18 December, 2006. Protein extracted from the leaves of plants from both sowing dates were used separately for experimentation. ELISA tests were developed with minor modifications as described initially by Engvall and Pedlman (1971) and later by Clark and Adams (1977). Here, microtitre plates were coated with different concentrations of proteins in coating buffers keeping the volume constant, i.e., 100 μl/well of soluble antigen. The plates were incubated for 1 hr at room temperature and kept overnight at 4°C. Following a standard washing procedure, the plates were washed with antibody dilution buffer. A 100 μl dilution of primary antibody (anti-HSP 90 sera) was added and the plates were incubated for 2 hrs at room temperature. The plates were washed again with antibody dilution buffer three times and a substrate of 1:1,000 times diluted alkaline phosphate conjugated secondary antibody were added to the plates (rabbit anti-goat I_gG-ALP conjugate) and incubated for 2 hrs at room temperature. After washing the plates three times with dilution buffer, 100-μl substrate solutions were added in each well and incubated for 30 min. The reaction was terminated by adding 100 μl of 1.5 M NaOH solution. The absorbance of the plates was taken 405 nm in an ELISA reader.

Table 1. Twelve wheat genotypes and their pedigrees used in the detection of heat-shock proteins.

Genotype	Pedigree
Acc 8528	not available
DBW 14	Raj 3765 / PBW 343
Halna (K 7903)	HD 1982 / K 816
HD 2808	WH 542 / DL 377-8
HI 385 (Mukta)	HYB 633 / Baza // PR / PKD 25
NP 846	NP 760 . RN
PBN 51	BUL 'S' / FLS 'S'
Raj 3765	HD 2402 / VL 639
Raj 4014	DL 802-5 / K 9011
UP 2425	HD 2320 / UP 2263
WH 147	E 4870 / C 303 // 5339 / PV 18
WH 1003	WEAVER / JACANA

Results and Discussion. In timely-sown conditions, we observed that the OD value at 405 nm ranged between 0.05 (Raj 3765 and HD 2808) to 0.42 (NP 846). In late-sown conditions, the OD value at 405 nm ranged between 0.05 (Halna) to 0.61 (NP 846). The OD values of both days of sowing of different genotypes are presented in Fig. 1.

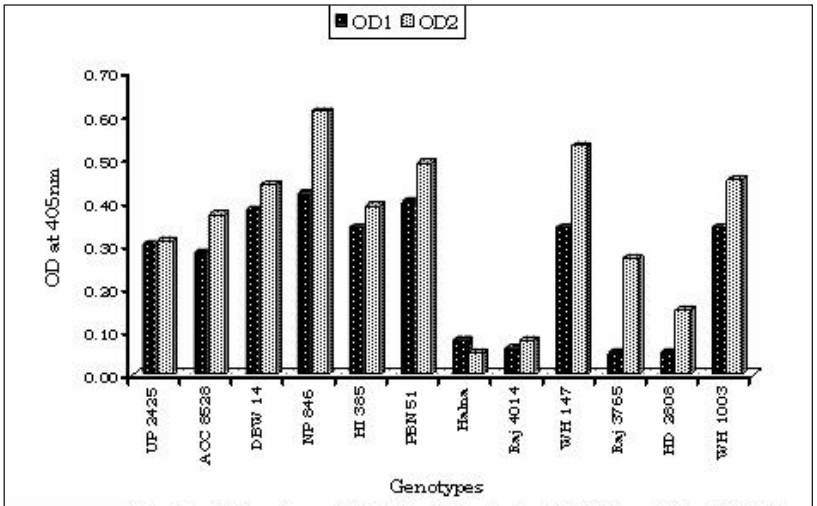

Fig. 1: OD value of ELISA in both D_1 (OD 1) and D_2 (OD 2)

In the ELISA study (which indicates the presence of heat-shock protein), we observed that a majority of the genotypes had high OD values under late-sown conditions compared with the timely sown, and a similar finding was reported by Sharma (2006). Cupina et al. (1979) studied 12 wheat cultivars of varying duration and found that late-maturing types contained more chlorophyll than early cultivars, particularly at heading. This finding indicates that there may be heat-shock protein expressed (HSP 90) in response to heat stress. We found higher ODs for those heat-tolerant genotypes, ACC 8528, DBW 14, NP 846, HI 385, and PBN 51, whereas Raj 4014 had a low OD value and was observed to be heat susceptible. Halna had a very low OD value although it showed heat tolerance on the basis of the heat susceptibility index (result not shown). Because Halna is a heat-tolerant cultivar but matures in a very short period (115 days) in both timely and late-sown conditions, it was not exposed to heat stress, which could be the most plausible explanation of its very low expression of HSP-90 resulting in a very low OD value.

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Performance of brown and black rust resistance genes in some wheat cultivars of central, peninsular, and south India.

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Some of the popular wheat cultivars grown in central, peninsular, and southern India were evaluated for seedling and adult-plant resistance to black and brown rusts. Because the source of rust inoculum for Central and Peninsular India lies mainly in Nilgiri Hills in southern India, the cultivars were tested only with Nilgiri pathotypes. Cultivars were raised as single lines in plastic trays (12 x 5 cm) each accommodating 10 lines (8 seedlings/line). Uredosporic dust of individual pathotypes prevailing in the Nilgiri Hills and maintained artificially at the IARI Regional Station, Wellington, was inoculated on the wet surface of the primary leaves of 7-day-old seedlings of the test cultivars by a uniform rub application from base to tip. Inoculated pots were kept in a fine mist created with a manually operated water sprayer making a free film of water on the leaf surface. The plants were kept in a high humidity atmosphere maintained in glass humidity chambers. After 24 hours, the pots were transferred to benches in the glasshouse. Optimum temperature (20°C for brown and 25°C for black rust) and a light regime of 16:8 hours light:dark cycle maintained in the glass houses permitted full expression of brown and black rust pustules after 12 days. Host–pathogen interactions were recorded by following standard international procedures of Johnston and Mains (1932) in brown rust and Stackman and Levine (1922) in black rust. Cultivars also were sown in an open field environment exposing them to natural rust pathotypes prevailing in Wellington to evaluate adult-plant resistance response. Rust intensities were recorded on these cultivars at growth stage 71 (Zadoks et al. 1974) following the Peterson scale (Peterson et al. 1948) for estimating adult-plant resistance.

Seedling and adult-plant response of cultivars are given in Table 1 (p. 81). In the Central Zone, seven of eight tested cultivars exhibited seedling resistance to all the pathotypes of brown and black rust prevalent in the Nilgiri Hills. These seven cultivars were HI 8498, HI 8381, HI 1544, HI 1531, HI 8627, DL 788-2, and HD 4672 were free of infection from brown and black rusts at the adult stage; their field resistance is robust only if the inoculum in central India originates from the Nilgiri Hills. Only cultivar HI 1500 of central India showed susceptibility but that was only to one race 77-5 (121R63-1) of brown rust. Fortunately, this genotype has strong adult-plant resistance to brown rust (0 rating). Partial susceptibility (10S) of HI 1500 to black rust is a very positive feature because such incomplete resistance restricts the epiphytotic development of disease so that economic losses do not exceed the threshold (field durability; Parlevliet 1977). The majority of the cultivars of the Central Zone possess gene *Sr2*, which is quite desirable for the purpose of preventing black rust epidemics in this zone. Because of the presence of *Sr2*, the rust resistance seems to be stabile in the Central Zone even after 4–5 decades of utilization of the cultivars possessing this gene. This gene is derived from the cultivar Hope, which is responsible for reducing yield losses to only negligible amounts since the late 1960s in

Table 1. Response of popular wheat cultivars of the Central, Peninsular, and South Hill Zones to individual pathotypes at the seedling stage and to a mixture of pathotypes at the adult-plant stage of brown, black, and yellow rusts.

Cultivar	Seedling reaction						Adult-plant reaction		Seedling resistance genes present		
	Brown rust pathotypes				Black rust pathotypes		Brown rust	Black rust	Black rust	Brown rust	Yellow rust
	77A	77-5	77-7	77-8	40A	40-1					
Central Zone											
HI 8498	;	;1	;1	;1	;	0	0	0	*Sr2*	*Lr23*	—
HI 8381	;2	;1	;2	;1	;2+	2+	0	0	*Sr2+Sr9e*	—	—
HI 1544	;2	0;	;1	;1	;1	;1	0	0	*Sr2*	—	—
HI 1531	;2	;2	;2	;2	;	;	0	0	*Sr2+Sr24*	*Lr24*	—
HI 8627	;1	;1	;1	;1	;	0	0	0	*Sr9e*	—	—
DL 788-2	;1	;1	1	0;1	;	0	0	0	*Sr2+Sr5+ Sr24*	*Lr24*	—
HD 4672	;2	;2	;1	;1	;1	1	0	0	—	*Lr23*	—
HI 1500	;1	3+	;2	;2+	;12+	;	0	10S	—	—	—
Peninsular Zone											
Raj 4037	2	3+	2+	;2	2+	2+	80S	20S	*Sr2*	—	—
DWR 162	2+	3+	2+	2+	2	2	60S	10MR	*Sr2+Sr31*	*Lr23+Lr26*	*Yr9*
MACS 2496	2+	3+	2+	22+	2	1	40S	10MR MS	*Sr2+Lr31*	*Lr1+Lr23+ Lr26*	*Yr9*
DDK 1001	;2	0;	;	;1	0;	;1	0	0	—	—	—
DDK1009	;1	;2	;2	;2	;	2	0	0	—	—	—
NIAW 917	0;	0;	0	0;	;1	0	0	0	*Sr2+Sr31*	*Lr26*	*Yr9*
DDK 1025	;2	;1	;1	0;	;	;	0	0	—	—	—
UAS 415	;2	;12	;1	;2	1	;	0	0	—	*Lr23*	—
DWR 195	2+	3+	2+	2+	0;1	2	20S	20MS	*Sr2+Sr31*	*Lr1+Lr23+ Lr26*	*Yr9*
NIAW 34	;2	;2	;2+	;2	;1	2+	60S	0	*Sr11*	*Lr13+Lr34*	*Yr18*
Raj 4083	2+	2+	2+	12+	;1	2	10S	0	—	*Lr23*	—
HD 2781	;1	;1	;1	;1	0	3+	0	0	*Sr2*	—	—
K9644	2+	2+	2+	2	0;	0	20S	0	*Sr2*	*Lr13*	—
MACS 1967	1	;2	2	2	2	2+	0	0	*Sr11*	—	—
AKDW 2997-16	;1	;2	;12	0;	1	;	0	0	—	—	—
Bijaga yellow	1	;1	;2	;2	;1	;	0	0	*Sr2+Sr11*	*Lr23*	—
South Hill Zone											
HW 1085	;1	;1	;1	0;1	0	0	0	0	*Sr24+Sr31*	*Lr24*	—
HW 2044	;1	;1	;2	;2	;1	;	0	0	*Sr2+Sr25*	*Lr19*	—
HW 2045	1	;1	;1	;1	0	0	0	0	*Sr2+Sr25*	*Lr19*	—
HW 3094	;2	;1	;	0;	0	;1	0	0	*Sr24+Sr31*	*Lr24+Lr26*	*Yr9*
HD 2833	22+	;1	;	;1	;1	;1	0	5MRMS	*Sr24*	*Lr24*	—
HW 3083	;	0;	;	0	0;	;2	0	0	—	—	—
HW 2000	;2	;1	;1	;1	;1	;	0	0	—	—	—
HW 5013	;2	;1	;1	0;	;1	;2	0	0	*Sr24+Sr31*	*Lr24+Lr26*	*Yr9*

South America. This resistance is based on the *Sr2* gene complex, which actually consists of *Sr2* plus 4–5 minor genes pyramided into 3–4 gene combinations (Rajaram et al. 1988). *Sr2* alone behaves as a slow-rusting gene. Because there have been no major stem rust epidemic in areas where CIMMYT germ plasm is grown worldwide, the resistance shows promise to be durable also in India. In addition to having *Sr2* protection against black rust, the two cultivars HI 1531 and DL 788-2 also possess *Lr24*, a gene currently resistant to all Indian pathotypes of brown rust and capable of providing simultaneous protection. Fortunately, the *Lr24* gene is present in combination with *Lr26* in cultivars HW 3094 and HW 5013 of the South Hill Zone (Table 1), which is an area of inoculum source. Such a combination may act as an

impediment to risng of new races. The presence of *Sr2* in a majority of cultivars of the Peninsular Zone (Table 1, p. 81) guarantees averting yield losses in this zone in the future bacause of the proven durability of this gene.

In the Peninsular Zone, 16 popular wheat cultivars were evaluated for seedling and adult-stage resistance and 11, DDK 1001, DDK 1009 , NIAW 917, DDK 1025, UAS 415, NIAW 34, Raj 4083, HD 2781, K 9644, MACS 1967, and AKDW 2997-16, showed excellent resistance to Nilgiri flora of black and brown rust pathogens at both the stages (Table 1, p. 81). Three cultivars, Raj 4037, DWR 162, and MACS 2496, were either completely or partially susceptible at seedling stage to brown rust and also susceptible to Nilgiri pathotypes of brown rust pathogen at the adult stage. Thus, the resistance of these three cultivars should be improved or they should be discouraged from cultivation if occupying large acreages in the states of Maharashtra and Karnataka. Nevertheless, these three cultivars need to be retained in the germ plasm pool because of their utility as partially resistant lines for black rust at the adult-plant stage. Such a trait makes these genotypes excellent genetic stocks for deriving durable resistance either for direct cultivation or for incorporation into other high-yielding but susceptible cultivars. Still another genotype, DWR 195, is susceptible to the most predominate pathotype 77-5 (121R63-1) but only at seedling stage. This cultivar holds promise, because it is resistant to black rust at the seedling stage and possesses excellent partial resistance to both black and brown rusts giving it potential to become a durably resistant cultivar in Peninsular India.

Seedling and adult-plant reaction of eight wheat cultivars released for cultivation in the Southern Hill Zone are given in Table 1 (p. 81). All exhibited high levels of resistance (≤ 2 as seedlings and 0–5MR as adult plants) to the Nilgiri flora of both brown and black rusts. In the Southern Hill Zone, wheat is cultivated only in a few thousand ha in the hilly areas of southern Karnataka and parts of Tamil Nadu (Jag Shoran et al. 2009). Because these are the areas where host–pathogen contact is maintained continuously and selection pressure can favor pathogen survival, new, virulent mutants can emerge if host cultivars have single, major genes. Regarding black rust resistance of cultivars released for the Southern Hill Zone, the situation is comfortable because the majority possess more than one gene making them suitable for cultivation in this zone without imminent danger of new pathogenic variants emerging. Brown rust resistance, however, is worrysome with some of the cultivars, e.g., HW 1085, HW 2044, HW 2045, and HD 2833, because they possess only single genes, either *Lr19* or *Lr24*. No virulence for gene *Lr24* is known in India (Mishra et al. 2001), but its singular presence HW 1085 and HD 2833, which are recommended for cultivation in the Southern Indian hills may contribute to new pathogenic mutants by virtue of year round culture. These new variants may not be so threatening for wheat cultivation in South Indian Hills because less area is under wheat cultivation, but they may become a potential constraint in production of *Lr24*-containing wheats such as HI 1531 and DL 788-2 in the Central Zone. Thus, pyramiding more genes in cultivars with *Lr24* grown in the Southern Hill Zone is needed so that they can be cultivated more safely in the rust source areas of hilly Tamil Nadu and southern Karnataka. Such multigenic complexes of rust resistance genes may curtail the arisal of new pathogenic mutants.

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Two new wheat cultivars, Pusa-Navagiri and CoW(SW)2, released for cultivation in the Southern Hill Zone and the nontraditional areas of South India.

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The two disease-resistant, heat-tolerant, high-yielding wheat cultivars developed at IARI, Regional Station, Wellington, were released for cultivation under conditions in the Southern Hill Zone of India. The bread wheat HW 5207 (Pusa Navagiri) was released through All India Co-ordinated Wheat Improvement Progrmme and a *T. turgidum* subsp. *dicoccum* (Samba) wheat cultivar named HW 1095 and also known as CoW(SW)2 was released by Tamil Nadu Agricultural University, Coimbatore, as a state variety for cultivation in the Southern Hill Zone.

The Southern Hills are known as the main foci for leaf and stem rust inoculum to the plains of India. Hence, the development of high-yielding, rust-resistant wheat cultivars and their saturation in these areas is of national importance in order to arrest the dissemination of uredospores to the plains of India.

In the Southern Hill Zone, wheat is not grown commonly except in the areas adjoining Western and Eastern Ghats, which covers some districts of the west and north Tamil Nadu and southern Karnataka states, because of very short winters and unfavorable conditions for cultivation. These areas also have comparatively high temperatures, and the crop is damaged from high infections of Sclerotium foot rot.

The agro-ecological conditions in the Southern Hill Zone, high altitudes prone to frost damage, midaltitudes with erratic monsoon, and low hills with frequent water shortages during the short winters, prompted us to develop the early maturing, thermo-tolerant, rust- and foot-rot resistant bread wheat genotype HW5207. This bread wheat fits well in the local crop rotation with wider adaptability. HW 5207 has a yield potential up to 5.96 t/ha under need-based/restricted irrigation (up to five irrigations) and exhibiting remarkable resistance to all three rusts. Because HW 5207 matures in 100–102 days, it could become a choice and alternative crop for the resource-poor farmers in the areas where erratic and unpredictable northeastern monsoons occur. HW 5207 consistently yields under varied levels of irrigation and has a 32.5% yield advantage over control cultivars under two irrigation levels. HW5207 will ensure both grain and fodder for sustaining the livelihood of resource-poor farmers.

Salient features of the proposed cutlivar HW 5207.

- The genotype HW 5207 (Pusa navagiri) recorded the highest mean grain yield (52.1 q/ha) over the best check COW(W)1(48.75 q/ha) over the testing period. The superiority yield ranged from 7–18%.
- HW 5207 ranked in the first nonsignificant group eight out of 12 times (66.6%) over four years of testing at different locations indicating its wider adaptability and stability in its performance.
- HW 5207 exhibited a high degree of resistance to stem, leaf, and stripe rusts under both artificial and natural epidemic conditions against all the pathotypes occurring in the Nilgiris. The resistance to rusts and powdery mildew is attributed to the likely presence of a combination of genes, *Sr2* (based on the presence of pseudo-black chaff, tightly linked to *Sr2*), *Sr31*, and *Sr24* for stem rust; *Lr24* and *Lr26* for leaf rust; *Yr9* and *Yr15* for yellow rust; and *Pm8* for powdery mildew. These genes likely were derived from the parents involved in the cross.
- HW 5207 yielded consistently higher over the best check HW 2044 when tested at more locations in areas adjoining the Nilgiri and Palani Nills and nontraditional areas, indicating its elasticity.
- HW 5207 recorded highest mean grain yield of 58.7 q/ha under two irrigation levels in trials as compared to the best check HW 2044 . The over-all gain with two irrigations is 32.5%, which is the most favorable feature of the cultivar. The 12.1% advantage in mean yield obtained over HW 2044 under different irrigation levels indicats an ability for increased yield under varied soil moisture levels.
- HW 5027 has the ideal plant height (90 cm) with strong and resilient stems that provide resistance to lodging. The very nutritious grain registers 40.5 g mean test weight with > 11% protein and a high levels of iron (53.1 ppm), zinc (46.3 ppm), copper (5.33 ppm), and manganese (47.5 ppm) when compared to the checks indicating the nutritional quality of the grain it produces. In addition, HW 5027 has high scores for bread-making quality (7 out of 10), chapatti quality (7.42 out of 10), a *Glu-1* score of 8 out 10, mean sedimentation value of 45.5, and a high hectolitre weight of 78.3 (kg/hl).

Cultivation of HW 5207 will provide an alternative to HW 2044 and Cow(w)1 and create additional genetic diversity to contain rust from the foci of rust inoculum and will have an added yield advantage as HW5207 shown better adaptability; suit cultivation in high altitudes, at middle elevations, and in lower hills as well as areas adjoining the hills; offer protection against the prevailing rusts and minor foliar diseases such as leaf blight, powdery mildew, and Sclerotium foot rot under field conditions; produce more grain (50 q/ha) along with fodder ensuring farm sustainability; and confer a high degree of resistance at field level in the zone, which could be attributed to the likely presence of *Lr24+Sr24*, *Sr31+Lr26+Yr9+Pm8*, and *Yr15* possibly derived from the parents involved in the cross, evidenced from the Seedling Response Test. In addition, the presence of prominent pseudo-black chaff, which is tightly linked to *Sr2* (a race nonspecific APR gene), in combination with other stem rust genes is expected to offer durable resistance against the most frequent pathotypes of rust in the Southern Hill Zone, a hot spot for foliar diseases of wheat in India.

Release of HW 1095, a semidwarf dicoccum as CoW(SW)2.

HW 1095, a semidwarf, disease-resistant, nutritionally rich, economically viable and high yielding dicoccum (Samba wheat) wheat developed at IARI, Regional Station, Wellington, using mutation techniques, is released for parts of Tamil Nadu and the Southern Hill Zone, including nontraditional areas, in collaboration with Tamil Nadu Agricultural University, Coimbatore, as state release. Wheat is one of the most important cereal crops in the world, ensureing food security to humankind. Although as many as 18 species of wheat were described and recognized by Percival (1921). only a few are of importance in agriculture. India is one of the very few countries in the world that cultivates all three important commercially cultivated species of wheat, *T. aestivum* subps. *aestivum* (common bread or chappati wheat), *T. turgidum* subsp. *durum* (macaroni or durum wheat), and *T. turgidum* subsp. *dicoccum* (emmer, dicoccum, or Samba wheat). Bread wheat is the most important species accounting for a little over 87% of the total wheat production in India followed by durum (about 12%) and dicoccum (about 1%). Unlike aestivum and durum wheat, dicoccum wheat is grown on only limited acreage in Tamil Nadu, Karnataka, and parts of Maharastra. Even today, a considerable area under dicoccum can be found in the northwestern Tamil Nadu, Karnataka, Maharastra, and parts of Andhra Pradesh states. The farmers have preserved this wheat species becaues of its nutritional, nonshattering, and drought-tolerant traits. Currently, the tall land races that were released as NP 200, NP201, and NP 202, from IARI, Wellington, during 1960s are under cultivation in the southern Indian states for the traditional food preparation are made from dicoccum.

Incorporating dietary fiber-rich, dicoccum, whole-wheat flour in the regular diet of a diabetic significantly reduced total lipids ($p \leq 0.01$), triglycerides ($p \leq 0.01$), and LDL cholesterol ($p \leq 0.05$) (Yenagi N et al. 2001). Dicoccum wheat has therapeutic properties that can effectively reduce the cardiovascular risk factors. Managing diabetes, a life-long ailment, with medicine is very expensive and a dicoccum diet plays a crucial role in reducing the levels of plasma cholesterol and lowering glycemic response. The hulled grain of dicoccum wheat is used mainly in the alternative or health food markets. Most of the suggested beneficial effects of this cereal is from the specific characteristics of the fiber. Pyrolysis fragments derived from the polysaccharide fraction were significantly more abundant in dicoccum than in the other genotypes, whereas the highest percentage of lignin-derived pyrolysis fragments was detected in durum wheat. Results suggest that dicoccum genetic material may represent a source of high-value dietary fiber; dicoccum is much higher in fiber than common wheat. Future wheat-breeding programs should aim to preserve such characters.

In India, first three dicoccum cultivars, NP 200, NP 201, and NP 202, which were selected from Rishi Valley collections in Andhra Pradesh, were released for commercial cultivation during 1960s from the IARI Regional Station, Wellington. These cultivars are tall, tend to lodge, and are susceptible to yellow rust. Attempts were made to develop semidwarf dicoccum cultivars using dwarfing gene(s) derived from closely related tetraploid durum species, and a number of semidwarf cultivars were released from the University of Agricultural Sciences, Dharwad (DDK 1001, DDK 1009, DDK 1026, and DDK 1029) and from the Agharkar Research Institute, Pune. Although the dwarfing gene(s) derived from durum helped in developing semidwarf dicoccum wheats, most of them are now susceptible to yellow, particularly against pathotype 'I' (38S102) prevalent in the Southern Hills, and also produced undesirable end-product, grain traits, such as slightly sticky, reduced-quality fiber Rawa 'Uppuma', and were less preferred by the millers.

Therefore, a meticulously planned, dicoccum-improvement program was undertaken at IARI, Wellington, during 2002 for developing semidwarf dicoccum wheats without altering the quality of NP200, NP 201, and NP 202 by mutation breeding. Gamma irradiation of 10 (100 Gy (Gray is the unit of absorbed dose and is 1 Joul/kg)), 20 (200 Gy), 30 (300 Gy), and 40 (400 Gy) Kr γ-rays was given at optimal seed moisture levels. The irradiated seed were sown as M_1

and desirable plants were selected in the M^2 at 200 Gy dose. A stable population was fixed at M_4 that was entered into the All India Co-ordinated Trials as HW 1095 in 2005.

The salient features of HW 1095 (released as CoW(SW)2).

– dicoccum wheat HW 1095 developed at IARI, Regional Station, Wellington, is a NP200-mutant through gamma irradiation (200 Gray) maturing in 110 days, belonging to the early duration group.
– Culture HW 1095 recorded a mean grain yield of 4,040 kg/ha, which is an increase of 26% over NP 200 in a total of 98 trials over the past five years. NP 200 was used as a check. The yield of NP 200 was 3,190 kg/ha.
– Culture HW 1095 has 10–12 productive tillers with long and slightly tapering ears. A special attribute of this culture is the broad and waxy green foliage, drooping leaves, lodging resistance, and nonshattering grains. Rich in protein (13.2%) with a high sedimentation value (25), the reddish colored grain provides a good grain appearance and score of 8.
– The culture is resistant to black (stem), yellow (stripe), and brown (leaf) rusts. No major incidence of pests occurred in this Samba wheat culture. In view of a high and stable yield performance over locations and resistance to leaf and stem rust diseases, the culture HW 1095 is proposed for release as wheat COW (SW) 2 in collaboration with Department of Millets, Tamil Nadu Agricultural University, Coimbatore, as state release.
– The released cultivar HW 1095-CoW(SW)2 was significantly superior in yield over NP 200 and DDK 1029 during the testing period.
– HW 1095 occurred 11/18 times in first nonsignificant group indicating wider adaptability and stability in performance across zones.

The release of this Samba wheat CoW(SW)2 is likely to boost the re-introduction of dicoccum wheat in the traditional dicoccum belt. In addition, resource-poor farmers will earn a better livelihood, because dicoccum grain garners a higher price in the market than other types of wheat. Our efforts at IARI, Wellington, now are to improve NP201 and NP202, and of these, one promising entry HW 1098 already has been entered in AICWIP Co-ordinated Trials.

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A protein marker as a tool to detect the Secale cereale-derived linked genes Sr31, Lr26, Yr9, and Pm8 genes in wheat.

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Introduction. Much of the widely adapted wheat germ plasm generated and distributed by CIMMYT throughout the spring wheat production areas in low latitude countries carry a T1BL·1RS translocation. The wheat-breeding community has relied particularly on the use of the *Sr31* gene derived from wheat–rye hybrid derivatives produced in Germany in the 1930s (Mettin et al. 1973; Zeller 1973) that gave continued protection against stem rust worldwide. The T1BL·1RS segment carries genes for resistance to three rusts, *Sr31*, *Lr26*, and *Yr9*, and *Pm8* for resistance to powdery mildew (Zeller 1973). However, in many genetic backgrounds, especially wheat lines of CIMMYT origin, the expression of *Pm8* is suppressed by a gene(s) located in chromosome 1A (Ren et al. 1997) or 7D (Zeller et al. 1993). In addition, the translocation may contribute positively to agronomic traits such as yield and drought tolerance (Rajaram et al. 1983). On the negative side, wheat lines with the translocation generally produce lower quality flour than their non-T1BL·1 RS counterparts (Dhaliwal et al. 1987), indicating that the rye genes present are responsible for low gluten quality.

Singh et al. (1990) used SDS–PAGE to examine the genetic linkage between the genes controlling secalins (*Sec-1*) and those for resistance to the three rust diseases. The rust resistance genes are located 5.4±1.7 cM from the *Sec-1* locus, suggesting a close linkage (Afshari 2006). Because of the lack of pairing between the wheat and rye chromatin (IB and TIBL·IRS) in a wheat background, *Sec-1* acts as a marker for *Sr31*, *Lr26*, *Yr9*, and *Pm8*.

The ineffectiveness of *Sr31* against the new stem rust race Ug99 (Singh et al. 2004, 2006), which threatens wheat grain production worldwide, offers much hope to diversify the genetic base of the cultivar by pyramiding effective genes with or without *Sr31*.

The six Indian popular wheat cultivars, HD 2329, HD 2285, HP 1205, WH 147, J 24, and Lok-1, already with *Sr24+Lr24* that were introgressed with the *Sr31* gene complex through conventional backcross methods, were obtained for the confirmation of the presence of *Sr31*.

For the molecular analysis, protein was extracted using a protein-extraction buffer and separated in a vertical dual-gel unit (Sigma-Aldrich). Electrophoresis was at a constant 30 mA or until the bromophenol blue dye migrated to 1.5–2 cm above the gel base. SDS–PAGE used Laemmli (1970) buffer. The gel was then rinsed with distilled water and destained in 10% (v/v) acetic acid and 30% (v/v) methanol for 20 minutes, followed by washing in distilled water for 50 minutes with gentle shaking. The protein bands were documented on a digital gel documentation unit. The data on phenotyping of the constituted lines was done at IARI, Regional Station, Wellington.

Results and discussion. The SDS–PAGE procedure revealed patterns of water-soluble proteins that detected the T1BL·1RS translocation in wheat cultivars. The SDS–PAGE results showed that all the wheat stocks introgressed with the *S. cereale*-derived, linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8*, HW 4042 (HD 2329 with *Lr28*), HW 4044 (Lok-1 with *Lr28*), HW 4047 (WH 147 with *Lr28*), HW 4049 (HD 2285 with *Lr28*), and HW 4062 (J 24 with *Lr28*), carried the *Sec-1* band and the presence of the linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8* thus confirming the T1BL·1RS translocation. The recurrent parent HP 1205 also with the *Sr31* gene complex shows the *Sec-1* band. The protein bands corresponded to the secalins of the rye parent, which were present in the wheat cultivars carrying T1B·1R translocation. The *Sec-1* band was not found in the recurrent parents HD 2329, HD 2285, WH 147, J 24, and Lok-1, which do not have *Sr31* and suggesting the absence of the T1B·1R translocation. The lines pyramided with *T. ponticum*-derived linked genes *Lr24+Sr24*, and the *S. cereale*-derived gene comples are expected to yield better than the recurrent parent under field conditions.

Table 2. Adult-plant response to black (Sr), brown (Lr), and yellow (Yr) rust and powdery mildew (Pm, 0–4 scale) diseases in wheat genotypes that carry specific rust-resistance genes and their recurrent parents.

Stock	Back-ground of recurrent parent	Genes	Adult-plant response			
			Sr	Lr	Yr	Pm
HW 2037	HD 2329	*Lr28*	90S	F	90S	2
HW 4042	HD 2329	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	10R–MR	F	F	3
HW 2038	HD 2285	*Lr28*	50MS–S	F	30S	2
HW 4049	HD 2285	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	10R–MR	F	F	3
HW 2036	J 24	*Lr28*	90S	F	100S	2
HW 4062	J 24	*Sr25*, *Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	20R–MR	F	F	4
HW 2032	Lok-1	*Lr28*	90S	F	80S	3
HW 4044	Lok-1	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	15R–MR	F	F	3
HW 2033	WH 147	*Lr28*	100S	F	90S	2
HW 4047	WH 147	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	15R–MR	F	F	3
HW 4444	HP 1205	*Sr25+Lr19*	30MS–S	F	90S	4
	HP 1205	*Sr25+Lr19*, *Sr31*, *Lr26*, *Yr9*, and *Pm8*	F	F	F	3

The phenotyping data (Table 2) showed that the recurrent parents HW 2037, HW 2036, HW 2032, and HW 2033 (all carrying the *Ae. speltoides*-derived leaf rust resistance gene *Lr28*) were highly susceptibility to all stem and stripe rusts, except HW 2038, which was attributed to the presence of the *Sr8+Sr9b+Sr11* gene complex. However, HW 4444 in the background of HP 1205 showed resistance to leaf and stem rust because of the presence of *Lr19+Sr25*. The stocks HW 4042, HW 4049, HW 4062, HW 4044, HW 4047, and HW 4444 with *Sr31*, *Lr26*, *Yr9*, and *Pm8* from *S. cereale* clearly showed remarkable resistance against all three rusts. The *Sec-1* band clearly demonstrates and confirms that these lines carry *S. cereale*-derived, *Sr31*+gene complex.

Because *Sec-1* is tightly linked with the three rust resistance genes, SDS–PAGE is a useful method to identify and confirm the presence of rye chromatin and the three genes. The protein marker band associated with *Sec-1* is 5.4±1.7 cM from the linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8* and can be exploited for detecting the T1RS·1BL translocation and developing lines with or without the *Sr31* gene complex (Fig 1.). Because *Sr31* is not effective against the emerging threat posed by the Ug99 stem rust pathotype and associated with poor gluten quality, this technique can be used to select lines without *Sr31*. *Sec-1* can be introgressed with other effective stem rust resistance genes such as *Sr24* (virulent pathotype 40-1 already reported from India), *Sr25*, *Sr26*, or *Sr27* for developing cultivars that produce better quality flour. Otherwise, *Sec-1* can be pyramided with other effective stem rust gene(s) to exploit the positive yield traits associated with the *Sr31* gene complex. The *Sec-1* marker will be a quick and economical method for screening large numbers of wheat germ plasm lines for the presence of *Sr31* in the laboratory without any greenhouse facility in a short period of time.

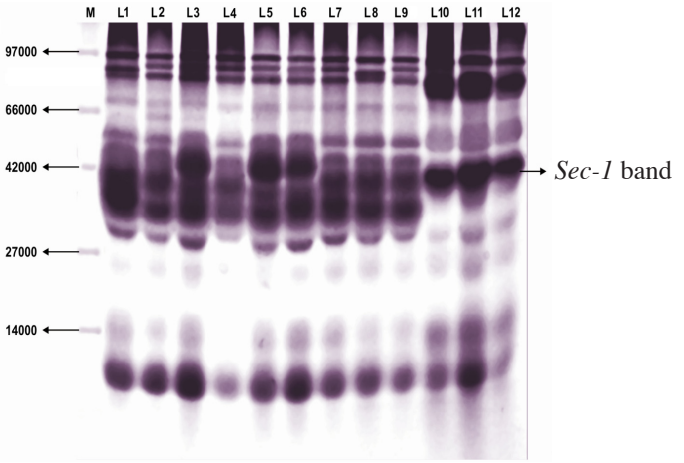

Fig. 1. Banding patterns of seed protein extracts from wheat stocks and various controls subjected to SDS-PAGE eletcrophoresis (lanes L to R: M, marker (14–97 Kda); L1, HW 4444 (+); L2, WH 542 (donor) (+); L3, HW 4049 (+); L4, HW4042 (+); L5, HW 2038 (rye parent) (–); L6, HW 2037 (Recurrent parent) (–); L7, HW 4062 (+); L8, HW 4044 (+); L9, HW 4047 (+); L10, R–1 (+); L11, R–2 (+); and L12, R–4 (+). The presence or absence of the Sec-1 band the presence or absence of T1BL·1RS is indicated by (+) and (–), respectively.

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Developing elite, durable disease resistant wheat cultivars combining high grain yield and end-use quality by introgressing effective genes employing conventional and modern breeding approaches.

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Introduction. A meticulously planned, wheat-improvement program employing back-cross methodology to introgress effective rust and powdery mildew resistance genes was initiated during late eighties and early nineties. Popular Indian bread wheat and dicoccum wheat cultivars were used. The reference stocks (RILs) obtained were initially evaluated for resistance, and only effective genes conferring resistance to existing pathotypes were taken for the program. The effec-

tive resistance genes were introgressed initially through a conventional back-cross hybridization method taking advantage of Wellington where in all three rusts and other foliar diseases occur on a susceptible line throughout the year and is considered as natural 'hot spot'. Later, when markers were made available, both conventional and MAS approaches are used. Initially, the number of backcrosses effected were 8–9, but now we stop with BC_3. For molecular confirmation, the mapping populations were used at the BC_1F_2 stage.

Alien rust-resistance genes in the back-cross program at IARI, Wellington (Table 3, p. 89).

Stem rust resistance genes:	*Sr2* (linked to pseudo-black chaff (*Pbc*)), *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr27* (linked to apical claw on spike), *Sr29*, *Sr30*, *Sr31*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr38*, *Sr39*, *Sr42*, and *Sr43*.
Leaf rust resistance genes:	*Lr9* (not effective in India), *Lr19* (new virulence reported), *Lr24*, *Lr26* (not effective in India), *Lr28*, *Lr32*, *Lr34* (adult-plant resistance (APR) is race nonspecific and linked to leaf tip necrosis), *Lr35* (APR), *Lr37*, *Lr39*, *Lr40*, *Lr41*, *Lr42*, *Lr45* (linked to pink awn/glume at milk stage under low temperature), *Lr46* (APR, race nonspecific), *Lr47*, *Lr48*, *Lr49*, *Lr53*, and *Lr57*.
Stripe rust resistance genes:	*Yr9*, *Yr10*, *Yr15*, *Yr16*, *Yr17*, *Yr18*, *Yr24*, *Yr25*, *Yr26*, *Yr29*, *Yr30*, *Yr35*, and *Yr40*.
Powdery mildew resistance genes:	*Pm6*, *Pm8*, *Pm38*, and *Pm39*

Pleiotropic or closely linked to genes (race nonspecific) exploited that are effective to other diseases include *Lr34*/*Yr18*/*Pm38*/*Bdv1*/*Sr* resistance/*Ltn*, *Lr46*/*Yr29*/*Pm39*/*Ltn*, and *Sr2*/*Yr30*/(*Lr27*)/*Pbc*.

Linked genes that are exploited include *Lr19*+*Sr25*, *Lr24*+*Sr24*, *Yr30*+*Sr2*+*Lr27*, *Lr26**+*Yr9*+*Sr31*+*Pm8*, *Lr37**+*Yr17*+*Sr38*, and *Sr39*+*Lr35*.

Pyramiding of effective stem rust-resistance genes currently under progress to over come threat from Ug99 and its variants of stem rust race virulent on *Sr31*, *Sr24*, and *Sr36* virulence spectrum of Ug99 (TTKSK). Genes that currently are effective against Ug99 are *Sr25* (*Lophopyrum ponticum*); *Sr28* [1], *Sr29* [2], and *SrTmp* [1] (*T. aestivum* subsp. *aestivum*); *Sr2*, *Sr13* [1,2], and *Sr14* [1] (*T. turgidum* subsp. *turgidum*); *Sr22* and *Sr35* (*T. monococcum* subsp. *monococcum*); *Sr36* [1] and *Sr37* (*T. timopheevii* subsp. *timopheevii*); *Sr32* and *Sr39* (*Ae. speltoides*); *Sr33* [2] and *Sr45* (*Ae. tauschii*); *Sr40* (*T. timopheevii* subsp. *armeniacum*); *Sr26* and *Sr43* (*Th. elongatum*); *Sr44* (*Th. intermedium*); and *Sr27* [1] and *Sr1A·1R* [1] (*S. cereale*). For genes marked with a [1], virulence for the gene is known to occur in other races; for those with a [2], the level of resistance conferred in the field usually insufficient (Singh et al 2008).

Markers available in public domain used at the Indian Agricultural Research Institute, Regional Station, Wellington. Stem rust: *Sr1A*, *Sr2*, *Sr9a*, *Sr11*, *Sr13*, *Sr14*, *Sr15*, *Sr17*, *Sr19*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr28*, *Sr29*, *Sr31*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr37*, *Sr38*, *Sr39*, *Sr40*, *Sr43*, *Sr44*, *Sr45*, *Sr46*, *SrR*, *SrTmp*, *SrTt3*, and *SrD5*; leaf rust: *Lr19*, *Lr24*, *Lr28*, *Lr32*, *Lr35*, *Lr37*, *Lr39*, *Lr26*, *Lr47*, *Lr50*, and *Lr51*; and yellow rust: *Yr9*, *Yr10*, *Yr15*, *Yr17*, *Yr18*, *Yr26*, and *Yr28* (Bariana et al. 2007).

Accomplishments.

- Combinations of *Sr24*+*Sr25, Sr25*+*Sr26, Sr25*+*Sr27*, *Sr25*+*Sr36*, *Sr25*+*Sr38*, *Sr24*+*Sr26*, *Sr24*+*Sr27*, and *Sr24*+*Sr36* are pyramided with *Yr10* in at least 20 adapted Indian bread wheat cultivars and the material is ready for sharing. Even stocks with *Lr19*+*Sr25*+*Sr36*+*Pm6* and *Yr15*, which are free from leaf, stem, and stripe rusts and powdery mildew have been developed and published (Table 4, pp. 90-91).
- Popular Indian bread wheat cultivars with *Lr24*+*Sr24* and *Lr19*+*Sr25* along with *Sr36*+*Pm6*, *Lr28*, and *Lr37* developed in 20 cultivar backgrounds have been completed and published.
- Corrective crosses for *Lr19*+*Sr25* where Sunstar was used are using 'wheatear'.
- Corrective crosses for *Lr32* (Thatcher *Lr32*) also is in progress at the BC_3F_2 stage.
- Incorporated of new leaf rust genes *Lr35*+*Sr39* (during Kharif 2010), *Lr39* (BC_3), *Lr42*, *Lr44*, *Lr45* (at BC_3F_3 stage) in 28 popular Indian bread wheat cultivars.
- Current efforts to incorporate/pyramid *Lr46*, *Lr47*, *Lr48*, and *Lr57* in combination with *Yr10* and *Yr15*.
- Pyramiding of *Sr24* with *Sr31*, *Lr19*+*Sr25* with *Sr31*, and *Lr19*+*Sr25* with *Lr24*+*Sr24* completed in 20 popular cultivars and published.
- *Lr28*, *Lr32*, and *Lr37* with *Sr36*+*Pm6* in 20 popular cultivars complete.

Table 3. Effective rust-resistance genes used in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington (* reference stock attributes are listed in Table 4, pp. 90-91).

Gene	Source	Reference stock used*	Chromosome location
Lr9 (ineffective at Wellington since 1995)	*Ae. umbellulata*	Abe	6BL
Lr19+Sr25, *Sr36+Pm6* (77-8 race reported in Peninsular Zone, India, during 2008)	*Th. ponticum*	Sunstar and Cook and now wheatear	7DL
Lr24+Sr24 (40-1 race reported in Wellington on *Sr24*)	*Th. ponticum*	Tr380-14*7/3Ag#14 Janz, Sunleg, RL6064, Agent	3DL
Lr26+Sr31+Yr9+Pm8 (77-1 race reported from Wellington for *Lr26*)	*S. cereale* (Petkus rye)	WH 542 (Bucanora)	T1BL1RS
Lr28	*Ae. speltoides*	CS 2A/2M 4/2	4AL
Lr32	*Ae. tauschii*	C86-8/KalyansonaF$_4$/ Thatcher *Lr32*	3DS
Lr34+Yr18+BDV1 Pm38+Sr resistance/*Ltn* (APR race nonspecific)	*T. aestivum* subsp. *aestivum* cultivar Terenizo	RL6058	7DS
Lr35+Sr39	*Ae. speltoides*	Thatcher+*Lr35*	2B
Lr37+Sr38+Yr17	*Ae. ventricosa*	Thatcher*8/VPM1, RL6081	2AS
Lr39	*Ae. tauschii*	KS92WGRC15, EZ 350692	2DS
Lr40	*Ae. tauschii*	LC+*Lr40*, KS89WGRC07	1D
Lr41	*Ae. tauschii*	EC381200, KS90WGRC10	2DS
Lr42	*Ae. tauschii*	EC381201, KS91WGRC11	1D
Lr44	*T. aestivum* subsp. *spelta*	EC381202, RL6147	1BL
Lr45	*S cereale* (Imperial rye)	EC 381203, RL6144	TAS·2R
Lr46	*T. aestivum* subsp. *aestivum*	Pavon 76, Dimond Bird	1BL
Lr47	*Ae. speltoides*	Pavon 7 S3 Lr47, KS90H450	7AS
Sr2+Lr27+Yr30+Pbc (pseudo-black chaff)	*T. aestivum* subsp. *aestivum*	Maden, Lok-1, HW 5207	3BS
Sr22 (APR)	*T. monococcum* subsp. *monococcum*		7AL
Sr24	*Th. ponticum*	Tr380-14*7/3Ag#14	3DL
Sr25+Lr19+Sr36+Pm6	*Th. ponticum*		7DL
Sr26	*Th. ponticum*	DARF*6/3Ag3/Kite	6AL
Sr27	*S cereale* (Imperial rye)	Kalyanasona*4/*Sr27*	3A
Sr29	*T. aestivum* subsp. *aestivum*	Pusa 4/Etoile de choisy	6DL
Sr30	*T. aestivum* subsp. *aestivum*	BtSr30Wst	5DL
Sr32	*Ae. speltoides*	CnsSr32 AS	2A, 2B, 2AS
Sr33	*Ae. tauschii*	RL5405	1DL, 1DS
Sr35	*T. monococcum* subsp. *monococcum*	Mq(2)/5*G2919	3AL
Sr36+pm6	*T. timopheevii* subsp. *timopheevii*	Cook*6/C 80-1	2BS
Sr38	*Ae. ventricosa*	Thatcher*8/VPM1, RL6081	2AS
Sr39	*Ae. speltoides* (APR)	Thatcher+*Lr35*	2B
Sr42	*T. aestivum* subsp. *aestivum*	EC381206	6DS
Sr43	*Th. ponticum*	EC381210	7DL
Sr44	*Th. ponticum*		7AS?, 7DS
Yr10	*T. aestivum* subsp. *spelta*	Moro, *Yr10*+WH 542	1BS
Yr15	*T. turgidum* subsp. *dicoccoides*	*T. dicocoides* G-25	1BL
Yr16	Capelle-Desprez	Capelle-Desprez	2DS
Yr17	*Ae. ventricosa*	Thatcher*8/VPM1, RL6081	2AS
Pm6	*T. timopheevii* subsp. *timopheevii*	Cook*6/C 80-1, Abe	2BS

Table 4. *Triticum aestivum* subsp. *aestivum* donor parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s)	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew
Abe	*Lr9 Sr36* (Not effective in India)	15R MR	F	40S	1
Sunstar*6/C80-1 (molecularly confirmed not carrying *Lr19*, 'wheatear' used now)	*Lr19 Sr25*	10R MR–30R MR	F	F	4
	Lr19+Sr25	F	F	10MR–MS	3
Cook*6/C 80-1	*Lr19 Sr25 Sr36 Pm6*	F	F	F	1
Tr380-14*7/3Ag#14	*Lr24 Sr24* (*Sr24* not effective in India)	15R MR	F	5MR	2+
DARF*6/3Ag3/Kite	*Lr24 Sr24 Sr26*	10R MR–20R MR	F	10MS	3
WH 542	*Lr26* (not effective in India) *Sr31 Yr9 Pm8*	10R MR	80S	F	3
CS 2A/2M 4/2	Lr28 Sr34 Yr8	90S	F	F	0–1
C86-8/Kalyansona F_4 (not carrying *Lr32*; Thatcher Lr32 used now	*Lr32*	70S	F	90S	3
	Lr32	60S	F	20S	2
RL6058	*Lr 34 Yr18 BDV1 Pm38*	F	30MR–MS	F	0–1
Thatcher+*Lr 35*	*Lr35* (Race specific APR) *Sr39*	F	F	F	2
Thatcher*8/VPM1, RL6081	*Lr37 Sr38 Yr17*	20R MR MS	F	15MS	4
KS92WGRC15, EZ350692	*Lr39*	40S	F	F	2
LC+*Lr40*	*Lr40*	S	S	F	2
EC381200	*Lr41*	5S	F	30S	3
EC381201	*Lr42*	F	F	40S	3
KS92WGRC16	*Lr43*	F	F	40S	2
EC381202	*Lr44*	20S	20S	F	2
EC381203	*Lr45*	S	F	S	3
Pavon 76	*Lr46*		20MS		
Pavon	*Lr47*	F	F	10S	2
Tr380-14*7/3Ag#14	*Sr24 Lr24*	15R MR	F	5MR	2+
DARF*6/3Ag3/Kite	*Sr24 Sr26 Lr24*	10R MR–20R MR	F	10MS	3
Sunstar*6/C80-1 (molecularly confirmed not carrying *Lr19*, 'wheatear' used now)	*Sr25 Lr19*	10R MR-30R MR	F	F	4
Cook*6/C 80-1	*Sr25 Sr36 Lr19 Pm6*	F	F	F	1
Kalyanasona*4/Sr27	*Sr27*	F–Tr	80S	90S	3
Pusa 4/Etoile de Choisy	*Sr 29*	F			
BtSr30Wst	*Sr 30*	F			
WH 542	*Sr31 Lr26 Yr9 Pm8*	10R MR	80S	F	3
CnsSr 32 AS	*Sr 32*	F			
RL5405	*Sr33*	F			
CS 2A/2M 4/2	*Sr34*	90S	F	F	0–1
Mq(2)/5*G2919	*Sr35*	F			
Abe	*Sr36*	15R MR	F	40S	1
	Sr37	F	80S	30S	2
Thatcher*8/VPM 1,RL 6081	*Sr38*	20R MR MS	F	15MS	4

Table 4 (continued). *Triticum aestivum* subsp. *aestivum* donor parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s)	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew
EC381198	*Sr38*	F	F	F	4
Thatcher+*Lr35*	*Sr39*	F	F	F	2
EC381204	*Sr39*	F	F	F	2
RL6087	*Sr40*	F	60S	F	2
EC381206	*Sr42*	F	40S	5S	2
EC381210	*Sr43*	F	80S	F	1
CS 2A/2M 4/2	*Yr8 Lr28 Sr34*	90S	F	F	0–1
WH 542	*Yr9 Lr26 Sr31 Pm8*	10R MR	80S	F	3
Moro, WH 542	*Yr10*	F	F	F	0–1
T. dicocoides G-25	*Yr15*	F	F	F	0–1
Capelle-Desprez	*Yr16*	F	F	F	0–1
Thatcher*8/VPM1, RL6081	*Yr17 Lr37 Sr38*	20R MR MS	F	15MS	4
EC463655	*Yr17*	F	90S	F	NA
EC463057	*Yr24*	F	40S	20S	NA
EC463658	*Yr26*	F	20S	30S	NA

Table 5. Number wheat cultivars released for commercial use developed through the alien gene backcross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Cultivar	Pedigree	Year of release	Release target zone
HW 2004 (Amar)	C 306//Tr 380-14*7//3 Ag # 14	1997	Central zone, rainfed
HW 1085 (Bhavani)	HW 2002A//CPAN 3057	1998	Southern Hill Zone, medium fertility, timely sown
HW 2044 (Kurinji)	PBW 226*5//Sunstar*6/C 80 -1	2000	Southern Hill Zone, medium fertility, timely sown
HW 2045 (Kaushambi)	HD2402*5//Sunstar*6/C80-1	2003	North Eastern Plain Zone, late sown
HS 375 (HIMGIRI) (In collaboration)	BB/G11/CJ 71/3/TAEST//KAL/BB	2003	Northern Hill Zone, very high altitude, timely sown
HS 420 (Shivalik) (In collaboration)	RAJ3302//cmh 73a-49*7/3*CNO 79	2003	Northern Hill Zone, late sown
HD 2833 (In collaboration)	PBW 226/HW 1042 (Tr 380-14*7/3 Ag#14)// HD 2285	2005–06	Peninsular Zone
MACS 6145 (HW 2034) (In collaboration)	C 306*9/CS 2A/2M*4/2	2004	North Eastern Plain Zone, rainfed
COW(W) 1 (HW 3094) (In collaboration)	HD 2646//HW 2002A/CPAN 3057	2004	Areas adjoining Southern Hills and hills in Tamil Nadu/Karnataka (wheat for warmer areas)
HW 5207 (Pusa Navagiri)	HW 3029//*Yr15*	2009–10	Southern Hill Zone, medium fertility, timely sown
Hw 1095 as CoW(SW)2 (Dicoccum)	NP200 - Mutant through Gamma Irradiation (y)(200 Gray)	2010	Areas adjoining Southern Hills and hills in Tamil Nadu/Karnataka (wheat for warmer areas)

Targeted breeding program to tackle the Ug99 threat accomplishments.

– Introgression of pyramided genes involving *Sr2* and *Sr22* with *Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr29*, *Sr30*, *Sr33*, *Sr35*, *Sr36*, and *Sr44* in at least 20 important, currently popular cultivars across the zones is under progress, many

Table 6. *Triticum aestivum* subsp. *aestivum* recurrent parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s) already carrying	Reaction to (adult-plant respone)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew (0–4 scale)
C 306	*Lr34+Yr18+BDV1+Pm38+Sr* resistance/*Ltn* (unknown resistance gene for yellow rust)	90S	90S	F	3
HD 2009		40S	60S	100S	3
HD 2285	*Lr23+Sr9b+Sr11+Yr2*	30MS	100S	30S	3
HD 2329	*Lr13+Lr10+Lr34*, *Sr8+Sr9b+Sr11+Yr2+Yr18*	80S	90S	90S	3
HD 2402	*Lr34*+ unknown resistance gene for yellow rust	30S	100S	F	3
HD 2687	*Sr31 Lr26 Yr9 Pm8*	15R MR	80S	F	3
HI 1077	*Lr14a*	30MS S	50S	40S	3
HS 240	Sr31 Lr26 Yr9 Pm8	5R MR	70S	F	3
HUW 234	*Lr14a+Sr9b+Sr11+Yr2*+(Ks) and *Sr31 Lr26 Yr9 Pm8*	20MS S	100S	F	3
J 24		90S	100S	100S	3
Kalyansona	*Yr2*	80S	90S	90S	3
Lok-1	*Lr13+Sr2+Sr9b+Sr11+Yr18*	70S	80S	80S	3
NI 5439	*Lr34+Yr18+BDV1+Pm38+Sr* resistance/*Ltn* and *Sr11+Yr2*	90S	90S	100S	3
PBW 226		20S	90S	F	3
Sonalika	*Lr11* and *Lr13* (Gupta et al. 1984; Rao et al. 2001)	60S	80S	60S	3
UP 262		50S	50S	50S	3
UP 2338	*Lr26+Lr34+Sr31+Yr9+Yr18*	10MR	60S	F	3
VL 421		60S	90S	80S	3
WH 147	*Lr34*	90S	90S	90S	3
WH 542	*Lr34*, *Sr31 Lr26 Yr9 Pm8*	10R MR	80S	F	3
WL 711	*Lr11* and *Lr13* (Gupta et al. 1984; Rao et al. 2001)	100S	100S	90S	3
HI 977		F	60S	40S	2
HP 1205		60SS	80SS	90S	3
PBN 51		20MR	40S	S	2
PBW 343	*Lr34*	20MR	60S	5S	3
Raj 3077		5MR	60SS	60SS	1
HD 2877	*Sr31*	5MR	40SS	F	3
HW 3070	*Lr24+Sr24*, *Sr31*	F	F	10MR-10S	2
HD 2733	*Sr31*	20MR	60S	F	3

at BC_2 stage in Rabi 2009–10.
– Simultaneous molecular confirmations are under taken
– More than 400 near isogeneic lines carrying various specific rust resistance genes developed.

Some salient observations made on the introgression lines with above-mentioned rust resistance genes.

– *Lr24+Sr24* are tightly linked, but snew pathotype virulent on *Sr24* (40-1/62G29) was reported from this station.
– *Sr31*, *Lr26*, *Yr9*, and *Pm8* are tightly linked and linked to slow senescence of leaf and high susceptility to powdery mildew. A new pathotype virulent on *Lr26* (77-5) was reported from Wellington, *Pm8* is ineffective in a spring wheat back ground, the virulent races available at Wellington were showing 5MR–MS reaction to yellow rust, *Sr31* gave a 20MR–MS reaction.
– *Lr28* and *Lr32* were observed to be associated with fast rusting to stem rust susceptibility and a reduced level of infection to powdery mildew, *Lr28* and *Lr32* have association with fast rusting to stem rust.
– *Lr24+Sr24* and *Sr27* are associated with phenotypical markers of apical claw on the spike.
– *Lr19+sr25* seems to be associated with slow leaf senescence and increased yield, however, the susceptibility level for powdery mildew increases.
– *Lr37+Sr28+Yr17* introgression not giving yellow rust resistance in all backgrounds indicating the existance of certain suppressor genes at that particular loci.
– *Sr31* is associated with red grain, in derivatives there is always a chance to get amber grains.

Table 7. Maintenance and utilization of wild species of wheat at the Indian Agricultural Research Institute, Regional Station, Wellington, under this program 2009–09.

Species	Gene pool	Genome	Ploidy level (2n)	Total accessions
Ae. biuncialis	Tertiary	UM	28	122
Ae. columanaris	Tertiary	$U^{co}M^{co}$	28	17
Ae. comosa	Tertiary	M	14	3
Ae. comosa var. *comosa*	Tertiary	M	14	1
Ae. comosa var. *subventricosa*	Tertiary	M	14	1
Ae. crassa	Secondary	DJ, DJX	28, 42	9
Ae. cylindrica	Secondary	CD	28	75
Ae. geniculata	Tertiary	$U^{g}M^{g}$	28	110
Ae. juvenalis	Secondary	DMU	42	1
Ae. kotschyii	Tertiary	USS	28	9
Ae. longissima	Secondary	SB	14	36
Ae. markgrafii	Tertiary	CC	14	39
Ae. neglecta	Tertiary	UM	28	102
Ae. peregrina	Tertiary	US	28	55
Ae. peregrina var. *brachythera*	Tertiary	US	28	3
Ae. peregrina var. *peregrina*	Tertiary	US	28	1
Ae. searsii	Secondary	SS	14	50
Ae. sharonensis	Secondary	S^{sh}	14	77
Ae. speltoides	Secondary	S	14	29
Ae. speltoides var. *ligustica*	Secondary	S	14	9
Ae. speltoides var. *speltoides*	Secondary	S	14	6
Ae. tauchii	Primary	D	14	81
Ae. triuncialis	Tertiary	UC	28	239
Ae.triuncialis var. *persica*	Tertiary	$U^{t}C^{t}$	28	2
Ae.umbellulata	Tertiary	U	14	52
Ae.uniaristata	Tertiary	Mt	14	2
Ae.ventricosa	Secondary	$D^{v}N^{v}$	28	1
T. monococcum subsp. *aegilopoides*	Primary	A^{m}	14	742
T. timopheevii subsp. *armeniacum*	Secondary	AG	28	252
T. timopheevi subsp. *timopheevii*	Secondary	AG	28	22
T. turgidum subsp. *dicoccoides*	Primary	AB	28	595
T. urartu	Primary	A		171
Secale cereale	Tertiary	R	14, 16, 20	136
Total accessions				2,938
Total from tertiary gene pool				155

– *Yr9* is ineffective in a spring wheat background.
– *Lr45* seems to linked to pink awn and glumes at milk stage under low temperature.
– *Lr32* and *Lr28* in combination with *Sr31* are observed to give enhanced yield, to be investigated and exploited.
– Lr35 and Lr45 seems to not enhancing the yield and need further investigation.
– *Lr45* can easily be selected for based on pink awn color.
– Combinations of major and minor genes pyramided in certain elite cultivars is the long-term solution.
– *Lr19* and *Sr31* seem to be associated with high susceptibility to powdery mildew.
– *Lr45* seems to be associated with lax spikes although fertility in the lowest spikelet is restored.

Other externally funded projects in operation now at IARI, Regional Station, Wellington include 1. a DBT-funded Net work project 'Molecular Marker Assisted development of biotic stress resistant wheat varieties' and 2. an Indo-Australian breeding program on 'Molecular markers for broadening the genetic base of stem rust resistance genes effective against strain Ug99'.

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Ug99 virulence of wheat stem rust pathogen yet not detected in India.

J. Kumar and M. Sivasamy.

The virulence of race Ug99 of *Puccinia graminis* Pers..f.sp. *tritici* Eriks. & E.Henn. causing stem rust of wheat was recognized first in Uganda during 1999. Ug99 has the potential of migrating into India as documented by other rust races migrating from eastern Africa to southern Asia. A huge area in India is under cultivation of the mega-cultivar PBW 343 and other Veery cultivars with the gene *Sr31*, which has been rated to be highly susceptible when tested in Kenya (Singh et al. 2006). Owing to the inherent capability of stem rust spores for wind dipersal for long distances, the Nilgiri Hills in Tamil Nadu the state of South India are one of the prospective Indian targets of Ug99 virulence. A continuous vigil thus becomes imperative for tracking the supposed introduction of Ug99 and variants at this location, especially because wheat and stem rust survives here throughout the year.

The Wellington Station of theIndian Agricultural Research Institute situated in the Nilgiri Hills of Tamil Nadu in India is an ideal place to undertake Ug99 surveillance because stem rust survives here in vivo on wheat grown year round as winter and summer (off-season) crops. This IARI research station is well prepared to track the field incidence (if it happens) of new pathogenic strains such as Ug99 with a battery of well-maintained greenhouses for accomplishing virulence analysis in wheat rust pathogens. A quick, differential set comprising wheat lines capable of capturing Ug99

and its variants is regularly planted in a staggered way with repeating sowing at three-month intervals to maintain adult-stage plants continuously in the field. The quick set is comprised of the wheat lines Morocco (no *Sr* gene), LMPG (no *Sr* gene), Seri–MACS 2496, Bacanora–WH 542, Attila–PBW 343, *Sr31*/LMPG, *Sr24* (Tr 380–14), *Sr36* (Cook-2), *Sr36* (Cook), and *Sr36* (LMPG).

In the month of November 2009, the quick set also was planted at all regional stations of IARI; Shimla (North Hill zone), the Wheat Division of IARI headquarters in Delhi (North Western Plain Zone), Indore (Central Zone), and Wellington (South Hill Zone). These station cover all the agro-ecological situations in India suitable for wheat cultivation. Uredosporic dust was collected from 146 leaf samples of stem rust from the premises of the IARI Regional Station, Wellington, between April 2009 and April 2010 from the regular winter (March–April 2009 and October 2009–April 2010) and the summer crops (July–November, 2009). Seedlings of the quick set were inoculated and seedling reactions recorded following Bahadur et al. (1985). These samples yielded only the existing Indian pathotypes and none resembled Ug99 or its reported variants. The adult-stage reactions recorded in the first week of April, 2010, following the scale of Roelfs et al. (1992) indicated that all lines of the quick set were free of stem rust except Morrocco, which was susceptible at Indore and Wellington. We have concluded that Ug99 has not yet reached in Nilgiri Hills or other parts of India so far.

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ITEMS FROM ITALY

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

Pyramiding of leaf rust-resistance genes in common wheat using marker-assisted selection.

F. Nocente, L. Gazza, L. Sereni, and M. Pasquini.

Foliar diseases, such as leaf rust caused by *Puccinia triticina* Eriks. (*Pt*), have been important factors limiting wheat production worldwide. This pathogen is regarded as potentially the most damaging causal agent of rust disease on wheat in Italy, where it is widespread and needs constant monitoring.

One strategy for increasing the durability of resistance in commercial cultivars is to pyramid multiple resistance genes into a single wheat genotype. Pyramiding two or more genes, irrespective of whether they are major or minor, with different modes of action can greatly delay or even prevent the breakdown of resistance. The introgression of two or more genes into the same genetic background is difficult to monitor by traditional phenotypic analysis alone because of the epistatic or dominance effects of some genes or the lack of pathotypes with virulences matching the corresponding resistance gene(s). The availability of specific molecular markers tightly linked to respective resistance genes makes the detection of multiple genes in one genotype possible; such markers are the basis for efficient marker-assisted selection (MAS) in breeding work to speed up the identification of lines carrying two or more resistance genes.

Several known genes for resistance to leaf rust, often derived from related species and genera, have confirmed their efficacy in Italy over a long period. Epidemiological field controls in different locations in Italy and greenhouse

tests were carried out over 5 years on a set of 36 Thatcher NILs, each with one gene (*Lr*) for resistance to *P. triticina*. As a result, five *Lr* genes were selected as the most effective in Italy (Table 1): *Lr9* (from *Ae. umbellulata*), *Lr10* (from *T. aestivum* subsp. *aestivum*), *Lr47* (from *Ae. speltoides*), and the *Lr24-Sr24* (from *Th. ponticum*), and *Lr37-Yr17-Sr38* (from *Ae. ventricosa*) clusters. Molecular markers (STS, CAPS, and SCAR) closely linked to these genes were validated and used for MAS.

Table 1. Resistance genes and related introgression lines used for pyramiding experiments at the Consiglio per la Ricerca e la Sperimentazione in Agricoltura, Roma, Italy.

Resistance gene	Chromosome location	Source	Introgression line
Lr9	6BL	*Ae. umbellulata*	Tc*6 / Transfer // Spada
Lr10	1AS	*T. aestivum* subsp. *aestivum*	Tc*6 / Exchange // Bolero Tc*6 / Exchange // Bilancia
Lr24–Sr24	3D	*Th. ponticum*	Tc*6 /Agent // Bolero Tc*6 /Agent // Spada
Lr47	7A	*Ae. speltoides*	T7AS-7S3#1S-7AS·7AL / Bilancia T7AS-7S3#1S-7AS·7AL / Colfiorito
Lr37–Yr17–Sr38	2AS	*Ae. ventricosa*	Tc8* / VPM1 // Bolero

The NILs carrying these genes were used as donor parents for a backcross program in order to introgress the selected genes in four susceptible, high-quality and locally adapted common wheat cultivars Bolero, Spada, Colfiorito, and Bilancia. Eight introgression lines were obtained (Table 1) and intercrossed in order to combine two or more resistance genes into the same wheat cultivar using a gene-pyramiding scheme (Table 2). The first gene combination was achieved by crossing 'Bolero+*Lr24*' with 'Bolero+*Lr9*' (Fig. 1) followed by selfing the progenies and then screening by MAS to identify individuals homozygous at both requested loci. The same breeding scheme was used for combining the other *Lr* genes into cultivars Spada, Colfiorito, and Bilancia. The introgression of the target genes was confirmed by both PCR amplification of molecular markers (STS, CAPS, and SCAR) linked to the genes and phytopatological tests to verify their phenotypic expression in the new genetic background. Further screening of *Lr24-Sr24+Lr9* cross combination was simplified and accelerated by the use of a high-throughput, multiplex PCR system that allows the simultaneous detection of both resistance gene (Fig. 2). Reaction conditions, such as annealing temperature, primer concentration, and type of polymerase, were optimized to obtain a robust amplification and reproducible genotype analysis. In addition, phytopathological analysis using specific rust pathotypes were performed in order to confirm the absence of suppressing or modifying effects due to the co-presence of the introgressed genes.

Table 2. Crosses for gene pyramiding through marker-assisted selection at the Consiglio per la Ricerca e la Sperimentazione in Agricoltura, Roma, Italy.

Bolero + *Lr24–Sr24*	/	Spada + *Lr9*
Bolero + *Lr24–Sr24*	/	Bolero + *Lr9* (Fig. 1)
Bolero + *Lr24–Sr24*	/	Bolero + *Lr37–Yr17–Sr38*
Spada + *Lr9*	/	Spada + *Lr24–Sr24*
Spada + *Lr24–Sr24*	/	Colfiorito + *Lr47*
Bilancia + *Lr10*	/	Bilancia + *Lr47*

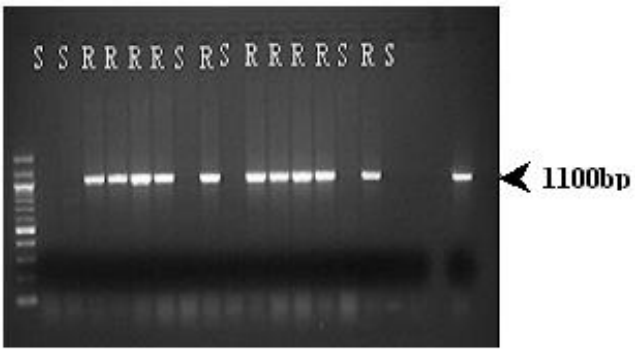

Fig. 1. STS marker-assisted screening of leaf rust resistance gene *Lr9* on the progny from a cross between the cultivar Bolero and a Thatcher NIL–*Lr9* (R = resistance and S = susceptible).

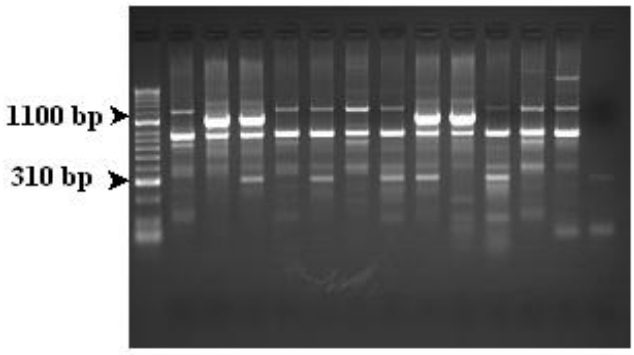

Fig. 2. Multiplex PCR on F_2 plants from a cross between Bolero+*Lr24* and Bolero+*Lr9*. A single, resolved band for each marker, 1,100 bp for *Lr9* and 310 bp for *Lr24*, was visualized on an ethidium bromide-stained agarose gel.

Different individuals were identified with favorable gene combinations: *Lr24-Sr24+Lr47*, *Lr24-Sr24+Lr37-Yr17-Sr38*, *Lr9+Lr24-Sr24*, and *Lr10+Lr47*. These combinations can prevent the breakdown and enhance the durability of resistance, expressed both in seedling and adult-plant stages, and possibly to more than one pathogen, as in the case of gene clusters *Lr24-Sr24* and *Lr37-Yr17-Sr38*, conferring resistance to leaf (adult-plant resistance), stripe, and stem rust.

Novel, selected genotypes are now available that could be useful as cultivars or for further breeding work. In conclusion, the pyramiding of relevant resistant genes in an agronomically superior genotype offers real solutions for a longer period of protection and for a shorter breeding time.

Table 3. Field behavior to natural powdery mildew infections of 6V disomic substitution and addition lines in different regions of Italy during 2007–08 and at Martonvásár, Hungary, in 2008–09. For infection type, the first digit gives the relative height of disease (1–9, a value of 5 corresponds to the midpoint of the plant), the second digit shows the disease severity as a percentage but in terms of 0–9 following the modified Cobb's scale (0–100%), Tr = trace, — = no data, and an * indicates symptoms on the susceptible line CS/V58 derived from CS lacking of chromosome 6V#4.

Line/cultivar	Lonigo (VC)		S. Angelo (LO)		S. Lazzaro (BO)		Viterbo (VT)		Foggia (FG)		Libertinia (CT)	Caltagirone (CT)	Martonvásár, Hungary	
	2007	2008	2007	2008	2007	2008	2007	2008	2007	2008	2008	2007	2008	2009
CS/V32	0	1–2	8–3	0	0	0	0	0	0	0	1–Tr	1–3	Tr	Tr
CS/V63	0	0	8–1	8–1	1–1	0	0	0	0	0	Tr	1–3	—	—
Chinese Spring (CS)	—	7–6	—	7–6	—	1–Tr	6–6	6–5	—	0	0	—	8–5*	8–5*
Fortunato (check)	6–4	6–6	8–4	8–3	9–6	7–4	7–6	7–5	0	5–3	1–Tr	5–3	—	—
Novosadska (check)	8–5	7–7	8–5	8–5	9–4	7–5	8–4	8–5	5–1	5–3	5–3	1–2	—	—
Irnerio (check)	8–7	7–7	8–5	8–4	9–7	7–7	—	8–6	1–2	7–5	7–8	1–4	—	—

Resistance to Blumeria graminis tritici and Puccinia triticina in aneuploid wheat lines with chromatin introgressed from Dasypyrum villosum.

M. Pasquini, F. Nocente, L. Sereni, and A. Matere; M. Bizzarri, D. Vittori, and C. De Pace (Department of Agrobiology and Agrochemistry, University of Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy); and G. Vida (Agricultural Research Institute of the Hungarian Academy of Sciences, Brunszvik u.2, H-2484 Martonvàsàr, Hungary).

Leaf rust and powdery mildew are important fungal diseases affecting wheat cultivation in Italy. National pathogenicity surveys and virulence determinations are annually performed in the most important wheat-growing areas to obtain data on disease severity and virulence composition of the pathogen population. The incorporation of effective and durable resistance is a valuable breeding strategy for wheat improvement, and the wild species prove to be a useful source for this character. *Dasypyrum villosum* Candargy (syn. *Haynaldia villosa*) (*Dv*) is an annual, diploid (2n=14), allogamous grass species, belonging to the tribe Triticeae. This species is widespread in the Mediterranean region and has been reported as carrying different genes conditioning useful characters, including resistance to several pathogens. One gene for resistance to *B. graminis* f.sp. *tritici* was reported to be located at locus *Pm21* on the short arm of chromosome 6V#2 introgressed in *T. astivum* subsp. *aestivum* from *D. villosum*. A study was made on the disomic addition (DA) (CS/V63) and substitution (CS/V32) (DS) lines of chromosome 6V#4 introgressed, by Prof. De Pace, into the Chinese Spring (CS) wheat chromosome complement from a *D. villosum* population collected in Latium. The disomic addition line (DA) CS/V63 was completely resistant to powdery mildew at adult-plant and seedling stages, in comparison with the disomic substitution line (DS) CS/V32, which was genetically unstable at the seedling stage (Tables 3 and 4). As matter of fact, monosomic and nullisomic

Table 4. Seedling inoculation with *B. graminis* pathotypes of control and wheat introgression lines. Infection type scoring was a 0–4 scale.

Line	Pathotype	
	O1	O2
CS / V63 95-97 2n=44	0	0
CS / V63 1.95 2n=44	0	0
CS / V32 v616-1 2n=42	0/3	0/3-
CS / V32 v623-3 2n=42	0/1++3=	0/3-
Chinese Spring (CS)	3/3+	3+
CS+6V (Sears)	3+	3+
Dv T v330	0	0
Dv 200 v346	0	0

plants for 6V#4 were observed in the progenies of CS/V32. In nursery plots designed for disease scoring under air-borne inoculum and grown in two-year field experiments in several Italian localities and at Martonvàsàr (Hungary), the two lines carrying chromosome 6V#4 confirmed their resistance in many environments (Table 5).

Table 5. Segregation for resistance to powdery mildew pathotype O2 in F_2 plants (* non significant).

Cross combination	Number of F_2 plants	Resistant	Susceptible	χ^2 (3:1)
CS / V63 // CS + 6V	356	270	86	0.284 *

The DA CS/V63 line was crossed to the susceptible DA line 6V#1, obtained by Prof. E.R. Sears. A suitable mapping population, segregating for powdery mildew resistance coming from chromosome 6V#4 of *D. villosum*, was obtained. The $F_{2:3}$ progenies were studied both by phytopathological (with a selected pathotype of *B. graminis*) and molecular (PCR marker) analyses in order to assess the genetic basis of resistance. The segregation for powdery mildew resistance indicated the presence of one dominant gene (called *PmVt*) controlling resistance, presumably located on 6VS (Table 5). Molecular analyses using the marker $OPH17_{1900}$, reported as linked to the *Pm21* gene, were used to confirm the location of this gene on 6VS and to verify its relationship with the *Pm21* locus. The preliminary analyses on resistant and susceptible F_3 progenies seem to confirm the location of *PmVt* on 6VS, but the marker and the resistance gene do not seem to be closely linked (Fig. 3).

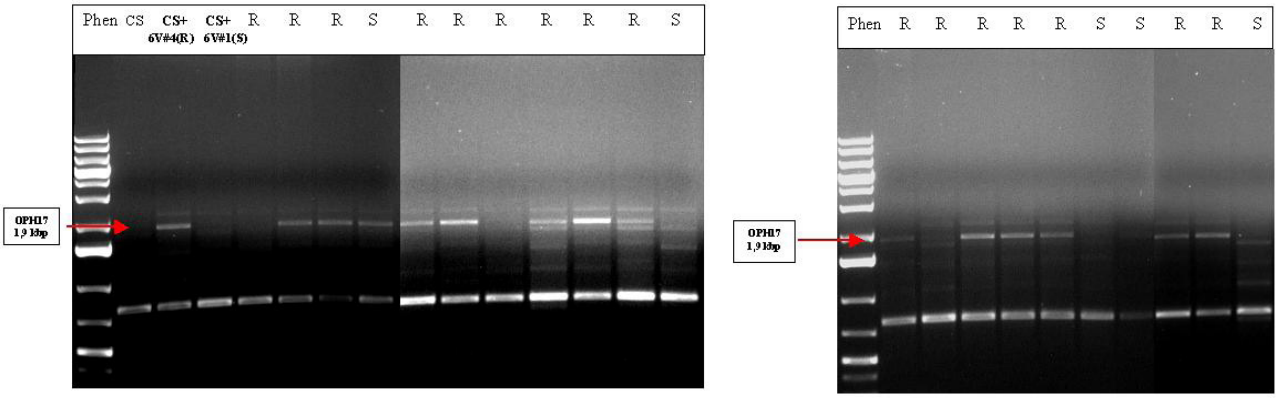

Fig. 3. Preliminary analysis on resistant and susceptible F_3 progeniew from the cross 'CS/V63//CS/6V' using the molecular marker $OPH17_{1900}$.

The lines also were tested for resistance to *P. triticina*. All lines were susceptible in experiments with different selected pathotypes at the seedling stage. When tested in the field in multilocation epidemiological trials, they showed adult-plant resistance (APR) to *P. triticina* (Tables 6 and 7, p. 99). The genetic basis of APR was studied in the same $F_{2:3}$ progenies, and the resistance surveyed in the 6V#4-introgression line could be controlled by a single resistance gene, different from those already present in Chinese Spring (*Lr12*, *Lr34*).

In conclusion, the *D. villosum* ecotypes coming from Latium resulted in resistance to *B. graminis*. A suitable mapping population, segregating for powdery mildew resistance on chromosome 6V of *D. villosum*, was obtained. One dominant gene (*PmVt*) controlling resistance to *B. graminis* was identified; adult plant resistance (probably under simple genetic control) to *P. triticina*, derived from *D. villosum*, was observed

Table 6. Seedling inoculation with *P. triticina* pathotypes of control and wheat introgression lines. Infection type scoring was a 0–4 scale.

Line	Pathotype		
	B-1	B-2	B-3
Chinese Spring (CS)	3+	3+	4
CS / V63 A (2n=44)	3+	3+ 4	4
CS / V32 S (2n=42)	3+ 4	3	4
CS 1BL/1VS	3+	3+	3+ 4
CS+6V (Sears)	3+	3+	3+ 4
Dv T	1–	0	0; 1=
Dv 200	1=	1–	1–
CS / V58 (2n=42)	3+	3+	3+
CS / V59 (2n=42)	3+	3+	3+
CS / V60 (2n=42)	3+	3+	3+

Table 7. Field behavior to natural leaf rust infections of 6V disomic substitution and addition lines in different regions of Italy during 2007–08 and at Martonvásár, Hungary, in 2008–09. For infection type, the first digit gives the relative height of disease (1–9, a value of 5 corresponds to the midpoint of the plant), the second digit shows the disease severity as a percentage but in terms of 0–9 following the modified Cobb's scale (0–100%), Tr = trace, — = no data, and an * indicates symptoms on the susceptible line CS/V58 derived from CS lacking of chromosome 6V#4.

Line/cultivar	S. Angelo (LO)		Grosseto (GR)	Montelibretti (RM)		Ussana (CA)		Foggia (FG)		Gela (CL)		Marton-vásár, Hungary	
	2007	2008	2007	2007	2008	2007	2008	2007	2008	2007	2008	2008	2009
CS/V32	—	0	3	0	5–1	0	0	—	0	7–3	1–3	Tr	Tr
CS/V63	—	8–2	3	Tr	Tr	0	0	—	0	—	8–2	—	—
Chinese Spring (CS)	—	8–4	—	—	8–4	—	8–4	—	0	—	8–4	8–5*	8–5*
Fortunato (check)	7–3	8–7	8	8–5	8–4	8–6	8–5	8–3	5–2	7–5	7–4	—	—
Novosadska (check)	7–2	8–5	2	1–1	5–1	0	8–Tr	0	0	1–1	5–4	—	—
Irnerio (check)	8–3	8–8	8	8–2	8–5	8–6	8–3	8–2	0	8–6	8–7	—	—

in the wheat introgression lines; new bread wheat genotypes were selected carrying useful genes controlling different characters.

Septoria disease complex on durum wheat in Italy.

A. Iori, A. L'Aurora, A. Matere, L. Sereni, F. Casini, and M. Pasquini.

The Septoria disease complex, caused by *M. graminicola* (anamorph *S. tritici*) and *Phaeosphaeria nodorum* (anamorph *St. nodorum*), has been observed on durum wheat during the last few years and an increase in its diffusion has been recorded (Fig. 4). The presence of the disease has been detected not only in northern regions of Italy but outside its typical area of spread as well (central and southern Italy).

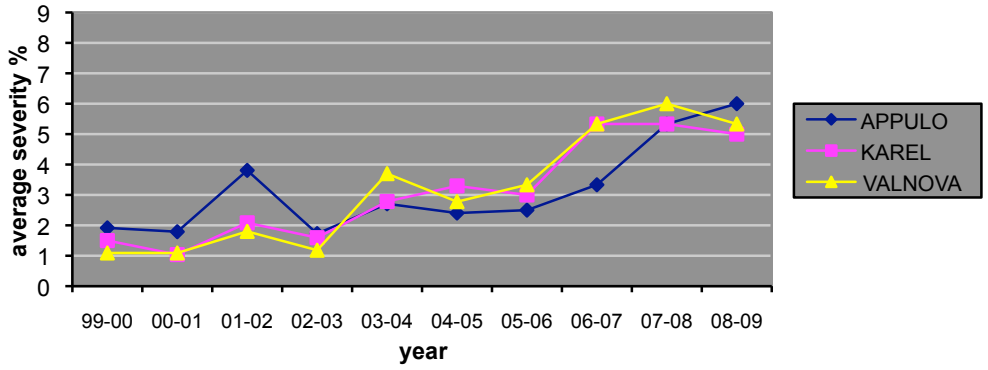

Fig. 4. Average severity of the Septoria disease complex on durum wheat check cultivars from 2000 to 2009.

National pathogenicity surveys and virulence determinations were conducted by organizing field nurseries in the most important durum wheat-growing areas. Twenty-three wheat genotypes, included in the National Durum Wheat Network, were grown in experimental fields situated in central and southern Italy, during a 4-year period. Data on disease severity were recorded using a double-digit scale, representing the vertical disease progress (first digit) and disease severity as a percentage (second digit). Naturally infected leaf samples were collected from the field; leaf segments were put in humidity chamber or on water agar medium at 20°C for 48 h and then analyzed with stereoscopic and compound microscopes for pathogen identification.

Climatic conditions favored the spread of Septoria disease complex on wheat plants in 2007 and 2009; moderate disease infections were observed in 2008 but not present on plants in 2006 (Table 8, p. 100). All genotypes were moderately or completely susceptible in the field to *S. tritici* and/or *S. nodorum* in the location/year where heavy infections of these pathogens were detected, such as in Sardinia in 2009. Microscopic analyses on infected leaf samples showed

Table 8. Behavior of durum wheat cultivars to the Septoria disease complex in central and southern Italy from 2006 to 2009 (R = resistant, MR = moderately resistant, MS = moderately susceptible, S = susceptible, and — = missing data).

Culitvar	2006			2007			2008			2009		
	Puglia (FG)	Sardinia (CA)	Lazio (RM)	Puglia (FG)	Sardinia (CA)	Lazio (RM)	Puglia (FG)	Sardinia (CA)	Lazio (RM)	Puglia (FG)	Sardinia (CA)	Lazio (RM)
Anco Marzio	R	R	R	R	MR	MS	MR	R	R	R	MS	MR
Canyon	R	R	R	MS	R	MS	MR	R	R	R	MS	MS
Casanova	R	R	MR	MR	MR	MS	MR	MR	R	R	MS	MR
Ciccio	R	R	R	MR	R	MS	R	MR	R	R	S	S
Claudio	R	R	R	MS	R	MS	R	R	R	R	S	MR
Creso	R	R	MR	R	MS	MR	R	MR	R	R	MR	MS
Duilio	R	R	MR	MS	R	R	MR	MR	MR	R	S	MR
Dylan	R	R	R	MS	R	—	MR	MR	R	R	S	MS
Grecale	R	R	R	R	MS	MS	R	R	MR	R	MS	MR
Iride	R	R	MR	MS	—	—	R	MR	R	R	S	MR
Levante	R	R	MR	MR	MR	MR	MS	R	MS	R	MR	MS
Maestrale	R	R	R	MS	R	—	R	—	MR	R	MS	MS
Meridiano	R	R	R	MS	R	—	R	MR	MR	R	S	MS
Neolatino	R	R	R	MR	MS	S	R	R	MR	R	S	MR
Normanno	R	R	R	R	MS	MR	MS	R	MR	R	S	MR
PR22D89	R	R	MS	R	MS	—	MS	R	MR	R	S	R
Sant Agata	R	R	R	MR	MS	MS	MS	MS	R	R	S	R
Saragolla	R	R	R	R	MS	MR	R	R	R	R	S	MS
Simeto	R	R	MS	MS	R	MS	R	MS	R	R	S	S
Solex	R	R	MR	MR	MR	MS	R	MR	MS	R	S	R
Svevo	R	R	MR	MS	R	MS	MS	MS	MR	R	S	S
Valerio	R	R	MR	MS	R	MS	R	MR	MS	R	S	MR
Virgilio	R	R	MS	R	MR	MS	R	MR	S	R	S	MR

that *S. tritici* and *S. nodorum* sometimes occur together and with other pathogens on durum wheat cultivars. *S. tritici* was isolated most during the last four years, whereas *S. nodorum* was identified only in 2008 and 2009 (Table 9).

Table 9. Isolation frequency (%) of fungal pathogens on infected leaf samples from field experiments.

	2006	2007	2008	2009
Number of samples	19	29	16	25
Septoria tritici	16	41	19	54
Stagonospora nodorum	0	0	6	29
Fusarium spp.	11	7	0	23
Helminthosporium spp.	63	66	19	29
Alternaria spp.	84	100	94	91
Cladosporium spp.	84	83	88	77
Epicoccum spp.	16	31	56	40
Stemphylium boryosum	26	38	31	40
Phoma spp.	5	3	0	6

Monitoring of powdery mildew and leaf rust infections in Italy: behavior of durum wheat cultivars.

A. Matere, F. Nocente, L. Sereni, A. L'Aurora, F. Casini, and M. Pasquini.

Fungal diseases affect wheat cultivation in Italy with economic consequences because of their influence on yield, grain quality, and healthiness. National pathogenicity surveys and virulence determinations are conducted annually, both in organic and conventional farming systems, to provide timely information about the structure of pathogen populations, which are relevant to breeding programs and resistance deployment.

Data on disease severity are recorded in the field, and artificial inoculations, at the seedling stage, are conducted in greenhouse by testing single pathotypes of the different pathogens on durum and common wheat cultivars and lines. For field evaluation, a double-digit scale, representing vertical disease progress (the relative height of the disease based on a 1–9 scale, with the value of 5 corresponding to the mid-point of the plant) and severity estimate (disease severity as a percentage following a modified Cobb's scale 0–100%) was used.

Among epigeous wheat diseases, powdery mildew and leaf rust occur annually throughout most Italian wheat-growing areas. Powdery mildew has shown a decrease in its frequency and severity over time, probably because of the cultivation of more resistant cultivars and the occurrence of climatic conditions unfavourable for fungal growth. The mean percentage of powdery mildew infections on the susceptible check cultivars Appulo (durum wheat) and Fortunato (common wheat) has not exceeded 44% during the last decade. Durum wheats appear to be more susceptible than bread wheat (Fig. 5)

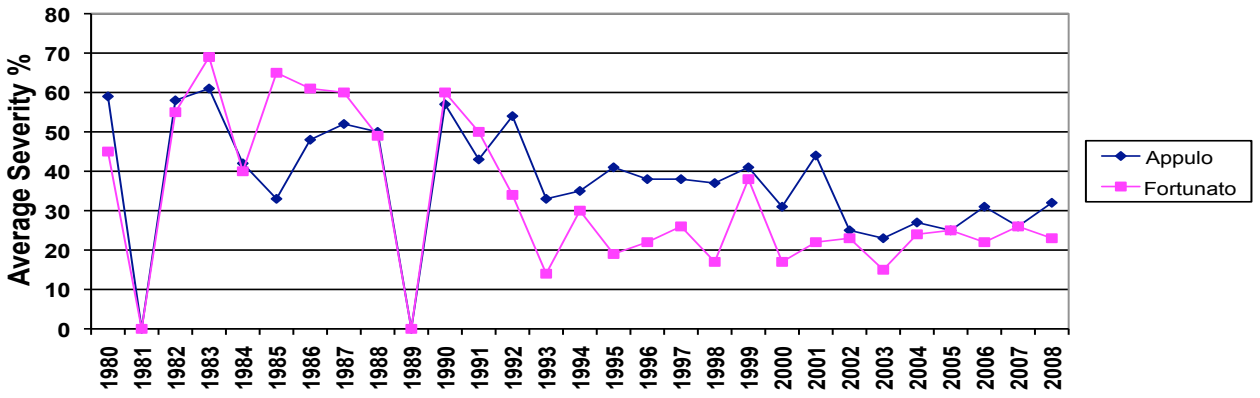

Fig. 5. Average powdery mildew severity in the field on durum (Appulo) and bread (Fortunato) wheat check cultivars from 1980 to 2008.

From 1981 to 1991, the mean percentage of leaf rust infections was generally over 50% on susceptible wheat cultivars; in the last years the disease has shown a moderate decrease in its frequency and severity (Fig. 6). The disease severity frequently appeared slightly higher on bread wheat than on durum cultivars. Durum wheat showed slightly higher percentages of infection in central and southern Italy than in the north.

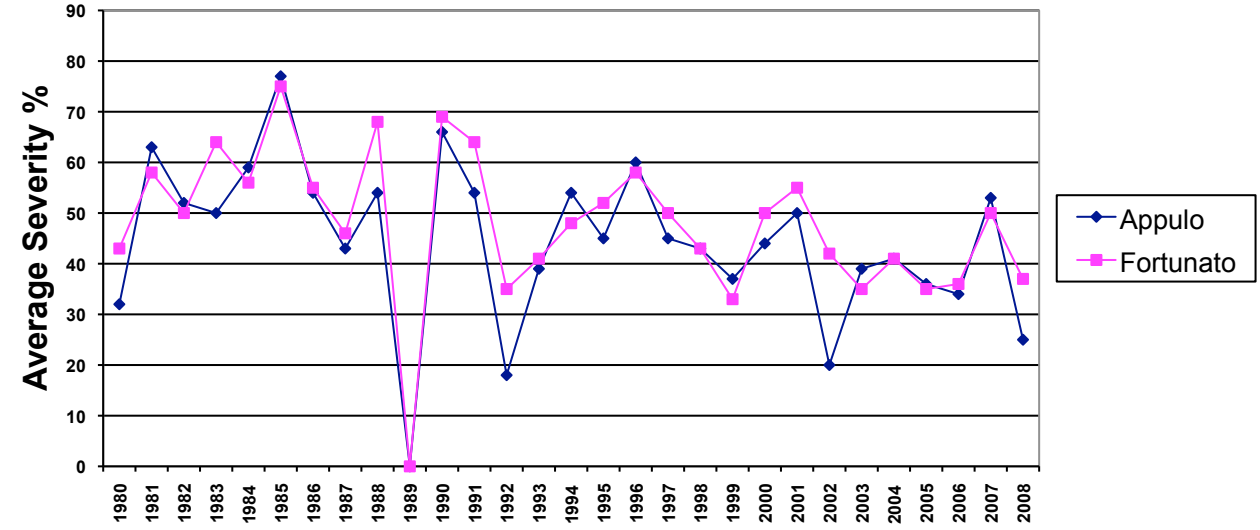

Fig. 6. Average leaf rust severity in the field on durum (Appulo) and bread (Fortunato) wheat check cultivars from 1980 to 2008.

During the last four years, data on field infections by powdery mildew and leaf rust on durum wheats have been recorded in central and southern Italy (typical durum wheat-growing areas) and included in the National Durum Wheat Network. Field nurseries were organized in different locations in Italy; in some, disease infections allowed a comparison of the varietal behavior.

Many durum wheats grown in Italy resulted resistant to powdery mildew in almost all the locations tested (Table 10, p. 103). With respect to leaf rust none of the cultivars was found completely resistant in the years/locations considered, but several genotypes (Casanova, Levante, Normanno, PR22D89 and Saragolla) showed only a moderate susceptibility in some wheat growing areas (Table 10).

Table 10. Field behavior to powdery mildew in central and southern Italy of durum wheat cultivars included in the National Wheat Network (R = resistant; MR = moderately resistant; MS = moderately susceptible; s = Susceptible; and — = missing data).

Cultivar	Locality												
	2005–06				2006–07					2007–08		2008–09	
	Sicily (CL)	Calabria (CS)	Puglia (FG)	Basilicata (MT)	Sicily (CL)	Sardinia (CA)	Calabria (CS)	Puglia (FG)	Basilicata (MT)	Sicily (CT)	Puglia (FG)	Sicily (CL)	Puglia (FG)
Anco Marzio	R	MS	R	R	R	R	R	R	R	MS	MS	R	R
Canyon	R	R	R	R	MR	R	R	R	R	R	R	—	R
Casanova	R	R	R	R	MR	R	R	R	R	R	R	R	R
Ciccio	R	MR	R	R	R	R	R	R	R	MR	MS	R	R
Claudio	R	R	R	R	R	R	R	R	R	R	R	R	R
Creso	R	R	R	R	R	R	R	R	R	R	R	—	R
Duilio	R	R	R	R	R	R	R	R	R	R	R	R	R
Dylan	R	MR	R	R	MR	R	R	R	R	R	MS	R	R
Grecale	R	MR	R	R	R	R	R	R	R	MS	R	R	R
Iride	R	R	R	R	—	R	R	R	R	R	R	R	R
Levante	R	MS	R	R	R	R	R	R	R	R	R	R	R
Maestrale	R	R	R	R	R	R	—	R	R	R	R	R	R
Meridiano	R	R	R	R	R	R	R	R	R	R	R	R	R
Neolatino	R	R	R	R	R	R	R	R	R	R	R	—	R
Normanno	R	R	R	R	R	R	R	R	R	R	MS	R	R
PR22D89	R	R	R	R	R	R	R	R	R	R	MR	—	R
Sant'Agata	R	R	R	R	MR	R	R	R	R	MR	MS	R	R
Saragolla	R	R	R	R	MR	R	-	R	R	MR	R	R	R
Simeto	R	R	R	R	R	R	R	R	R	MS	MR	R	R
Solex	R	R	R	R	R	R	—	R	R	R	R	—	R
Svevo	R	R	R	R	MR	R	—	R	R	R	R	R	R
Valerio	R	R	R	R	MR	R	—	R	R	R	R	R	R
Virgilio	R	R	R	R	MR	R	R	R	R	R	R	—	R

The same durum wheat cultivars were artificially inoculated in greenhouse, at the seedling stage, with different pathotypes of *B. graminis* and *P. triticina*, identified within the pathogen populations during the 2005–06 to 2008–09 crop seasons. Infection types were scored on a 0–4 scale. The reaction of genotypes to the different pathotypes anually identified has been reported (Table 11, p. 103). The cultivars Canyon, Dylan, Grecale, Iride, Levante, Maestrale, Meridiano, Normanno, Saragolla, and Svevo had a resistant or variable behavior with respect to both pathogens between 2005 and 2009 (Table 12, p. 103).

In conclusion, the risk of heavy epidemics is potentially in Italy high because of the selection of new virulent variants within the pathogen populations; increased cultivation of susceptible cultivars, often from foreign countries;

Table 11. Field behavior to leaf rust in Central and Southern Italy of durum wheat cultivars included in the National Wheat Network (R = resistant; MR = moderately resistant; MS = moderately susceptible; s = Susceptible; and — = missing data).

Cultivar	Locality																
	2005–06			2006–07						2007–08				2008–09			
	Calabria (CS)	Puglia (FG)	Basilicata (MT)	Sicily (CL)	Sardinia (CA)	Calabria (CS)	Puglia (FG)	Basilicata (MT)	Lazio (RM)	Sicily (CL)	Puglia (FG)	Sardinia (CA)	Lazio (RM)	Sicily (CL)	Puglia (FG)	Sardinia (CA)	Lazio (RM)
Anco Marzio	R	R	R	MS	R	R	R	R	S	MS	R	R	R	R	R	R	R
Canyon	MR	MR	MS	MS	S	MR	MS	R	MS	MR	R	R	R	—	R	MS	MR
Casanova	R	R	R	MS	MR	R	MR	R	MR	R	R	—	R	R	R	MS	R
Ciccio	MS	MR	R	S	S	MR	MS	MS	MS	MR	R	R	R	MR	MR	R	MR
Claudio	R	R	R	S	S	R	MS	MS	S	R	R	—	R	R	MR	MS	R
Creso	MR	R	MS	MS	S	R	R	MR	MR	R	R	MR	R	—	R	R	MS
Duilio	MS	MR	R	S	S	R	MS	MR	MS	R	MR	MR	R	R	R	R	R
Dylan	R	R	MS	MS	S	R	MS	R	S	MR	R	MR	R	R	R	R	MS
Grecale	MR	R	R	MS	S	R	R	R	R	R	R	R	R	R	R	R	R
Iride	MR	MR	R	—	S	R	MS	R	S	MR	R	R	R	R	R	R	MS
Levante	R	R	R	MS	R	R	MR	R	MS	R	R	R	R	R	R	R	MS
Maestrale	R	R	R	MR	S	R	MS	R	MS	MS	R	R	R	R	R	MR	MR
Meridiano	MS	MR	MR	MR	S	MR	S	R	MS	R	R	R	R	R	R	R	MS
Neolatino	MR	MR	MR	MR	S	MR	MS	MR	MS	MS	R	R	R	—	R	MS	R
Normanno	R	R	R	MS	MR	R	R	R	MS	MS	R	R	R	R	R	MS	R
PR22D89	MR	R	MS	MS	MR	MR	MR	MR	MS	MR	MR	R	R	—	R	R	R
Sant'Agata	MS	MS	R	MS	S	MR	MS	MR	S	MS	R	MR	R	R	MR	MR	MR
Saragolla	MR	R	R	MS	MR	R	R	R	R	MS	R	R	R	MR	R	R	MR
Simeto	MS	MR	R	MR	S	MR	MR	MR	S	R	R	MR	R	R	MR	R	MS
Solex	MS	R	R	MS	MR	R	MR	R	S	R	R	R	R	—	R	MR	R
Svevo	MS	MR	MR	MS	S	MR	MS	R	S	MR	R	R	R	R	R	MR	S
Valerio	MS	MS	MR	MS	S	MR	MS	R	S	MR	R	MR	R	MS	R	MR	MS
Virgilio	MS	R	R	S	MS	MR	MS	R	S	R	R	R	R	—	R	R	MR

Table 12. Seedling behavior of durum wheat cultivars artificially inoculated with different, annually identified pathotypes (R = resistant to the whole spectrum of virulence tested; S = susceptible to the whole spectrum of virulence tested; V = variable, the genotype is carrying some gene for resistance; and — = missing data).

Cultivar	*Blumeria graminis*				*Puccinia triticina*			
	(2 pathotypes) 2006	(3 pathotypes) 2007	(2 pathotypes) 2008	(2 pathotypes) 2009	(4 pathotypes) 2006	(5 pathotypes) 2007	(4 pathotypes) 2008	(4 pathotypes) 2009
Anco Marzio	S	S	R	V	R	V	V	R
Canyon	V	V	V	V	V	V	V	V
Casanova	S	S	R	R	V	R	R	V
Ciccio	S	S	V	V	V	R	R	V
Claudio	S	S	V	V	V	V	S	V
Creso	S	V	R	R	R	R	R	R
Duilio	S	S	S	V	V	V	V	R
Dylan	R	R	R	R	R	V	—	R
Grecale	V	V	R	V	V	V	—	R
Iride	R	V	V	V	R	V	R	R
Levante	R	R	R	R	R	R	R	R
Maestrale	R	R	R	V	R	R	R	R
Meridiano	R	V	R	V	R	V	R	R
Neolatino	V	S	S	V	R	V	R	V
Normanno	R	V	R	R	R	V	R	R
PR22D89	S	S	S	V	V	V	R	V
Sant'Agata	V	V	S	V	V	V	R	R
Saragolla	R	V	R	R	R	R	—	R
Simeto	S	V	V	V	V	V	—	V
Solex	V	V	S	V	R	V	R	V
Svevo	V	R	R	R	V	V	V	R
Valerio	V	S	V	S	R	R	R	V
Virgilio	S	S	S	S	V	V	S	V

inoculum migration from adjacent wheat-producing regions; and modified cultural practices. Selecting new wheat genotypes, characterized by multiple and durable resistance to different pathogens, by classic and nonconventional breeding is important.

2007–09 national network of conventional durum wheat cultivar trials.

Andreina Belocchi, Maria Grazia D'Egidio, Mauro Fornara, Ester Gosparini, Valerio Mazzon, and Fabrizio Quaranta.

Since 1972, the Research Unit for the Qualitative Valorization of Cereals of the Italian Council for Research in Agriculture (CRA–QCE, Rome) has coördinated the national network for the evaluation of the performance of conventionally managed durum wheat cultivars. The aim of this network is to provide useful information about the qualitative and quantitative traits of durum wheat cultivars managed conventionally, testing at the same time their suitability to specific agroclimatic conditions. Field trials are kept in diverse locations, in collaboration with some important national and local agencies involved in agricultural research. Between 2007 and 2009, field experiments were carried out in 54 locations, grouped into six main geographical and pedoclimatic areas (Sicily, Southern Italy, Sardinia, Thyrrenic–Central Italy, Adriatic–Central Italy, and Northern Italy). Several cultivars were evaluated; some were tested in all the environments, whereas others were considered suitable only for a part. Three replicate trials were grown in each field. The agronomic

performance of ten genotypes evaluated in all the areas between 2007 and 2009 are given in Table 13. Such cultivars represent a considerable amount of the durum wheat commercialized seed in Italy. For all the observed parameters and all growing areas, the mean data of the cultivars equalled the values obtained considering all the tested genotypes.

Table 13. Yield, grain protein content, and test weight of ten Italian durum wheat cultivars tested during a three- year period (2007–09) in six areas of Italy (for length of growing cycle, E = early, ME = medium early, M = medium, ML = medium late, and L = late).

Cultivar	Length of growing cycle	Yield							
		Index (yield / column mean * 100)							t/ha
		Sicily	Sardinia	South	Thyrrenic–Central	Adriatic–Central	North	Mean	Mean
Anco Marzio	E	106	100	101	104	102	104	**103**	**5.28**
Ciccio	E	95	95	92	87	92	90	**92**	**4.73**
Duilio	E	106	97	99	98	97	99	**99**	**5.11**
Saragolla	E	109	112	107	107	109	107	**109**	**5.60**
Iride	ME	104	108	103	104	101	102	**104**	**5.34**
Simeto	ME	86	93	97	94	97	93	**94**	**4.81**
Claudio	M	105	104	104	100	103	105	**104**	**5.32**
Normanno	M	97	104	105	107	105	103	**104**	**5.34**
Dylan	ML	105	94	103	107	99	108	**103**	**5.27**
Creso	L	87	91	89	91	93	88	**90**	**4.63**
Mean (t/ha)		**4.46**	**5.81**	**4.13**	**4.76**	**6.24**	**5.47**	**100**	**5.14**
		Grain protein content							
		Index (grain protein content / column mean * 100)							**% D.M.**
Anco Marzio	E	101	105	100	100	100	98	101	**13.4**
Ciccio	E	97	95	97	97	98	99	97	**13.0**
Duilio	E	98	102	100	100	100	101	100	**13.4**
Saragolla	E	98	101	98	98	98	98	98	**13.1**
Iride	ME	97	96	96	96	97	98	97	**12.9**
Simeto	ME	104	101	102	103	104	104	103	**13.8**
Claudio	M	100	99	100	100	100	101	100	**13.4**
Normanno	M	101	101	102	101	100	101	101	**13.5**
Dylan	ML	101	98	1011	100	99	99	100	**13.3**
Creso	L	103	103	105	104	103	101	103	**13.8**
Mean (% D.M)		**80.5**	**80.6**	**80.5**	**78.8**	**78.9**	**75.4**	**100**	**79.1**
		Test weight							
		Index (test weight / column mean * 100)							**kg/hl**
Anco Marzio	E	102	102	102	102	102	103	102	**80.7**
Ciccio	E	100	101	101	99	100	100	100	**79.1**
Duilio	E	99	99	100	99	100	100	99	**78.7**
Saragolla	E	99	99	98	99	99	98	99	**78.2**
Iride	ME	100	99	99	99	99	98	99	**78.3**
Simeto	ME	97	97	98	97	97	96	97	**76.8**
Claudio	M	102	103	102	103	103	104	103	**81.3**
Normanno	M	98	99	99	99	100	99	99	**78.5**
Dylan	ML	101	100	100	102	100	102	101	**79.7**
Creso	L	101	101	101	102	101	101	101	**79.9**
Mean (kg/hl)		**80.5**	**80.6**	**80.5**	**78.8**	**78.9**	**75.4**	**100**	**79.1**

The average national yield for the period reached 5.14 t/ha; the highest production was achieved in Adriatic–Central Italy, whereas the lowest was from Southern Italy (6.24 t/ha and 4.13 t/ha, respectively). Four of the cultivars (the early cultivars Anco Marzio, Saragolla, and Iride, and the medium Claudio) reached yield indexes higher than 100 in all six environments. On the contrary, Creso, Ciccio, and Simeto were clearly below the average in every area.

Grain protein content was the highest in Northern Italy (14.0%, the nationwide average was 13.4 %) and lowest in Sardinia (12.7 %). The cultivars Creso, Normanno, and Simeto were above average in every area, and Ciccio and Iride were characterized by at all locations as lower than the national average. No genotype was high for both yield and protein content, but Dylan and Normanno showed a satisfactory compromise between high yield and good protein level .

Test weight values were not much different from each other, with the exception of northern Italy, where the aveage (75.4 kg/hl) was clearly below the others. The national mean value was 79.1 kg/hl with the best results in Sardinia (80.6 kg/hl) and Sicily and southern Italy (80.5 kg/hl). No great differences were detected between the cultivars if Simeto is excluded. The average test weight for Simeto during the period was 76.8 kg/hl; other values ranged from 81.3 kg/hl (Claudio) to 78.2 kg/hl (Saragolla). Claudio, Anco Marzio, Creso, and Dylan exceeded the local average in every area, Duilio, Iride and Saragolla were slightly under average, and Simeto was the only cultivar whose test weight was remarkably under the mean data in every growing area.

2007–09 national network of organic durum wheat cultivar trials.

Fabrizio Quaranta, Andreina Belocchi, Maria Grazia D'Egidio, Mauro Fornara, Sahara Melloni, Massimiliano Camerini (University of Molise, Dip. to S.A:V.A), and Stefano Pucciarmati.

In 2003, Italian Ministry of Agriculture established a national network in order to supply to farmers useful information concerning the qualitative and quantitative performance and suitability of durum wheat cultivars to specific agrosystems managed by organic farming. The Research Unit for Qualitative Valorization of Cereals of the Italian Council for Research in Agriculture (CRA–QCE, Cereal Quality Research Unit in Rome) coördinated this network, which was carried out in collaboration with diverse national agencies and universities. In the period between 2007 and 2009, 16 durum wheat cultivars (representing about 70% of the commercialized seed) were evaluated in 18 experimental fields, representative of three Italian geographical macroareas (Southern, Thyrrenic Central, and Adriatic Central–Northern Italy). Three replicate trials were grown in each field.

The agronomic performance of the tested genotypes are given in Table 14 (pp. 105-106). The average national yield for the period 2007–09 reached 3.72 t/ha.

Table 14. Yield, grain protein content, and test weight of 16 organically managed, Italian durum wheat cultivars tested during a three-year period (2007–09) in three main cropping areas of Italy (for length of growing cycle, E = early, ME = medium early, M = medium, ML = medium late, and L = late).

		Yield				
		Index (yield / column mean * 100)				t/ha
Cultivar	Cycle	South	Thyrrenic Central	Adriatic Central and North	Mean	Mean
Ciccio	E	104	100	93	**99**	**3.67**
Duilio	E	106	101	104	**104**	**3.86**
Karalis	E	96	101	104	**100**	**3.75**
Saragolla	E	108	105	111	**108**	**4.02**
Svevo	E	105	97	103	**102**	**3.80**
Meridiano	ME	111	101	109	**107**	**3.99**
Simeto	ME	106	98	100	**101**	**3.76**
Claudio	M	112	106	112	**110**	**4.10**
Colosseo	M	101	101	98	**100**	**3.73**
Normanno	M	99	111	110	**106**	**3.97**
San Carlo	M	88	90	100	**93**	**3.48**
Vinci	M	97	110	102	**103**	**3.83**
Dylan	ML	104	111	103	**106**	**3.94**
Grazia	ML	94	94	99	**96**	**3.56**
Cappelli	L	76	71	58	**68**	**2.52**
Mean (t/ha)		**3.53**	**3.62**	**4.02**	**3.72**	**3.72**
		Grain protein content				
		Index (grain protein content / column mean * 100)				%D.M.
Ciccio	E	95	100	99	98	**12.3**
Duilio	E	98	99	98	99	**12.4**
Karalis	E	104	102	101	102	**12.8**
Saragolla	E	95	95	94	95	**11.9**
Svevo	E	103	104	104	104	**13.0**
Meridiano	ME	98	97	96	97	**12.2**
Simeto	ME	101	104	103	103	**12.9**
Claudio	M	97	97	99	98	**12.3**
Colosseo	M	95	96	96	96	**12.0**
Normanno	M	99	96	97	97	**12.2**
San Carlo	M	104	101	102	102	**12.9**
Vinci	M	98	97	95	97	**12.2**
Dylan	ML	98	96	96	97	**12.2**
Grazia	ML	103	101	101	102	**12.8**
Cappelli	L	110	113	118	114	**14.3**
Mean (t/ha)		**12.6**	**12.4**	**12.8**	**12.6**	**12.6**

Table 14 (continued). Yield, grain protein content, and test weight of 16 organically managed, Italian durum wheat cultivars tested during a three-year period (2007–09) in three main cropping areas of Italy (for length of growing cycle, E = early, ME = medium early, M = medium, ML = medium late, and L = late).

		Yield				
		Index (yield / column mean * 100)				t/ha
Cultivar	Cycle	South	Thyrrenic Central	Adriatic Central and North	Mean	Mean
Ciccio	E	101	100	100	**100**	**79.7**
Duilio	E	99	99	100	**99**	**79.0**
Karalis	E	100	102	101	**101**	**80.3**
Saragolla	E	98	98	98	**98**	**78.0**
Svevo	E	100	101	101	**100**	**79.8**
Meridiano	ME	97	96	98	**97**	**77.0**
Simeto	ME	98	97	97	**98**	**77.5**
Claudio	M	102	102	103	**102**	**81.2**
Colosseo	M	101	101	100	**101**	**80.1**
Normanno	M	99	100	100	**100**	**79.2**
San Carlo	M	100	100	103	**101**	**80.2**
Vinci	M	98	98	98	**98**	**77.9**
Dylan	ML	100	101	101	**101**	**80.0**
Grazia	ML	102	102	103	**102**	**81.1**
Cappelli	L	102	100	98	**100**	**79.3**
Mean (t/ha)		**80.4**	**80.2**	**77.7**	**79.4**	**79.4**

The highest value was recorded in the Adriatic Central–Northern Italy region (4.02 t/ha), however, yields in the Southern and Thyrrenic–Central Italy were close (3.53 t/ha and 3.62 t/ha, respectively). Five cultivars, Claudio, Duilio, Dylan, Meridiano, and Saragolla, had yield indexes greater than 100 in all three areas. The cultivars Claudio and Saragolla had indexes that were remarkably above the average value in every growing area. To the contrary, generally negative results were given by the old cultivar Cappelli, basically because of intense lodging to which this tall genotype is subject, even when managed organically.

Grain protein content had an average value of 12.6%. Once again, production from the Adriatic Central–Northern Italy region were the best (12.8%) but even in this case, no large differences were observed between this region and those from Southern (12.6%) and Thyrrenic–Central Italy (12.4%). Overall, protein content seems to be negatively related to yield. The highest percentages were obtained by the cultivar Cappelli, whereas lower values were recorded in the most productive cultivars. Eight genotypes, Cappelli, Creso, Duilio, Grazia, Karalis, San Carlo, Simeto, and Svevo, reached the important commercial value of 12.0% in every environment and, among these, Svevo obtained a good protein content level (13.0%), brilliant from a productive point of view. The protein content of Saragolla was below 12.0%.

The nationwide average test weight was 79.4 kg/hl. The highest value was recorded in Southern Italy (80.4 kg/hl). Data from Thyrrenic–Central Italy were not much different, with an average value of 80.2 kg/hl. However, production from Adriatic–Northern Italy were the worst (77.7 kg/hl). The cultivars Claudio and Grazia gave above average test weights in all the environments, with a mean greater than 81.0 kg/hl. Meridiano, Simeto, and Vinci were clearly below average in all areas (< 78.0 kg/hl).

Weed control and nitrogen supply in organic durum wheat in Italy.

Sahara Melloni, Andreina Belocchi, Massimiliano Camerini (University of Molise, Dip. to S.A:V.A), Valerio Mazzon, and Fabrizio Quaranta.

Weed control and nitrogen supply are two crucial factors in organic farming (Hansen 2000). In Mediterranean areas, winter-grown cereals are heavily affected by low temperatures and high autumn–spring rainfall causing low nitrogen availability in the soil rooting layer. Weed control is possible only with crop rotation and mechanical methods. Intercropping is used widely to enhance the efficiency of the cropping systems, basically using species exhibiting complementary use of nitrogen, water, and other resources. Cereal–legume temporary intercropping, aimed only at increasing nitrogen supply for the former crop, is a less used practice (Vandermeer 1989; Pristeri 2006). Our effort was to evaluate the effect of durum wheat–legume temporary intercropping and mechanical weeding on grain yield, weed control, nitrogen availability, and protein content.

Field experiments were carried out in 2004–05 and 2005–06 in Rome using a randomized split-plot design with three replicates. Three Italian, durum wheat cultivars (Cappelli, Creso, and Duilio) were grown with three cropping techniques: i) no weeding (control), ii) mechanical weeding (harrowing) at tillering (weeded), and iii) with a temporary intercrop of field bean. No N fertilizers were added. The intercrop was made by sowing single wheat rows 45-cm apart and a legume species was sown in the 45-cm interrow. Weed density was determined at wheat harvest by counting the weedy plants in a 1-m^2 sample area. At harvest, grain yield and grain protein content were measured. Means for each cultivar and technique were compared using a Fisher LSD at P = 0.05. No significant differences were found for the 'cultivar x technique' interaction.

Intercropping and harrowing were effective in reducing weed density, but no significant differences were detected between treatments and between cultivars (Fig. 7). For yield, intercropping was a less effective tool and no difference was found between the weeded and control treatments. Between cultivars, Duilio had the higher yield.

Grain protein content was higher in the intercrop-managed field even with lower yields, whereas no significant differences were found between weeded and untreated plots. In particular, we emphasize that intercropping increased the amount of protein in all cultivars above the market-required standards. Cappelli had a higher protein level content even if due to low yields.

The main advantage of temporary intercropping certainly is related to the direct effect of nitrogen derived from the atmosphere and supplied to the system with biomass incorporation, although positive effects also may come from nitrogen transfer from legume roots before incorporation, the modification of wheat root development, and improved efficiency in the use of resources other than nitrogen. Our results indicate that temporary intercropping may supply an important amount of nitrogen to cereals, leading to an increase of grain quality traits. This technique and harrowing also give positive effects in controlling weeds. Temporary intercropping may be considered an environmentally sustainable technique that can improve organic wheat production in Mediterranean areas. Further studies are needed concerning the feasibility of this agronomic practice and to confirm that harrowing is convenient for improving yield and reducing the number of weeds.

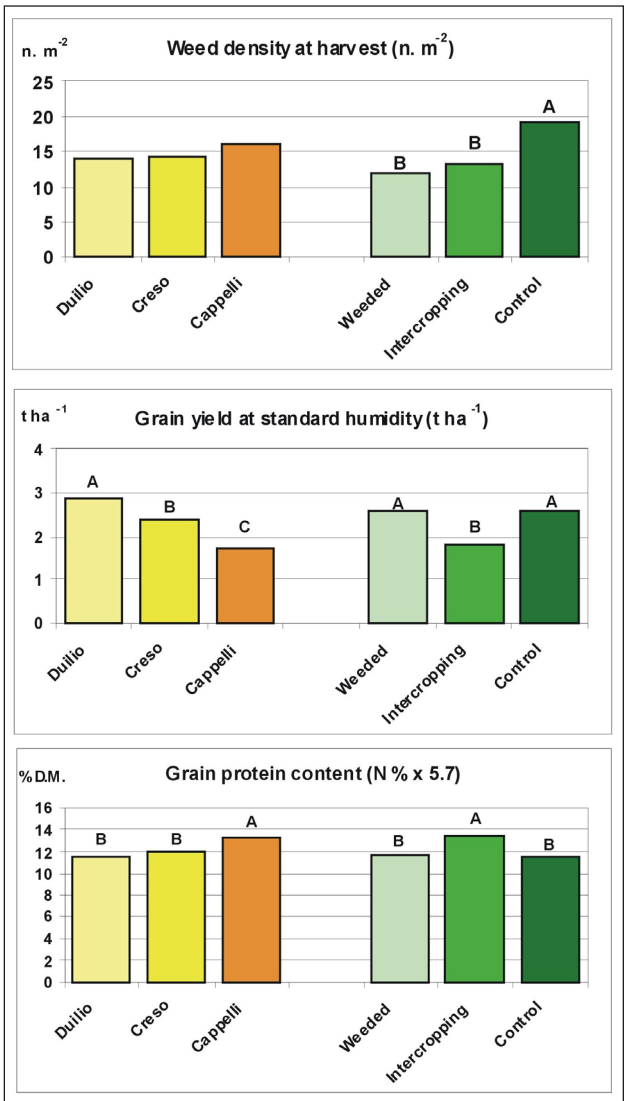

Fig. 7. Weed density, grain yield, and protein content of three durum wheat varieties under three different weed management techniques during 2004–05 and 2005–06 in Rome, Italy.

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The quality of organic durum wheat grown in Italy.

Maria Grazia D'Egidio, Cristina Cecchini, Sahara Melloni, Salvatore Moscaritolo, Valeria Scla, and Fabrizio Quaranta.

Cereal-based products play a primary role in the growing attention by consumers and producers about organic farming products. Durum wheat is the choice raw material for pasta production and, consequently, its quality characteristics are related strictly to requirements of the milling and pasta-making industries. This study investigated the quality aspects of durum wheat grown in an organic cropping system in experimental fields in Italy . The survey was carried out within the 'BIOCER' National Project with financial support from the Italian Agriculture Ministry.

Nine durum wheat cultivars (Ciccio, Duilio, Simeto, Iride, San Carlo, Claudio, Grazia, Creso, and Cappelli) from among the most widely grown in Italy, and differing from each other for the length of the growth cycle (early, medium-early, medium, medium-late, and late), were grown over four years (2004–07) under controlled, organic, crop-management conditions in experimental fields located in the most representative regions for durum wheat cultivation in Italy. A randomized block design with three or four replicates was used in all environments. Diverse parameters were used to characterize the quality of raw materials: test weight, protein content (Dumas-Leco combustion method), gluten Index (UNI 10690 method), alveographic test (UNI 10453 method), and yellow index (Minolta Chromameter CR-300). Semolina flour obtained by a pilot milling plant (Buhler MLU 202) also was used to produce pasta samples (spaghetti shape, Ø = 1.65 mm) employing a low temperature drying diagram (Tmax 50°C). Pasta cooking quality was evaluated by sensory analysis according to D'Egidio et al. (1993). Analytical data for the mean of repeated analyses and differences between replicates were included within the specific ranges of each method. Results related to quality aspects were expressed as average values in the three main macroclimactic areas considered (north, center, and south).

Yield data are reported in Fig. 8. The highest yield was in the northern area (4.48 t/ha) and the lowest in the south (3.33 t/ha). Among the cultivars, Claudio had the best production; Iride was a highlight, especially in the north. Production by the old cultivar Cappelli was quite poor because of the plant height and frequent lodging. Average test weight values were quite similar in all environments; San Carlo, Claudio, and Grazia were the highest; however, all the cultivars presented levels above 80 kg/hl, considered a good value for the durum wheat grading (UNI 10709). Protein content (Fig. 9), a critical parameter in organic conditions because of absorption and the availability of nitrogen, is considered an essential factor for organic crops. An average value above 12.0% was found for all three environments. The best protein content (average value 12.7%), even if associated with lower yield, was in southern Italy, a suitable agroclimatic area for durum wheat. Relevant differences were detected among the genotypes: Cappelli had the highest protein content, owing to the lowest production level, San Carlo, Creso, and Simeto had levels equal to or higher than the average value of the environment, and Iride had the lowest levels in all trials.

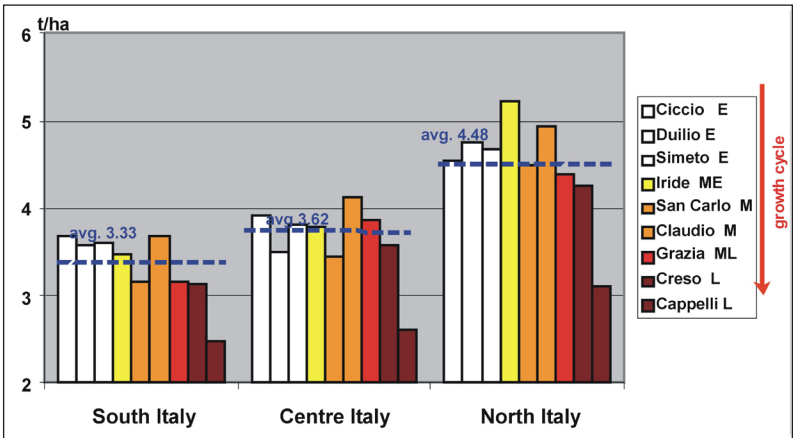

Fig. 8. Production (t/ha) of nine durum wheat cultivars grown between 2004–07 in controlled organic crop-management condition at three locations in Italy (E = early, ME = medium early, M = medum, ML = medium late, and L = late cultivars).

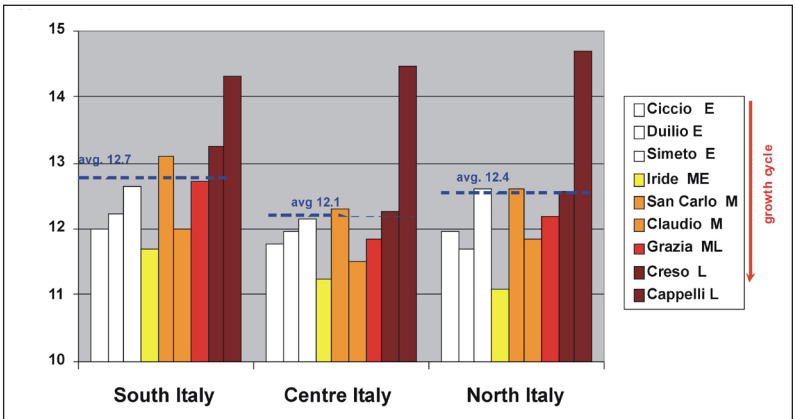

Fig. 9. Protein content (% D.M.) of nine durum wheat cultivars grown between 2004–07 in controlled organic crop-management condition at three locations in Italy (E = early, ME = medium early, M = medum, ML = medium late, and L = late cultivar).

Rheological characteristics were evaluated by different methods (SDS, gluten index, and alveographic test). Results of the SDS tests (Fig. 10) showed similar average values in all environments; the highest value was detected in southern Italy. The cultivars maintained the same order of sedimentation levels in all the areas, even if with different values. San Carlo was the highest. For gluten index, no statistical differences were observed between the environments, and all the cultivars except Cappelli had good values. However, because a low gluten content can provide an overestimate of the gluten index (D'Egidio et al. 2008), data from different methods should be integrated to correctly estimate cultivar performance. Average levels for the alveographic parameter (W) were not particularly high in any environment (Fig. 11); the highest values were recorded in southern Italy (140) and for San Carlo among the cultivars. Quality traits (gluten quality and color) are characterized by a high genotypic effect. The response of each cultivar in different environments can change in magnitude, but the rank of cultivars does not significantly change among the environments (Mariani et al. 1995). Therefore, the choice of cultivars suitable for specific agroclimatic environments represents an effective tool for obtaining raw materials having a suitable qualitative levels for the industrial requirements.

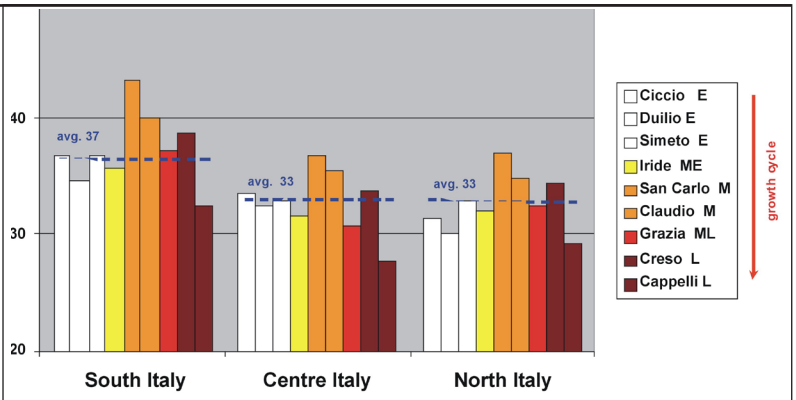

Fig. 10. Average SDS sedimentation rates (mL) of nine durum wheat cultivars grown between 2004–07 in controlled organic crop-management condition at three locations in Italy (E = early, ME = medium early, M = medum, ML = medium late, and L = late cultivars).

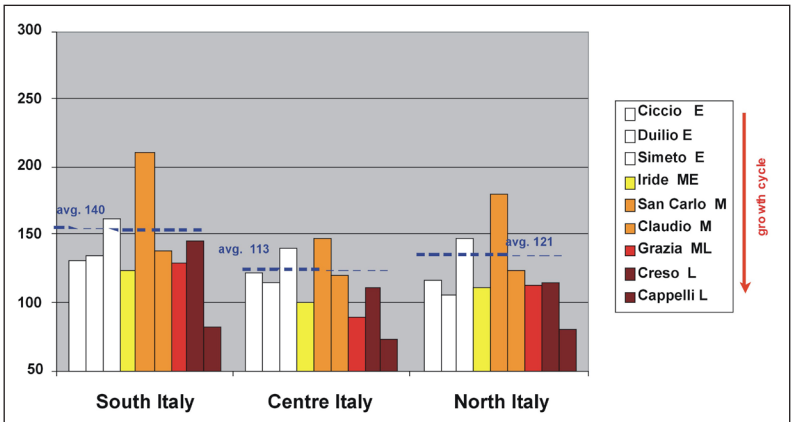

Fig. 11. Average levels of Alveographic parameter (W (J x 10^{-4})) of nine durum wheat cultivars grown between 2004–07 in controlled organic crop-management condition at three locations in Italy (E = early, ME = medium early, M = medum, ML = medium late, and L = late cultivars).

Semolina flour color, expressed as a yellow index, showed significant differences between the cultivars as expected because of the strong genetic inheritance of this character. The cultivar San Carlo had the highest values in all environments. Considering the levels required by pasta-making industry, average values in the agroclimatic areas were not high, however, until recently, colour was not considered in breeding programs. Consequently, several old genotypes are characterized by low yellow index values. Better results were generally recorded in the southern area over those in the center and north, confirming the findings of Johnston et al. (1983) that the positive influence of warm, droughty conditions on the synthesis and accumulation of carotenoid pigments. Evaluations for pasta cooking quality were not significantly different, always medium quality.

Protein level is the main factor to be improved for durum wheat grown in an organic cropping system. However, a suitable choice of cultivars can provide higher guarantees, without added costs, in order to meet industrial requirements for products of high quality. Cultivating organic durum wheat in suitable agroclimatic areas will produce raw material meeting the criteria for health and quality. Not using chemical products causes production to be unsatisfactory only in some unfavorable years and environments. Although it is more difficult to ensure regularly good protein levels, the use of good quality, modern cultivars can provide raw material suitable for the requirements of pasta-making industry when good agronomic practices are applied. The demand for food with high quality and safety levels is increasing all the time. In this context, enhancing the traceability along the entire production chain could make organic products appreciated more and more.

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Grain yield, quality, and deoxynivalenol (DON) contamination of organic and conventional durum wheat.

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Durum wheat has the most widespread cultivation in Italy (approximately 1.60 x 10^6 ha) with an important and growing quota in the organic cropping system. The increasing area of the wheat grown in the organic cropping system could mean a greater presence of deoxinivalenol (DON) in foodstuffs because of the ban on the use of synthetic pesticides. In addition, lower grain yields and protein contents created uncertainty about the use of organic agricultural techniques for durum wheat. Recent studies concerning the particular safety practices adopted in organic farming systems show a lower incidence of *Fusarium* spp. than in conventional systems (Edwards 2009; Vànovà et al. 2008; Pussemier et al. 2006). We evaluated the incidence of the sources of variability for yield, protein content, and DON contamination in raw durum wheat grown in comparable environments under both organic and conventional cropping systems in south-central Italy.

Six cultivars (Ciccio (early), Simeto (early), Duilio (early), Iride (medium-early), Claudio (medium), and Creso (late)) with different biological cycles were used. Samples were collected from several experimental fields in both conventional and organic cropping systems during a three-year period between 2006 and 2008. The following fields were selected as representative of the durum wheat-growing areas in Italy: Jesi, Pollenza, and Papiano in central Italy and Campobasso, Foggia, and S.Stefano Quisquina in southern Italy. Agronomic data were collected throughout the course of the experiment. Whole-meal samples were extracted in distilled water, and the filtered extract was employed for DON analysis using the enzyme-linked immunosorbent assay (ELISA). Statistical analysis were used to elucidate the influence of cultivar, cropping system, year, and field location on grain yield, protein content (having a normal distribution), and DON contamination (using a generalized linear model).

For yield, the cropping system factor was highly significant; its contribution to explain variability was 73% also taking into account the interaction with location. This result confirms that the most important factor in explaining the differences in production is the cropping system, with a grain yield significantly greater in the conventional. The average grain yields obtained in the three years at the six locations reflected the production expectations for the different areas of Italy, both for conventional (5.85 t/ha) and organic (4.91 t/ha) cropping systems. Years were not significant for grain yield, explaining only 1% of the total variability. No significant differences were recorded among the six cultivars. Higher yields were obtained from Iride, Claudio, and Duilio in both cropping systems, and Creso had the lowest (Fig. 12, p. 111).

Cropping system, location, and year significantly affected grain protein content; the cultivar factor was negligible. Location and cropping system had the same weight (their contribution to the explanation of variability was 35% (location) and 37% (cropping system); year was slightly lower (24%). No interactions were significant.

Protein content was inversely affected by the lower yields obtained in the organic system and by climatic conditions that influenced the absorption of available nitrogen. Widespread variability between locations and years was

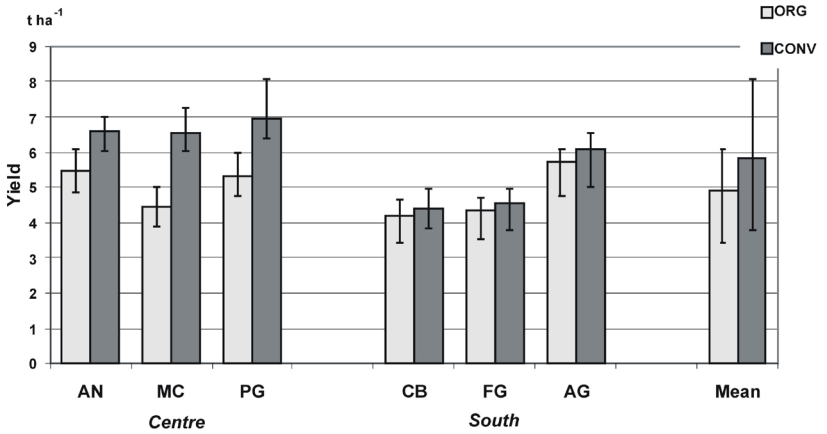

Fig 12. Comparison for grain yield (t/ha at 13% moisture) of the national networks in the organic and conventional cropping systems. Means are for six cultivars (Ciccio (early), Simeto (early), Duilio (early), Iride (medium-early), Claudio (medium), and Creso (late)) in two different agroclimatic areas of Italy (Jesi–AN, Pollenza–MC, and Papiano–PG (central Italy) and Campobasso–CB, Foggia–FG, and S.Stefano Quisquina-AG (southern Italy)). Vertical bars are the maximum and minimum values.

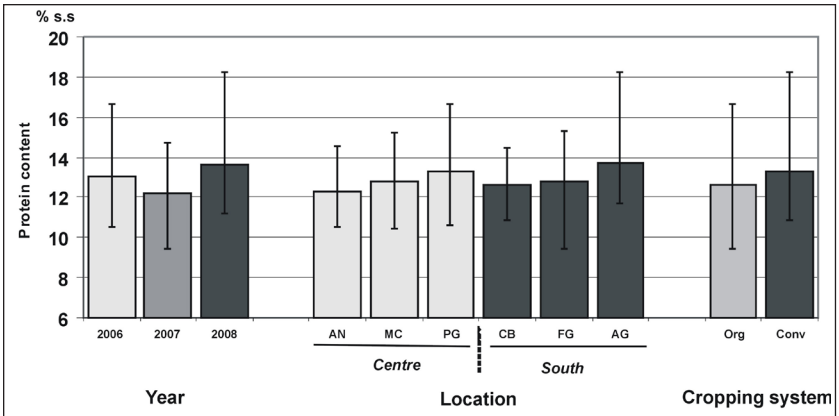

Fig 13. Grain protein content (13% DM) of the national networks in the organic and conventional cropping systems in Italy. Means are for year, location (see Fig. 12 for abbreviations), and cropping system. Vertical bars are the maximum and minimum values.

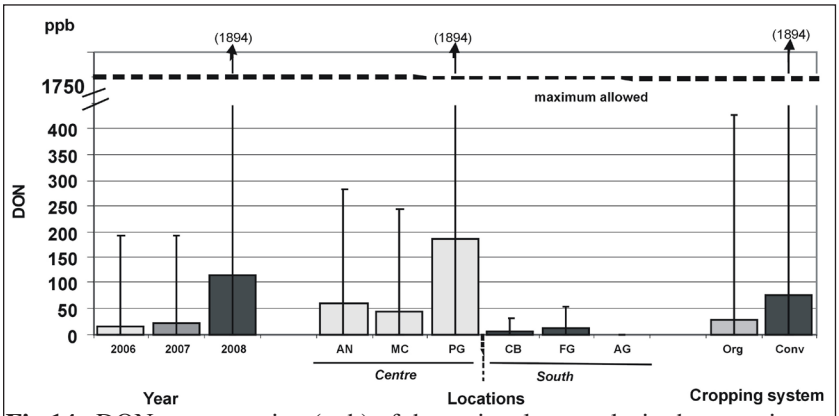

Fig 14. DON concentration (ppb) of the national networks in the organic and conventional cropping systems in Italy. Means are for year, location (see Fig. 12 for abbreviations), and cropping system. Vertical bars are the maximum and minimum values.

observed, whereas the tested cultivars showed greater homogeneity, the differences between organically and conventionally cropped plots for any cultivar were never significant for both central and southern Italy (Fig. 13).

Most of the variability in DON contamination was due to location. Considering only the simple effects, over 35% of the variability may be attributed to location. DON concentration at the locations in central Italy were higher than those in the south. The variability increased considerably for the interaction with year (almost 70%).

Cropping system and cultivar, although significant, had a low influence, however, their interaction accounted for 13% of the total variation. The 'cropping system x location' interaction accounted for 5% of the total variability. Mean levels of DON contamination were generally lower with only one sample during the three year-period exceeding the legal limit of 1,750 ppb (Reg. CE 1881/2006). In organic durum wheat, contamination during both 2006 and 2007 was characterized by lower contamination with *Fusarium* spp. than in 2008. The levels of DON contamination in the six fields had higher mean values in the central locations than in the south, where climatic conditions are characterized by lower rainfall and low atmospheric relative humidity (Fig. 14).

These results point out clearly the absence of a significant correlation between DON levels and type of cultivar cycle (0.090 n.s). No correlation was observed between production and DON concentration. Particularly interesting is the positive correlation between DON values and number of spikes/m^2 (r = 0.210**). We confirmed the known positive correlation with protein content (r = 0.179**) and number of spikes/m^2 (r = 0.210**). A negative, highly significant correlation exists between 1,000-kernel weight (–0.243 ***) and test weight (–0.476***), both probably due to the direct effects of damage from *Fusarium* fungi on the kernel.

The results of this study revealed some interesting issues. A low DON presence was confirmed in each location in southern Italy; in some there was a complete absence of contamination in all the years of trials for both conventional and organic cropping systems. Lower DON concentrations were detected in organic wheat samples, both in less favorable years for the occurrence of *Fusarium* (2006 and 2007) and in the more favorable one (2008). The organic cropping system allowed good results not only in the locations where fungal infections was limited (southern Italy) but even in locations in central Italy, which are more exposed to the risks of fungal pathogens attacks. The hypothesis of higher levels of DON in durum wheat grown under organic cropping system, based mainly on the consideration that chemical plant-protection is banned, does not seem supported by evidence. Although the choice of cultivar has a reduced influence on the possibility of contamination, some cultivars appear more susceptible to contamination by DON, likely due to the fact that they are more suitable to southern Italy, where the selective pressure for Fusarium is less. Our results largely confirm the importance of the southern vocational areas for growing durum wheat, which is a important primary crop for the economy and typical of such areas.

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2007–2009 conventional bread wheat cultivar trials in central Italy.

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The Research Unit for the Qualitative Valorization of Cereals of the Italian Council for Research in Agriculture (CRA–QCE, Rome) has field trials to evaluate the performance of conventionally managed bread wheat cultivars in central Italy. The aim of these trials is to provide useful informations about the qualitative and quantitative traits of bread wheat cultivars managed conventionally, testing at the same time their suitability to specific agroclimatic conditions. In the period between 2007 and 2009, field experiments at four locations, grouped into two regions (two in Latium and two in Molise). The agronomic performance of the 12 genotypes was evaluated in all the regions in the period between 2007 and 2009 (Table 15). The trials

Table 15. Yield and test weight of 12 Italian bread wheat cultivars tested during a three-year period (2007–09) in two regions of Italy (Latium and Molise) (for ISQ class, FF = Frumento di Forza (improver wheat, strongest), FB = Frumento da Biscotto (wheat for biscuits, weakest), FPS = Frumento Panificabile Superiore (superior bread-making wheat), and FP = Frumento Panificabile (ordinary bread-making wheat); yield index = yield/column mean*100; test weight index = test weight/column mean*100).

		Yield			Test weight		
		Index		Mean	Index		Mean
Cultivar	ISQ class	Latium	Molise	(t/ha)	Latium	Molise	(kg/ha)
Bologna	FF	96	90	5.46	103	102	81.1
Apache	FPS	95	104	5.85	99	98	78.5
Blasco	FPS	100	103	5.97	105	105	83.4
Egizio	FPS	97	95	5.62	104	103	82.1
Aubusson	FP	103	99	5.95	98	99	78.2
Azzorre	FP	100	97	5.79	97	97	76.8
Exotic	FP	112	114	6.63	97	98	77.1
Isengrain	FP	101	107	6.10	100	99	79.2
Mieti	FP	84	87	5.04	99	99	78.6
PR22R58	FP	113	103	6.34	99	99	78.7
Profeta	FP	101	97	5.80	102	102	80.8
Artico	FB	98	104	5.93	96	98	77.1
		Mean (t/ha)			Mean (kg/ha)		
		5.95	5.80	5.87	77.7	80.9	79.3

were replicated three times in each field. These cultivars represent a considerable amount of the commercialized bread wheat seed in Italy.

The tested cultivars are catalogued according with the Synthetic Quality Index method (Indice Sintetico di Qualità, ISQ), from the strongest type FF (Frumento di Forza, improver wheat), particularly used for manufacturing products with a strong and well leavened structure, to the weakest type FB (Frumento da Biscotto, qheat for biscuits), more appropriate to lend friableness to the products. The intermediate categories are FPS (Frumento Panificabile Superiore, superior bread-making wheat) and FP (Frumento Panificabile, ordinary bread-making wheat).

The average yield during the three-year period reached 5.87 t/ha. The production of both regions were quite similar (Latium: 5.95 t/ha; Molise: 5.80 t/ha). Three of cultivars (Exotic, PR22R58, and Isengrain, each of the FP class), reached yields exceeding 6.0 t /ha with indicies higher than 100 in every region. Blasco (class FPS) had satisfactory indicies in both regions associated to the best test weight (83.4 kg/hl), whereas most of the other cultivars were characterized by test weights not optimal for the requirements of the milling industry.

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2007–08 triticale cultivar trials in central Italy.

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The Research Unit for the qualitative valorization of Cereals of the Italian Council for Research in Agriculture (CRA–QCE, Rome) carries out field trials for the evaluation of the performance of triticale cultivars in central Italy. The aim of these trials is to provide useful information about the qualitative and quantitative traits of triticale cultivars, testing at the same time their suitability to specific agroclimatic conditions. Between 2007 and 2008, field experiments were carried out in two locations in central Italy (Leonessa, RI, 42°33'59" N, an inner mountain environment), and Rome, 41°58'04" N, where fields are in a tight river plain). The trials were replicated three times in each field.

The agronomic performance of nine genotypes evaluated in the period between 2007 and 2008 is given in Table 16. The average yield of the period was 3.84 t/hda. Two of the cultivars (Bienvenue and Wilfried), both with medium growth cycles, reached yields remarkably exceeding the average in every location. These cultivars also exhibited the best test weights.

Table 16. Growth cycle, grain yield, and test weight of nine Italian triticale cultivars tested during a two-year period (2007–08). Mean data are from two locations of central Italy.

Cultivar	Heading date (days after 1 April)	Grain yield t/ha	Grain yield index	Test weight kg/hl
Rigel	30	3.43	89	66.9
Oceania	32	3.86	100	65.8
Catria	34	3.53	92	64.0
Mizar	34	3.67	95	70.4
Bienvenue	38	4.77	124	71.9
Wilfried	39	4.50	117	71.3
Frontera	44	3.73	97	70.5
Magistral	45	3.45	90	65.5
Talentro	49	3.65	95	71.3
Mean	38	3.84	100	68.6

2006–08 barley cultivars for livestock feeding in the Molise Region of Italy.

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The Research Unit for the Qualitative Valorization of Cereals of the Italian Council for Research in Agriculture (CRA-QCE, Rome) carries out field trials to provide useful informations about the qualitative and quantitative traits of barley cultivars for livestock feeding, testing at the same time their suitability to specific agroclimatic conditions. In the period between 2006 and 2008, field experiments were carried out in Colletorto (CB), a location in the Molise region (41°40' N,

an inner hill environment, 515 msl, surrounded by the Central Apennine Mountain Range). The trials were replicated in triplicate.

Agronomic performance of 14 genotypes were evaluated during the two-year period between 2006 and 2008 (Table 17). The average yield of the period was 4.91 t/ha. Four of the cultivars, Ninfa and Sixtine (early-medium and medium growth cycle) and Ketos and Mattina (both with late growth cycles), reached yields that exceeded the average. At the same time, these cultivars also exhibited the best test weights. For plant height, the cultivar Sixtine, with an average height of about 1 m, appears to be more subject to lodging; conversely the cultivar Ninfa has a fairly low average height.

Table 17. Growth cycle, height plant, grain yield and test weight of 14 Italian barley cultivars for livestock feeding tested at Colletorto during a three-year period (2006–08).

Cultivar	Heading date (days after 1 April)	Height cm	Yield t/ha	Yield index	Test weight Kg/hl
Vega	30	85	4.66	95	70.6
Nure	33	93	4.79	98	73.2
Amillis	33	94	4.77	97	73.0
Ninfa	33	82	5.08	104	74.3
Lutece	34	95	5.37	109	69.9
Aliseo	34	87	4.55	93	71.0
Sixtine	35	101	5.11	104	72.3
Baraka	35	91	4.69	96	73.4
Sonora	36	91	4.91	100	71.0
Dasio	36	66	3.63	74	69.2
Siberia	37	87	5.11	104	70.3
Aldebaran	38	91	5.37	109	68.0
Ketos	38	90	5.44	111	73.2
Mattina	40	94	5.20	106	71.8
Mean	35	89	4.91	100	71.5

Valorization of the emmer wheat crop in marginal environments of central Italy.

Andreina Belocchi, Mauro Fornara, Massimiliano Camerini (University of Molise, Dip.to S.A:V.A), Sahara Melloni, and Fabrizio Quaranta.

Emmer wheat was one of the first crops domesticated in the Near East. Widely cultivated in the ancient world, emmer wheat is now a relict crop in mountainous regions of Europe and Asia. The mounting interest for organic food in Italy has brought an increasing demand fur such hulled cereals. In 2001–02, the Experimental Institute for Cereals (currently Research Unit for the Qualitative Valorization of Cereals of the Italian Council for Research in Agriculture, CRA–QCE) carried out agronomic trials in two different environments of Central Italy.

At Leonessa (42°34' N, 969 masl), situated in a small plain at the foot of Mt. Terminillo, one of the highest mountains of the Apennine range, two different emmer genotypes were compared; a local one, Leonessa, and a recent cultivar, Farvento, patented by the former Institute of Germplasm of the National Council for Research. Trials dealt with the effects of seeding rate and nitrogen fertilization. Three different seeding rate were used (250, 300, and 350 germinating seeds/m^2), and nitrogen was supplied in six combinations, varying dose and supply date. Both genotypes were sown at the same date (14 March). The main results of the trial comparing Leonessa and Farvento indicated a delayed heading date (+13 days) and a taller height (+14 cm) (Table 18). Leonessa had a higher yield (1.13 t/ha) than that of Farvento (0.74 t/ha). A significant, posi-

Table 18. Growth cycle, plant height, and grain yield of two different emmer genotypes, six combination of nitrogen supply, and three seeding rates (seeds/m^2) in a field trial at Leonessa, Italy, 2001.

Treatment		Heading date (days after 1 April)	Plant height (cm)	Yield (t/ha)	Yield index
Nitrogen dose	0	89	80	0.76	81
	0 + 30	87	87	0.95	101
	30 + 30	87	88	0.79	84
	0 + 60	87	94	1.10	117
	30 + 60	87	89	0.88	94
	0 + 90	88	90	1.14	121
Genotype	Farvento	94	95	0.74	79
	Leonessa	81	81	1.13	120
Seeding rate	250	87	88	0.86	91
	300	88	88	0.95	101
	350	87	87	0.97	103
Mean		87	88	0.94	100

tive effect from nitrogen fertilization was recorded shen nitrogen was supplied at the beginning of stem elongation.

In Rome (41°58' N), trials were conducted on volcanic soils and dealt with the effect of a previous crop and fertilization on the emmer genotypes Leonessa and Garfagnana. All plots where sown on 18 January with a seeding rate of 300 germinating seeds/m^2. The effect of three different previous crops (emmer, sunflower, and chickpea) and three nitrogen supply levels (30, 60, and 90 kg/ha) supplied as inorganic (urea) and organic form (poultry manure, supplied prior to sowing) were measured (Talbe 19). A leguminous forecrop exerted a positive effect on yield, whereas no differences were ascribed to either of the two fertilizer types. Indeed, plots that received a greater dose of nitrogen gave, on average, higher yields. The genotype Garfagnana was slightly taller, later in heading, and more productive than Leonessa.

Table 19. Growth cycle, plant height, and grain yield of two different emmer genotypes, three different forecrops, two forms of fertilizer, and three different nitrogen supplies of two different emmer genotypes grown in the field in Rome, Italy, in 2001.

Treatment		Heading date (days after 1 April)	Plant height (cm)	Yield (t/ha)	Yield index
Previous crop	emmer	40	82	2.20	93
	chickpea	39	94	2.63	111
	sunflower	38	91	2.27	96
Fertilizer	poultry manure	39	90	2.36	100
	urea	39	88	2.36	100
Nitrogen dose	30 kg/ha	39	89	2.31	98
	60 kg/ha	39	88	2.33	99
	90 kg/ha	39	90	2.49	106
Genotype	Leonessa	39	87	2.32	98
	Garfagnana	40	91	2.41	102
Mean		39	89	2.36	100

Reactions of bread and durum wheat cultivars artificially inoculated at the seedling stage with Stagonospora nodorum.

A. Iori and A. L'Aurora.

Stagonospora nodorum (teleomorph *Phaeosphaeria nodorum*) is the fungal pathogen that causes Stagonospora nodorum blotch on wheat. In Italy, this fungus attacks seedlings and spikes causing yield losses of both durum and bread wheat. We evaluated 20 durum wheat and 18 bread wheat cultivars tested with *S. nodorum* isolates at the seedling stage in the greenhouse.

The pathogen was picked from naturally infected durum and bread wheat leaves collected in several Italian regions. Leaf segments with pycnidia were first washed with tap water, then with sterile distilled water, plated on water agar (15 g/L) in Petri dishes, and incubated at 20°C under a 12 h photoperiod. Single cirrhi of *S. nodorum* were isolated and tranferred to plates containing potato dextrose agar (PDA; 39 g/L) and kept at 20°C to develop colonies. Isolates were transferred to fresh plates every 7–10 days. Nine *S. nodorum* isolates collected from durum wheat and two isolates from bread wheat were used to inoculate durum wheats; whereas eight isolates gathered from durum wheat and four isolates from bread wheat were tested on bread wheats. Inoculum was prepared before inoculation. Cultures were washed with sterile distilled water, the spore suspension filtered, and the concentration was adjusted to 1 x 10^6 spores/mL with the aid of a hemacytometer. Finally, two drops of Tween 20 per 20 mL of inoculum were added. About 20 seeds for each bread or durum wheat cultivar were sown in pots in the greenhouse, and the seedlings were inoculated when the second leaf was emerging. Plants were maintained in a humid chamber for 72 h and returned to a greenhouse bench with a 12 h photoperiod at 20 °C. Disease severity was evaluated at 5, 8, and 10 days-after-inoculation using a 0 to 5 scale (Liu et al. 2004). Seedlings with two different lesion types were registered as an intermediate reaction type.

Artificial inoculations with different *S. nodorum* isolates showed that durum wheat genotypes were more susceptible than bread wheat cultivars at the seedling stage. The durum wheat cultivars Dylan, Meridiano, and Svevo were found to be resistant or moderately resistant with several isolates obtained from durum and bread wheat, whereas cultivars Anco Marzio, Ciccio, Claudio, Creso, Lesina, Solex, and Virgilio proved to be susceptible to all the isolates tested (Table 20, p. 116).

By contrast, many bread wheat cultivars showed resistance or moderate resistance to several isolates from both durum and bread wheat leaves. Cultivars Artico and Bologna tested with eight isolates from durum wheat and four isolates from bread wheat were resistant to all those isolates except Sn 15891. Cultivars Africa and Nomade were resistant as well; however, these cultivars were tested with a minor number of isolates (Table 21, p. 119). Unlike durum wheat, no bread wheat cultivars showed moderate or complete susceptibility to all the isolates used for artificial inoculation.

Table 20. Reaction of durum wheat cultivars artificially inoculated at the seedling stage with *Stagonospora nodorum* isolates collected from durum (*) and bread (^) wheat leaves collected in several Italian regions. Symptom severity was evaluated using a 0–5 scale (Liu et al. 2004), where 0 = highly resistant; 1 = resistant; 2 = moderately resistant; 3 = moderately susceptible; 4 = susceptible; 5 = highly susceptible. — = missing data. Average values based on repeated trials are reported.

Cultivar	AIND 1 (*)	Sn 15091 (*)	Sn 15147 (*)	Sn 15163 (*)	Sn 15465 (*)	Sn 15690 (*)	Sn 15570 (*)	Sn 15793 (*)	Sn 15891 (*)	Sn 15230 (^)	Sn 16037 (^)
Anco Marzio	3.0	4.0	3.5	3.0	4.5	4.3	3.5	4.5	4.5	4.0	3.5
Canyon	4.0	4.0	2.0	4.0	4.0	3.8	4.5	4.8	4.5	4.3	4.5
Ciccio	3.5	4.0	3.5	3.0	4.5	4.8	4.0	4.8	4.5	4.3	4.0
Claudio	4.0	4.0	3.5	3.5	4.5	4.8	4.5	4.5	4.5	4.5	4.0
Creso	4.0	4.0	4.0	4.0	4.5	4.5	4.3	4.5	4.5	4.5	4.5
Duilio	4.0	4.0	2.5	2.5	4.5	4.5	3.0	4.3	4.5	4.5	3.5
Dylan	2.0	1.0	3.5	2.5	4.0	4.0	0.0	2.5	3.0	2.0	0.0
Grecale	3.5	4.0	4.0	4.0	4.5	4.5	4.0	2.8	4.0	4.5	2.0
Iride	4.0	4.0	4.0	3.5	4.0	4.5	0.5	2.5	4.0	4.5	0.5
Lesina	4.0	4.0	4.0	4.0	4.5	4.5	4.0	3.5	4.5	—	4.5
Levante	4.0	3.8	4.0	4.0	4.0	4.0	0.5	2.5	4.5	4.5	2.5
Maestrale	—	—	—	—	4.0	4.0	0.5	1.8	2.5	4.5	0.5
Meridiano	3.0	2.8	2.5	2.0	2.5	—	1.0	2.3	3.5	4.5	0.5
Normanno	3.5	2.5	3.0	2.5	—	—	3.5	3.5	4.0	4.0	1.0
Simeto	3.0	1.8	2.0	3.5	4.5	—	4.3	4.3	4.5	4.5	2.5
Solex	3.8	3.8	3.0	4.0	4.0	—	4.0	4.3	4.5	4.5	4.0
Svevo	0.5	0.3	0.0	0.0	0.5	—	1.0	2.3	1.5	2.8	0.0
Valerio	2.5	2.3	3.5	3.5	4.0	—	3.5	3.5	4.5	4.5	3.0
Vinci	3.5	3.5	4.0	4.0	4.0	—	4.5	4.0	4.5	—	2.5
Virgilio	4.0	3.5	3.5	3.5	4.5	—	4.5	4.3	4.5	4.5	4.5

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Table 21. Reaction of bread wheat cultivars artificially inoculated at the seedling stage with *Stagonospora nodorum* isolates collected from durum (*) and bread (^) wheat leaves collected in several Italian regions. Symptom severity was evaluated using a 0–5 scale (Liu et al. 2004), where 0 = highly resistant; 1 = resistant; 2 = moderately resistant; 3 = moderately susceptible; 4 = susceptible; 5 = highly susceptible. — = missing data. Average values based on repeated trials are reported.

Cultivar	Sn 15091 (*)	Sn 15147 (*)	Sn 15163 (*)	Sn 15690 (*)	Sn 15570 (*)	Sn 15793 (*)	Sn 15891(*)	Sn 16268 (*)	Sn 15230 (^)	Sn 16037 (^)	Sn 16165 (^)	Sn 16357 (^)
A416	3.5	4.0	4.3	4.0	3.3	2.0	4.5	—	4.1	3.0	—	—
Africa	0.0	0.0	2.0	1.8	1.5	2.5	—	—	0.0	—	—	—
Albachiara	0.0	0.0	2.5	1.8	2.3	0.8	4.5	3.0	1.8	2.5	-	2.2
Artico	0.0	0.0	0.0	0.0	0.0	0.8	4.0	2.5	1.0	1.5	1.5	2.0
Aster	0.0	4.0	4.0	3.8	2.3	2.5	4.5	—	1.5	3.5	—	—
Aubusson	2.0	0.0	3.8	2.3	3.0	3.7	4.0	2.0	1.4	2.0	2.0	2.0
Avorio	0.0	0.0	3.0	2.5	0.0	0.0	—	—	0.0	—	—	—
Bilancia	2.0	3.0	4.0	2.0	2.0	1.5	—	—	1.8	—	—	—
Blasco	4.0	2.0	2.0	0.0	1.8	0.2	4.5	2.5	2.3	3.0	2.0	0.5
Bolero	2.0	2.0	4.3	1.8	2.0	1.5	5.0	2.0	3.1	2.3	—	4.0
Bologna	0.0	0.0	1.8	0.8	1.0	0.8	4.5	0.5	1.0	2.0	1.5	1.0
Bramante	0.0	3.0	4.0	1.8	2.0	1.7	4.5	1.5	2.3	3.5	—	—
Kalango	0.0	—	4.0	1.3	2.0	1.5	3.0	—	1.0	2.0	—	—
Mieti	0.0	2.0	3.5	2.5	2.8	2.7	4.5	2.0	3.1	2.5	—	3.0
Nomade	0.0	0.0	1.8	1.0	—	—	—	—	0.3	—	—	—
PR22R58	—	—	2.3	2.3	3.5	3.7	4.0	0.0	2.5	4.0	—	0.5
Sagittario	2.0	3.5	3.5	1.3	1.8	2.0	4.0	—	1.8	3.0	—	—
Serpico	0.0	—	4.0	1.0	0.0	0.5	—	—	0.5	—	—	—

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ITEMS FROM JAPAN

NATIONAL INSTITUTE OF CROP SCIENCE (NICS) – NATIONAL AGRICULTURE AND FOOD RESEARCH ORGANIZATION (NARO)
Tsukuba, Ibaraki 305-8518, Japan.

Kannon lines Nos. 1–51 with high flour yield, Japanese common wheat germ plasm for udon noodles.

Hiro Nakamura.

I report here the release of 51 germ plasm lines (Kannon No. 1–No. 51) of a Japanese common wheat used for udon noodle production. Kannon Nos. 1–51 are full-season, common wheat lines with a high grain and flour yields that have excellent milling and good udon noodle-making qualities. By using wheat flour particle size distribution measurements, I selected high flour yielding breeding materials among Japanese and Chinese wheat germ plasm, lines, and cultivars for breeding the udon-quality wheat lines with a high flour yield. The Kannon wheat lines were bred by crossing the selected Japanese and Chinese breeding materials with high flour yield with Japanese udon cultivars with high grain yield.

Japan produces about one million tons of wheat a year, maintaining ~15% self sufficiency in udon-quality wheat in a country of low overall food self-sufficiency, except for rice, which is near 100% self-sufficiency, or about 10 million tons/year. To improve the international competitiveness of the udon wheat grown in Japan, enhancing grain quality and developing cultivars with a higher flour yields are important in order to satisfy the demands of local milling companies. Therefore, breeding udon-quality wheat lines with excellent milling is the most important in the Japanese udon wheat-breeding program.

Wheat has been the staple food of Japan since ancient times, and it still makes frequent appearances on the dining table. The roots of a soft noodle such as udon lie in China, however, udon as we know it today developed independently in Japan. Of the many ways to eat wheat flour, it is the main ingredient in udon noodles. The kind of flour used has a great impact on the flavor and texture, therefore udon noodles are made of soft flour and not a hard bread flour. Each chef has his or her own unique formula; some blend several types of wheat flour, whereas others mix in other kinds of flour to give the udon noodles a chewier texture. Udon are popular with young and old alike, the cost of one bowl is low, and udon shops can be found nationwide. Some people in Japan eat udon almost every day.

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ITEMS FROM MEXICO

NATIONAL INSTITUTE FOR FORESTRY, AGRICULTURE, AND LIVESTOCK RESEARCH (INIFAP–CIRNO)
Campo Experimental Valle del Yaqui, Apdo. Postal 155, km 12 Norman E. Borlaug, entre 800 y 900, Valle del Yaqui, Cd. Obregón, Sonora, México CP 85000.

CEVY Oro C2008, a new durum wheat cultivar for southern Sonora, Mexico.

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Introduction. Wheat production in Mexico is estimated at 3.4 x 10^6 tons, which do not satisfy the consumer needs of 6.3 10^6. The Mexican milling industry produces approximately 3.5 x 10^6 tons of flour, which includes semolina; 43% of the wheat is produced in Mexico and 57% is imported. Of the total amount of wheat that the industry processes, 65.3% corresponds to bread wheat, 26.3% corresponds to wheat used for cookies, and only 8.4% is used for pasta. In northwest Mexico (Sonora, North Baja California, Sinaloa, and South Baja California), 63.18% of all wheat in the country was grown on 457,419 ha during the agricultural season autumn–winter 2008–09. The production value was about $350 x 10^6 USD in 2007. Wheat in this region is spring type and is cultivated under irrigation.

Before the 1990s, bread wheat was the dominant class in northwest Mexico. In the state of Sonora, bread wheat occupied more than 50% of the area dedicated to wheat from the agricultural season 1983–84 to 1993–94. However, many wheat producers decided to start growing durum wheat, because the mexican government implemented the domestic quarantine No. 16, which limited the cultivation of bread wheat in fields where Karnal bunt had been detected at levels greater than 2% infected grains. Other important factors were that durum wheat showed a greater grain yield than that of bread wheat, and during that period of time, did not have problems with leaf rust. In addition, there were opportunities for export of durum wheat.

Despite the economic and operational problems caused by Karnal bunt at the beginning of the 1980s, during 1990–91 bread wheat was still grown on 220,409 ha, which represented 89% of the total area dedicated to wheat in the state. However, durum wheat was consolidated as the dominat class grown in Sonora from the agricultural season 1994–95. Altar C84 was the dominant cultivar up to 2002–03, despite the fact that its resistance to leaf rust had already been overcome by a wheat race, which caused production losses during 2000–01 and 2001–02. Seed production of the cultivar Júpare C2001 (resistant to leaf rust) through a collaborative project between the Mexican National Institute for Forestry, Agriculture, and Livestock Research (INIFAP) and the International Maize and Wheat Improvement Center (CIMMYT) with support by the farmer´s union (PIEAES) of the Yaqui Valley, made it the most grown cultivar in southern Sonora from 2003-04 to 2008-09 (Table 1).

Table 1. Percent of the wheat-growing area (ha) in southern Sonora, Mexico during the agricultural season 2008–09.

Cultivar	Area (ha)	Percentage
Durum wheat		
Júpare C2001	119,327.38	42.34
Átil C2001	53,106.07	18.84
Samayoa C2004	29,062.75	10.31
Banámichi C2004	13,652.76	4.84
Platinum	7,741.92	2.75
Aconchi C89	1,067.14	0.38
Altar C84	491.66	0.17
Rafi C97	478.20	0.17
Nácori C97	10.00	0.004
TOTAL	224,937.90	
Bread wheat		
Kronstad F2004	29,818.81	10.58
Tacupeto F2001	23,733.23	8.42
Tarachi F2000	1,615.60	0.57
Rayón F89	1,045.33	0.37
Abelino F2004	638.18	0.23
Navojoa M2007	9.60	0.003
Roelfs F2007	9.60	0.003
TOTAL	56,870.34	

However, most of the durum wheat production for human consumption is for export, and the cultivar Júpare C2001 does not comply with the expected protein content in the grain and color, which are very important parameters of quality. In addition, new races of leaf rust present during 2008–09 overcame the resistance of Júpare C2001; therefore, cultivar options

for this region must be increased, so that they contribute to help the long-lasting use of cultivars by wheat producers in Sonora and in northwest Mexico, and at the same meet current minimum quality requirements for export.

After evaluating grain yield since the agricultural season of 2001–02 at the Yaqui Valley Experimental Station (CEVY), we proposed to release the experimental durum wheat line 'SCRIP_1//DIPPER_2/BUSHEN_3/4/ARMENT// SRN_3/NIGRIS_4/3/ CANELO_9.1' as the cultivar CEVY Oro C2008. Yield and quality comparisons are given with respect to cultivar check Júpare C2001, which was the most cultivated durum wheat cultivar in southern Sonora up to 2008–09. Information also is provided about the main phenotypic and agronomic characteristics as well as the reaction to diseases of this new cultivar.

CEVY Oro C2008 is a spring-type, durum cultivar that originated from hybridizations made in the Durum Wheat Breeding Program of CIMMYT. The cross number and history selection is CDSS02Y00381S-0Y-0M-19Y-0M (Table 2). Shuttle breeding was carried out between the experimental stations of El Batán, state of Mexico (B) (19°30'N and 2,249 msnm), San Antonio Atizapán, state of Mexico (M) (19°17'N and 2,640 msnm), and the Yaqui Valley (Y) (27°20'N and 40 msnm), in Sonora.

Table 2. Selection history and localities where cultivar CEVY Oro C2008 was evaluated (seasons are F–W = Fall–Winter and S–S = Spring–Summer; Irrigation was RR = regular rainfed and N = normal). Planting dates for the INIFAP yield trials were 15 and 30 November, 15 December, and 1 January.

Activity	Locality	Season	Irrigation
Simple genetic cross	Cd. Obregon, Sonora	F–W/2001–02	N
F_1 Generation	El Batan, Mexico	S–S/2002	RR
F_2 Generation	Cd. Obregon, Sonora	F–W/2002–03	N
F_3 Generation	Atizapan, Mexico	S–S/2003	RR
F_4 Generation	Cd. Obregon, Sonora	F–W/2003–04	N
F_5 Generation	Atizapan, Mexico	S–S/2004	RR
F_6 Generation	Cd. Obregon, Sonora	F–W/2004-05	N
Yield trials by CIMMYT			
Yield trials by INIFAP at different planting dates	Cd. Obregon, Sonora	F–W/2006–07 F–W/2007–08 F–W/2008–09	N

Description. The most important phenotypic characteristics of this cultivar, according to the International Union for the Protection of New Varieties of Plants (UPOV), are shown in Table 3 (p. 122). Cultivar CEVY Oro C2008 and check cultivar Júpare C2001 have a similar biological cycle with an average of 121 days for physiological maturity; however, the cycle is shortened due to the lack of cold hours, if planting is late and may average 108 days when sowing is done at the end of December. CEVY Oro C2008 is tall with an average height of 93 cm (Fig. 1), with a maximum of 105 and a minimum of 85. Plant growth habit is erect and shows no or low frequency of recurved flag leaves. The shap of the spike in profile view is tapering, density is medium, and the length excluding awns is short; awns are longer than spike. Spike is weakly glaucous, and the awns are distributed along the entire length and are brown. At maturity, the spikes become white. Glume shape is ovoid (spikelet in middle third of the spike) and are not hairy on the external surface. The shape of the shoulder is rounded and narrow in width; the beak is short and slightly curved. Grain shape is semi-elongated (Fig. 2, p. 122), and the length of brush hair in dorsal view is short. Grain coloration when treated with phenol is none or very light (Fig. 2, p. 122).

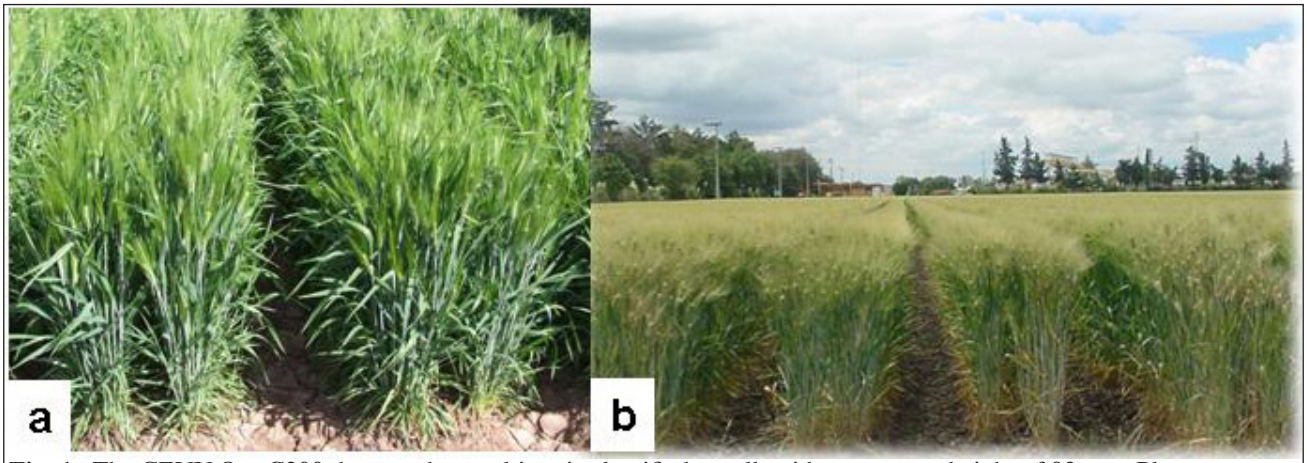

Fig. 1. The CEVY Oro C200 durum wheat cultivar is classified as tall, with an average height of 93 cm. Plants are erect and present no or a very low frequency of recurved flag leaves (a – heading; b – repening).

Table 3. Characteristics and description of phenotypic components of cultivar CEVY Oro C2008.

Structure	Characteristic	Description
Coleoptile	Anthocyanin coloration	Medium
First leaf	Anthocyanin coloration	Weak
Plant	Growth habit	Erect
	Frequency of plants with recurved flag leaves	Absent or very low
	Length (stem, spike and awns)	Long
	Seasonal type	Spring
Spike	Time of emergence	Early
	Glaucosness	Weak
	Distribution of awns	Whole length
	Length excluding awns	Short
	Hairiness of margin of first rachis segment	Wheat
	Color (at maturity)	White
	Shape in profile view	Tapering
	Density	Medium
Flag leaf	Glaucosness	Medium
	Glaucosness of blade	Weak
Awn	Anthocyanin coloration	Absent or very weak
	At tip of spike in relation to whole spike	Longer
	Color	Brown
Culm	Hairiness of uppermost node	Absent or very weak
	Glaucosness of neck	Weak
Grain	Shape	Semi-elongated
	Length of brushhair in dorsal view	Short
	Coloration with phenol	None or very light
Lower glume	Shape (spikelet in mid-third of ear)	Ovoid
	Shape of shoulder	Rounded
	Shoulder width	Narrow
	Length of beak	Short
	Shape of beak	Slightly curved
	Hairiness on external surface	Absent
Straw	Pith in cross section (half way between base of ear and stem node below)	Medium

Agronomic characteristics. CEVY Oro C2008 and the check cultivar Júpare C2001 are phenotypically very similar during early stages of development. Days-to-heading, physiological maturity, and plant height are very similar (Table 4, p. 123); however, after heading, the awns of CEVY Oro C2008 turn brown in contrast to the white awns of Júpare C2001. Because the height of CEVY Oro C2008 may reach 105 cm and the stems are thin, the lowest nitrogen rate is recommended, particularly when the third complementary irrigation (during the milky stage of the grain) is applied, in order to avoid lodging.

Fig. 2. Grain shape of the CEVY Oro C2008 durum wheat cultivar is semielongated. In the dorsal view (left), pubescence is short. Grain coloration after treatment with phenol is none or very light (right).

Reaction to disease. The evaluations carried out during the last three wheat seasons have shown that CEVY Oro C2008 and Júpare C2001 are different in resistance to leaf rust. Júpare C2001 became susceptible to this disease during the agricultural season 2007–08 when new races of the fungus were present in southern Sonora, whereas CEVY Oro C2008 showed resistance during all seasons of evaluation. The release of this new cultivar will allow wheat producers more economic benefits, because they will not have to rely on fungicides for control of leaf rust. Regarding Karnal bunt, CEVY Oro C2008 and Júpare C2001 have shown infection levels below 1% when artificially inoculated, so they are considered resistant (Table 4, p. 123).

Grain yield. Evaluation of grain yield and industrial quality of CEVY Oro C2008 started in season 2006–07 at the Yaqui Valley Experimental Station. The average yield was 5.5 t/ha, 200 kilograms lower than that of the check cultivar Júpare C2001 (Table 5). Based on statistical analysis, the best planting dates for CEVY Oro C2008 are between 15 November and 1 December. In two farmers' fields, CEVY Oro C2008 showed an average yield potential of 7.1 t/ha during the 2008–09 season (Table 6).

Table 4. Agronomic characteristics (average) and reaction to diseases of cultivar CEVY Oro C2008 and the check cultivar Júpare C2001 during the agricultural seasons 2006-07 to 2008-09, at the Yaqui Valley Experimental Station in Sonora, Mexico (R = resistant and S = susceptible).

Characteristic	Cultivar	
	CEVY Oro C2008	Júpare C2001
Heading (days)	81	80
Physiological maturity (days)	121	121
Plant height (cm)	93	92
Leaf rust	R	S
Karnal bunt	R	R

Quality. Several physico-chemical parameters affect the industrial quality of durum wheat cultivars. However, protein content, quality, and the pigment present in the endosperm of the grain noticeably affect the evaluation parameters of semolina used for pasta making. Although protein content and quality are affected by crop management, mainly by nitrogen fertilization, cultivar and yield potential are associated with protein present in the grain. Evaluations from 2006–07 to 2008–09 have shown that CEVY Oro C2008 is consistently superior to the check cultivar Júpare C2001 in yellow pigment content (Fig. 3). CEVY Oro C2008 produces a grain with an average specific weight of 83 kg/hl, and 13.5% protein at 12% moisture content. These two parameters are similar to those of the cultivar check Júpare C2001 (Table 7). From the farmer's point of view, grain yield has been the main parameter for choosing a cultivar; however, in the case of durum wheat, pigment is a very important factor to consider for export. The intensity of yellow pigment in the endosperm of CEVY Oro C2008 grain has an average of 28.1 points on the Minolta b scale, whereas Júpare C2001 has an average of 20.7.

Table 5. Experimental average grain yield (t/ha) of cultivar CEVY Oro C2008 and the check cultivar Júpare C2001 during agricultural seasons 2006–07 to 2008–09 grown at the Yaqui Valley Experimental Station in Sonora, Mexico. Experimental trials were at four planting dates with a total of four irrigations.

Agricultural season	Cultivar	
	CEVY Oro C2008	Júpare C2001
2006–07	5.970	5.962
2007–08	4.749	6.185
2008–09	5.965	5.134
Average	5.561	5.760

Table 6. Grain yield (t/ha) of cultivar CEVY Oro C2008 and the check cultivar Júpare C2001 in two farmers' fields during the agricultural season 2008–09 in the Yaqui Valley, Sonora, Mexico.

Season	Block	Cultivar	
		CEVY Oro C2008	Júpare C2001
2008–09	609	6.7	6.7
	2518	7.5	7.9
Average		7.1	7.3

Table 7. Industrial quality characteristics of cultivar CEVY Oro C2008 and the check cultivar Júpare C2001 during the agricultural seasons 2006–07 to 2008–09 at the Yaqui Valley Experimental Station, Sonora, Mexico.

Characteristic	Cultivar	
	CEVY Oro C2008	Júpare C2001
Specific weight (kg/hl)	83.0	83.6
Grain protein (%)	13.1	13.8
Color (Minolta b value)	28.1	20.7

Fig. 3. CEVY Oro C2008 (right) produces a greater concentration of pigment compared with Júpare C2001 (left).

The information for the release of durum wheat cultivar CEVY Oro C2008 was generated in southern Sonora, however, based on agroecological data, this cultivar can be grown in the irrigated areas of northwest Mexico, which includes the states of South Baja California, North Baja California, Sinaloa, and Sonora. CEVY Oro C2008 represents a new option in durum wheat with an acceptable grain yield potential and better quality for pasta making, for those farmers interested in wheat grain for export.

Acknowledgements. The authors wish to thank Dr. Karim Ammar, Head of the Durum Wheat Breeding Progam of the International Maize and Wheat Improvement Center (CIMMYT), for providing the advanced lines from which CEVY Oro C2008 originated. They also thank Rigoberto Lepe-Lomelí, Ramón Saucedo-Cruz, Luis Carlos Aceves-Rodríguez, and Jesús Hernández-Ortiz for their technical assistance.

Evaluation of agronomic characteristics in durum wheat cultivars and advanced lines for northwestern Mexico during 2008–09.

Pedro Figueroa-López, Víctor Valenzuela-Herrera, Guillermo Fuentes-Dávila, Gabriela Chávez-Villalba, José Luis Félix-Fuentes, and José Alberto Mendoza-Lugo.

Introduction. In northwestern Mexico, comprised of the states of Sonora, South Baja California, North Baja California, and Sinaloa, wheat is the crop with the greatest area planted in the country (approximately 63% of the total area). In southern Sonora, the area grown with wheat occupies about 300,000 ha. For the agricultural season 2008–09, the average grain yield was 5.9 ton/ha with a total production of 1.8 x 10^6 ton (OEIDRUS 2010). Wheat in this region is spring type, cultivated during the autumn–winter under irrigation (Huerta and González 2000). Beginning with the crop season 1994–95, durum wheat was consolidated as the wheat class more cultivated in the state of Sonora and during 2008–09 occupied about 225,000 ha in the southern part of the state. Because southern Sonora is in a coastal area, the relative humidity is high and leaf rust is a recurrent disease that develops rapidly in susceptible cultivars. New, more virulent races of the pathogen, which cause loss of resistance in the most widely grown cultivars (Herrera-Foessel et al.,2005; Singh et al. 2003), occurred in the 2000–01 and 2007–08 growing seasons with cultivars Altar C84 (Figueroa-López et al. 2002), Átil C2000, and Júpare C2001 (Figueroa-López 2009). In order to generate and release a cultivar as a new alternative for wheat producers, the germ plasm must feature resistance to diseases, acceptable grain yield, good agronomic characteristics, and industrial quality. The collaborative wheat breeding program between the Mexican National Institute for Forestry, Agriculture, and Livestock Research (INIFAP) and the International Maize and Wheat Improvement Center (CIMMYT) is generating advanced lines and cultivars of durum wheat with good yield potential and other characteristics in order to widen the options for wheat production in northwestern Mexico. Our objective was to evaluate the agronomic characteristics of a group of durum wheat cultivars and elite lines at several sowing dates under furrow irrigation.

Establishment of the trial. The study was carried out at the Yaqui Valley Experimental Station (the station was named Norman E. Borlaug Experimental Station–CENEB, in March, 2010), which belongs to the Northwest Regional Research Center (CIRNO) of INIFAP, during the wheat season of the autumn–winter 2008–09. The genetic material consisted of nine commercial cultivars of durum wheat and sixteen advanced lines from CIMMYT (Table 8, continued on p. 125). The experimental design was a split plot randomized complete block with three replications. Main plots were the sowing dates and the subplots consisted of the different cultivars and lines. Experimental plots were 4-m long on beds with two rows; space between beds was 0.8 m. Sowing dates were 15 November, 2008, 1 and 15 December, and 1 January, 2009, in dry soil using 100 kg of seed per hectare. Fertilization consisted of 300 kg/ha of urea and 130 kg/ha of monomonium phosphate before seeding. The trial was irrigated immediately after seeding and later during the season, three complementary irrigations were provided. Before the first complementary irrigation, 100 kg/ha of urea were applied. The herbicide Situi® xl at 25 g/ha of commercial product was sprayed over the trial 30 days after sowing.

Table 8. Durum wheat comercial cultivars and elite lines evaluated during the agricultural season 2008–09, at the Yaqui Valley Experimental Station, Sonora Mexico.

Entry	Cultivar/line	Selection history
1	Átil C2000	CD91B1938-6M-030Y-030M-4Y-0M
2	Júpare C2001	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B
3	Banámichi C2004	CDSS95B00803M-D-0M-1Y-0B-3Y-0B-0Y-0B-15EY-0Y
4	Samayoa	C2004CDSS95B00181S-0M-1Y-0B-1Y-0B-0Y-0B-14EY-0Y
5	CEVY ORO C2008	CDSS02Y00381S-0B-0Y-0M-19Y-0M-0Y
6	CIRNO C2008	CGSS02Y00004S-2F1-6Y-0B-1Y-0B
7	PATRONATO ORO C2008	CDSS02Y00390S-0Y-0M-8Y-0Y
8	Sáwali Oro C2008	CDSS02Y00786T-0TOPB-0Y-0M-2Y-0Y
9	Platinum	

Table 8 (continued). Durum wheat comercial cultivars and elite lines evaluated during the agricultural season 2008–09, at the Yaqui Valley Experimental Station, Sonora Mexico.

Entry	Cultivar/line	Selection history
10	CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/4/STOT//ALTAR 84/ALD/5/CNDO/PRIMADUR//HAI-OU_17/3/SNITAN	CDSS02Y01208T-0TOPB-0Y-0M-22Y-0Y
11	GUAYACAN INIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN	CDSS02B00562S-0Y-0M-2Y-1M-04Y-0B
12	PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/POHO_1/10/DIPPER_2/BUSHEN_3//SNITAN	CDSS02B01115T-0TOPB-0Y-0M-1Y-4M-04Y-0B
13	TGBB/CANDEF//LALA/GUIL/3/BONVAL/4/TILO_1/LOTUS_4/5/TILO_1/LOTUS_4	CDSS02B01344T-0TOPB-0Y-0M-2Y-2M-04Y-0B
14	COMARA//SOOTY_9/RASCON_37/3/2*AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9	CDSS02B00743S-0M-1Y-06Y-1M-1Y-0B
15	NUS/SULA//5*NUS/4/SULA/RBCE_2/3/HUI//CIT71/CII*2/5/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	CDSS04Y00888T-0TOPB-26Y-0M-06Y-2M-1Y-0B
16	KOFA/10/LD357E/2*TC60//JO69/3/FGO/4/GTA/5/SRN_1/6/TOTUS/7/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/8/SOMBRA_20/9/STOT//ALTAR 84/ALD	CDSS04SH00003S-25Y-8M-2Y-1M-1Y-0B
17	MOHAWK/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CHEN/ALTAR	DSS04SH00022S-22Y-2M-5Y-1M-1Y-0B
18	KOFA/3/SOMAT_3/PHAX_1//TILO_1/LOTUS_4	CDSS04SH00001S-27Y-10M-5Y-3M-1Y-0B
19	CMH83.2578/4/D88059//WARD/YAV79/3/ACO89/5/2*SOOTY_9/RASCON_37/6/1A.1D 5+10-6/3*MOJO/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13	CDSS02B00720S-0Y-0M-8Y-1M-04Y-0B
20	CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/4/STOT//ALTAR 84/ALD	CDSS02B00250S-0M-1Y-06Y-2M-1Y-0B
21	CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/7/CHEN_11/POC//TANTLO/5/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/6/MINIMUS/COMB DUCK_2//CHAM_3	CDSS04Y00864T-0TOPB-17Y-0M-06Y-1M-1Y-0B
22	CHEN/ALTAR 84/3/HUI/POC//BUB/RUFO/4/FN-FOOT/5/STOT//ALTAR 84/ALD/3/PATKA_7/YAZI_1/6/CNDO/PRIMADUR//HAI-OU_17/3/SNITAN	CDSS04Y00786T-0TOPB-18Y-0M-06Y-4M-1Y-0B
23	CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/7/CHEN_11/POC//TANTLO/5/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/6/MINIMUS/COMB DUCK_2//CHAM_3	CDSS04Y00864T-0TOPB-1Y-0M-06Y-2M-1Y-0B
24	SOMAT_4/INTER_8//VERDI/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13/8/RAFI97/9/MALMUK_1/SERRA-TOR_1	CDSS04Y01242T-0TOPB-4Y-0M-06Y-3M-1Y-0B
25	KOFA/4/DUKEM_1//PATKA_7/YAZI_1/3/PATKA_7/YAZI_1	CDSS04SH00008S-16Y-6M-2Y-4M-1Y-0B

Data analysis. Grain yield, specific weight (kg/hl), days-to-heading (50% of ears completely emerged), physiological maturity (loss of rachis coloration), and plant height were recorded. An analysis of variance was performed and multiple LSD (0.05) was used to compare means. A correlation was analyzed between specific weight as the independent variable and grain yield as the response variable.

Results and Discussion. The analysis of variance showed significant differences ($p < 0.001$) in grain yield, specific weight, days to heading, and plant height, and the interactions between genotypes and sowing dates. The mean comparison between cultivars and lines for grain yield and other agronomic characteristics is shown in Table 9. Cultivar CIRNO C2008 had an average of 6,421 kg/ha compared to Átil C2000 with 4,105 kg/ha. This difference in yield is related to the incidence of leaf rust and the difference in susceptibility–resistance. CIRNO C2008 originated from the cross between Átil C2000 with the line Camayo, which is resistant to leaf rust (Foessel-Herrera et al. 2005). Other cultivars that showed lower yields than that of CIRNO C2008 were Júpare C2001 (5,134 kg/ha), Banámichi C2004 (4,767kg/ha), and Platinum (3,931 kg/ha). Of the genotypes evaluated, eight produced more than 6,000 kg/ha (compared with the average regional yield in 2007–08 of 5,900 kg/ha). Outstanding were 'CIRNO C2008', 'GUAYACAN INIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN', and Samayoa C2004, which are characterized as possessing resistance genes from Camayo, Guayacan/INIA, and *Lr14a*, respectively (Herrera-Foessel et al. 2005, 2008). Grain yield was positively correlated with specific weight with a determination of coefficient of $r^2 = 0.78$ (Fig. 4). The general average of this last variable was reduced from 82.7 kg/hl at the first sowing date to 80.3 kg/hl at the last one, which could be attributed to the effect of different factors that affect grain filling, such as leaf rust severity. A compensating effect between grain weight and number of grains/spike was noticed, because at the later sowing dates, a difference in grain distribution in distal part is expressed as smaller in size and, therefore, cause a reduction in the average grain weight (Slafer et al. 1996). In general, the cultivar CEVY ORO C2008 was the tallest (96.2 cm), with the longest vegetative cycle (79 days to heading and 120 to physiological maturity) in contrast with the cultivar Platinum (67 days to heading and 110 to physiological maturity), which has been described as a cultivar with a vegetative short cycle. Solis et al. (2006) reported a shortening of the wheat vegetative cycle to physiological maturity as leaf rust severity increases, whereas Soto et al. (2009) pointed out the importance of the duration of the vegetative state of the foliar area measured from spike emergence to physiological maturity, which is related to grain yield. The environmental conditions that prevailed during the wheat season during this study al-

Table 9. Grain yield and agronomic characteristics of durum wheat commercial cultivars and advanced lines, evaluated during the agricultural season 2008–09 at the Yaqui Valley Experimental Station, Sonora, Mexico.

Entry No.	Yield (kg/ha)	Specific weight (kg/hl)	Days-to-flowering	Days-to-physiological maturity	Plant height (cm)
6	6,421	83.56	76.00	119.8	74.58
13	6,335	83.57	73.75	116.6	87.92
11	6,275	83.63	71.67	114.3	83.33
15	6,181	84.10	76.25	117.5	90.00
14	6,163	83.68	72.58	117.4	85.00
18	6,130	84.06	74.58	117.7	90.83
24	6,056	82.81	71.67	116.6	84.17
4	6,012	82.23	71.33	116.1	80.42
5	5,965	83.29	79.67	120.7	96.25
17	5,959	82.14	74.58	118.3	81.25
10	5,940	82.33	73.75	117.5	83.75
25	5,901	81.80	78.58	120.1	93.33
19	5,878	83.75	78.50	120.3	87.50
7	5,865	83.05	77.58	119.7	84.17
8	5,825	83.07	76.92	120.7	88.33
20	5,691	81.45	74.17	117.2	87.50
16	5,617	82.49	73.42	118.1	86.67
23	5,590	82.47	70.92	115.3	85.83
21	5,510	83.04	74.75	116.8	90.83
22	5,344	81.58	75.50	119.1	84.58
12	5,159	80.62	73.33	117.4	87.50
2	5,134	82.63	75.67	118.7	90.83
3	4,767	80.43	72.92	116.8	79.17
1	4,105	79.78	78.50	119.3	82.50
9	3,931	78.20	67.08	110.4	65.00
LSD (0.05)	390	0.50	0.63	1.2	2.79

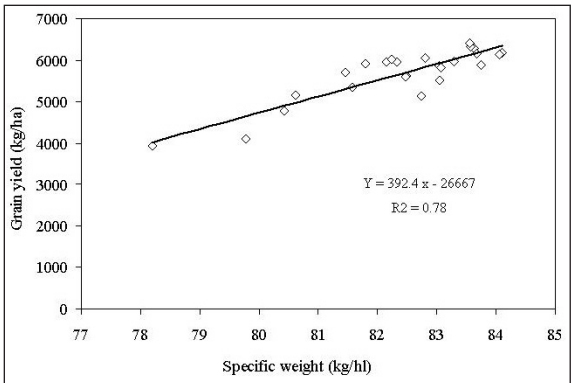

Fig. 4. The correlation between specific weight and grain yield of a group of durum wheat cultivars and advanced lines evaluated during the agricultural season 2008–09 at the Yaqui Valley Experimental Station, Sonora, Mexico.

lowed us to evaluate the effect of leaf rust, grain yield potential, and other agronomic characteristics of genotypes, some of which can be considered as the best options for durum wheat production in southern Sonora.

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Evaluating grain yield in ten genotypes of durum wheat at different sowing dates and irrigation conditions at the Yaqui Valley Experimental Station, Sonora, Mexico.

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Introduction. High produciton levels make wheat is the most important crop in northwestern Mexico. Of the wheat classes cultivated in the state of Sonora, durum wheat has occupied the greatest area for the last several years; influenced by grain yield potential. To evaluate the performance of the material generated by breeding programs, it is necessary to measure stability of genotypes in the prevailing environments (Solano et al. 1998). Selection of the most appropriate genotypes for specific environments might be relatively easy, however, as environments diversify and cover a wider area, the variability in climatic factors increases and, consequently, plants can not maintain productivity within a range of high yields. Our objective was to evaluate the grain yield potential of ten genotypes of durum wheat at different sowing dates and irrigation conditions.

Table 10. Durum wheat lines evaluated during the agricultural season 2006–07 at the Yaqui Valley Experimental Station, Sonora, Mexico.

Line	Cross and selection history
1	SOMAT_4/INTER_8 CDSS95B00181S-0M-1Y-0B-1Y-0B-0Y-0B-14EY-0Y
2	CS/TH.CU//GLEN/3/GEN/4/MYNA/VUL/5/2*DON87/6/2*BUSCA_3 CDSS95B00803M-D-0M-1Y-0B-3Y-0B-0Y-0B-15EY-0Y
3	ADAMAR_15//ALBIA_1/ALTAR84/3/SNITAN/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9 CDSS02Y00214S-0Y-0M-5Y-0Y
4	GREEN_2/HIMAN_12//SHIP_1/7/ECO/CMH76A.722//YAV/3/ALTAR84/4/AJAIA_2/5KJOVE_1/6/ MALMUK_1/SERRATOR_1 CDSS02Y00287S-0Y-0M-10Y-0Y
5	1A.1D 5+106/3*MOJO//RCOL/3/SNITAN/SOMAT_3//FULVOUS_1 /MFOWL_13 CDSS02Y00405S-0Y-0M-18Y-0Y
6	1A.1D5+10-6/3*MOJO//RCOL/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1 CDSS02Y00408S-0Y-0M-6Y-0Y
7	MUSK_1//ACO89/FNFOOT_2/4/MUSK_4/3/PLATA_3//CREX/ALLA/5/OLUS*2/ILBOR//PATKA_7/YAZI_1 CDSS02Y00786T-0TOPB-0Y-0M-2Y-0Y
8	STOT//ALTAR 84/ALD*2/3/KHAPLI CGSS01B00033T-099Y-099B-099B-147Y-0B
9	SOOTY_9/RASCON_37/3/STOT//ALTAR 84/ALD CGSS02Y00002S-2F1-48Y-0B-11Y-0B
10	SOOTY_9/RASCON_37//CAMAYO CGSS02Y00004S-2F1-6Y-0B-1Y-0B

Materials and Methods. A grain yield trial was carried out at the Yaqui Valley Experimental Station (27°22 LN, 109°55 LW, at 37 masl; the station was named Norman E. Borlaug Experimental Station – CENEB, in March, 2010), during the agricultural season 2006–07 in the southern part of Sonora. In this region, the climate is warm, extreme warm, and dry BW (h') and BS (h¨) according to Koppen's classification, modified by García (1964). The soil is heavy clay. The genetic material consisted of ten durum wheat advanced lines (Table 10, p. 127) sown on four dates (15 November, and 1, 15, and 29 December), with two and three complementary irrigations (Table 11). Experimental plots were 5-m long in two beds with two rows each with a density of 100 kg/ha under a randomized complete block design with three replications. The agronomic management followed the technical recommendations made by the National Institute for Forestry, Agriculture, and Livestock Research (INIFAP) for the region. Climatic conditions during the course of the trial were recorded from the agroclimatic network system in the Yaqui Valley, station block 910 (Table 12; AGROSON 2009).

Table 11. Sowing dates and number of irrigations for ten durum wheat lines, during the agricultural season 2006–07 at the Yaqui Valley Experimental Station, Sonora, Mexico.

Sowing date	# of irrigations	Irrigation dates
15 November	2	5 January and 14 February
15 November	3	29 December, 2 and 28 February
1 December	2	23 January and 28 February
1 December	3	12 January, 16 February, and 12 March
15 December	2	6 February and 8 March
15 December	3	29 January, 1 and 23 March
29 December	2	26 February and 27 March
29 December	3	12 February, 9 March, and 3 April

Table 12. Climatic data registered at station block 910, Yaqui Valley, during November 2006 to May 2007 in Sonora, Mexico (accumulated rain = 24.4 mm; accumulated cold hours = 512).

Month	Year	Average temperature (°C)	Maximum average temerature (°C)	Minimum average temperature (°C)	Maximum relative humidity (%)	Minimum relative humidity (%)	Maximum average solar radiation (kwatt/m²)
November	2006	20.53	30.40	12.28	87.93	25.37	0.74
December	2006	15.35	24.52	7.56	87.00	27.30	0.70
January	2007	13.59	21.72	6.22	88.00	33.54	0.72
February	2007	15.49	25.18	7.34	92.00	31.53	0.88
March	2007	17.63	28.62	8.23	91.09	26.35	0.96
April	2007	19.65	29.23	10.85	91.62	25.55	0.98
May	2007	24.21	34.15	13.56	82.64	19.06	1.05

Results and Discussion. Significant differences were found between lines sown on 15 November with two irrigations (Table 13, p. 129). Average yield for the ten lines was 5,432 kg/ha with two irrigations and 6,769 for three. Average yield of individual lines ranged from 4,285 to 5,983 kg/ha. Wheat lines (9) SOOTY_9/RASCON_37 /3/STOT//ALTAR84/ALD, (7) MUSK_1//ACO89/FNFOOT_2/4/MUSK_4/3/PLATA _3//CREX/ALLA/5/OLUS*2/ILBOR//PATKA_7/ YAZI_1, and (1) SOMAT_4/INTER _8 had the highest yield. For the 15 November sowing date with three irrigations, average yield for individual lines ranged from 5,854 kg/ha to 7,608. Lines 7 and 9 showed the highest yield with 7,608 and 7,479, respectively. Both lines showed 1,639 and 1,496 kg more than with two irrigations.

For the second sowing date with two irrigations, average yield for the ten lines was 5,159 kg/ha; for three irrigations it was 6,240. The average yield of the individual lines with two irrigations ranged from 4,517 to 5,612 kg/ha. Line 9 showed the highest yield, followed by lines 2 (CS/TH.CU//GLEN/3/GEN/4/ MYNA/VUL/5/2*DON87/6/2*BUSCA_3) and 7. For the same sowing date with three irrigations, average yield of individual lines ranged from 5,581 to 6,663 kg/ha. Lines 7, 9, and and 1 showed the highest yield with 6,663, 6,658, and 6,583 kg/ha, respectively. These lines had 1,242, 1,046, and 1,225 kg/ha more than with two irrigations.

For the third sowing date with two irrigations, the average yield for the ten lines was 4,853 kg/ha and for three irrigations it was 5,494. The average yield of individual lines with two irrigations ranged from 4,320 to 5,411

Table 13. Grain yield and physiological maturity of ten experimental durum wheat lines with two and three complementary irrigations in four sowing dates at the Yaqui Valley Experimental Station, Sonora, Mexico (means in columns with the same latter are statistically similar DMS, 0.05; PMat = days-to-physiological maturity).

Line	15 November				1 December				15 December				29 December			
	2 irrigations		3 irrigations		2 irrigations		3 irrigations		2 irrigations		3 irrigations		2 irrigations		3 irrigations	
	Yield	PMat	Yield	PMat	Yield	PMat	Yield	PMat	Yield	PMat	Yield	PMat	Yield	PMat	Yield	PMat
1	5,927 az	126 e	16,829 cd	129 d	5,358 ab	120 ef	6,583 a	122 d	4,973 a	115 cd	5,476 bcd	114 de	4,634 ab	104 d	5,324 a	110 a
2	5,591 ab	126 e	6,625 cde	129 d	5442 ab	119 f	6161 bc	121 d	5,071 a	112 e	5,683 abc	113 e	3,845 de	103 e	5,212 a	106 b
3	5,375 bc	130 bc	6,904 cd	133 bc	5,146 bc	123 bcd	6,429 ab	126 b	4,495 a	118 ab	5,462 cd	117 ab	4,290 bc	108 a	5,458 a	111 a
4	4,285 e	132 a	5,854 f	134 ab	4,517 d	124 abc	5,658 d	128 a	4,735 a	117 abc	5,912 ab	117 ab	4,251 bcd	108 ab	5,272 a	112 a
5	4,713 de	131 ab	6,454 de	135 a	4,787 cd	125 a	6,027 c	128 a	4,320 a	118 ab	5,105 d	118 a	3,648 e	109 a	5,068 a	112 a
6	5,028 cd	130 ab	6,125 ef	133 ab	4,700 d	124 ab	5,581 d	127 ab	4,780 a	119 a	5,519 abcd	117 ab	4,241 bcd	108 ab	4,941 a	111 a
7	5,969 a	128 cde	7,608 a	130 d	5,421 ab	122 cd	6,663 a	126 bc	4,406 a	116 bcd	5,173 cd	116 bc	4,057 cde	108 ab	5,149 a	111 a
8	5,686 ab	129 bcd	6,733 cd	129 d	5,350 ab	122 cd	6,070 c	123 d	5,071 a	116 bcd	5,233 cd	115 cd	3,957 cde	108 ab	5,149 a	110 a
9	5,983 a	127 de	7,479 ab	131 cd	5,612 a	121 de	6,658 a	125 c	5,411 a	114 de	5,327 cd	116 bc	4,362 bc	107 bc	5,575 a	111 a
10	5,766 ab	129 bcd	7,088 bc	131 cd	5,263 ab	122 cd	6,573 a	125 c	5,274 a	116 abc	6,050 a	116 abc	4,810 a	106 cd	5,661 a	110 a
CV (%)	4.89	0.96	4.32	0.98	4.09	0.83	2.86	0.73	10.63	1.34	5.96	0.93	6.07	0.89	7.11	1.3

kg/ha. Line 9 showed the highest yield, followed by lines 10 (SOOTY_9/RASCON_37//CAMAYO), 2, and 8 (STOT//ALTAR 84/ALD*2/3/KHAPLI). For the same sowing date with three irrigations, the average yield of individual lines ranged from 5,105 to 6,050 kg/ha. Lines 10, 4 (GREEN_2/HIMAN_12//SHIP_1/7/ECO/ CMH76A.722//YAV/3/ALTAR84/4/AJAIA_2/5KJOVE_1/6/MALMUK_1/SERRATOR_1), and 2 showed the highest yield with 6,050, 5,912, and 5,683 kg/ha, respectively; these lines had 776, 1,177, and 612 kg/ha more than with two irrigations.

For the fourth sowing date with two irrigations, the average yield for the ten lines was 4,209 kg/ha and for three irrigations it was 5,280. The average yield of individual lines with two irrigations ranged from 3,648 to 4,810 kg/ha. Line 10 showed the highest yield, followed by line 1. For the same sowing date with three irrigations, average yield of individual lines ranged from 4,941 to 5,661 kg/ha. Lines 10 and 9 showed the highest yield with 5,661 and 5,575 kg/ha, respectively; these lines had 851 and 1,213 kg/ha more than with two irrigations.

The average yield of the group of lines showed a continuous decrease with later sowing dates (Fig. 5, p. 130) in this particular agricultural season (2006–07). The maximum average yield difference at the different sowing dates with two irrigations was 1,223 kg/ha and for three it was 1,489. Six lines showed a consistent grain yield reduction from the first to the second sowing dates, then to the third and the fourth sowing dates when two complementary irrigations were applied, whereas for three irrigations, eight lines showed the same pattern. The most outstanding line for grain yield under two irrigations was SOOTY_9/RASCON_37 /3/STOT//ALTAR 84/ALD, which produced the highest yield in the first three sowing dates (5,983, 5,612, and 5,411 kg/ha, respectively) and was third (4,362 kg/ha) at the fourth date. These results clearly indicate that this line has the capacity to perform well under water stress. Other lines that showed acceptable performance under these conditions were SOOTY_9 /RASCON_37//CAMAYO, which was first in yield in the fourth sowing date (4,810 kg/ha) and second in the third date (5,274 kg/ha); SOMAT_4/INTER_8, which was second in yield in the fourth sowing date (4,634 kg/ha) and third in the first date (5,927 kg/ha); and MUSK_1//ACO89/FNFOOT_2/4/MUSK_4/3/PLATA_3//CREX/ALLA/5/OLUS*2/ ILBOR//PATKA_7/YAZI_1, which was second in yield in the first sowing date (5,969 kg/ha) and third in the second date (5,421 kg/ha). In overall average grain yield at the four sowing dates under two complementary irrigations, SOOTY_9/RASCON_37 /3/STOT//ALTAR84/ALD was first, SOOTY_9/RASCON_37//CAMAYO second, and SOMAT_4/INTER_8 third. For the overall average grain yield in the four sowing dates under three complementary irrigations, SOOTY_9/RASCON_37//CAMAYO was first, SOOTY_9/RASCON_37/3/STOT//ALTAR84/ALD second, and MUSK_1//ACO89/ FNFOOT_2/4/MUSK_4/3/PLATA_3//CREX/ALLA/5/OLUS*2/ILBOR//PATKA_7/YAZI_1 third. This last line produced the highest average yield in the whole trial with 7,608 kg/ha. There was a tendency to greater grain

yield by early wheat lines at the first two sowing dates (November 15 and December 1) as compared to late sowing (December 15 to January 1) (Table 13, p. 129), where earliness was not a factor that determined yield of lines under the prevailing conditions during the study.

The maximum, minimum, and average daily temperatures from the day of wheat emergence are given in Fig. 6. The data indicate that stress conditions were present and affected the experimental genotypes during different phenological stages. During December–January, the average maximum temperature was 24 and 21°C, respectively, which was favorable for wheat growth. At this phenological stage, good soil coverage is achieved and tillers are completely developed. On the other hand, plants are exposed continuously to environmental stimuli that affect their development and productivity. For some species, small changes in the levels of stimuli might become stress factors. Environmental stress may be present in different ways but, in general, their common effect is the hydric status of the plant (Bohnert et al. 1995). The plant response to such conditions will depend on species, because the mechanisms that confer tolerance to stress, in many instances, have evolved specifically for certain groups. Similarly, response to stress is based on the stage of development in which plants have experienced unfavorable conditions (Bohnert and Jensen 1996). Fokar et al. (1998) and Savin et al. (1997) found significant variation in the reduction of number and grain weight/spike under heat; on the other hand, under cool conditions (10°C), the plant expresses the real yield potential, because there is a high correlation between yield and cold hours. Under this scheme, there was a 22% yield reduction in treatments with two and three irrigations during the fourth sowing date with respect to the first date.

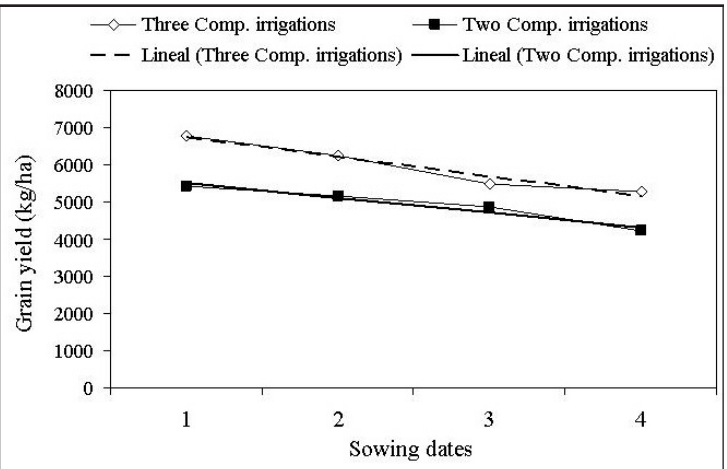

Fig. 5. Average grain yield in four sowing dates and the tendency wity two and three complementary irrigations of ten durum wheat advanced lines during the agricultural season 2006–07 at the Yaqui Valley Experimental Station, Sonora, Mexico.

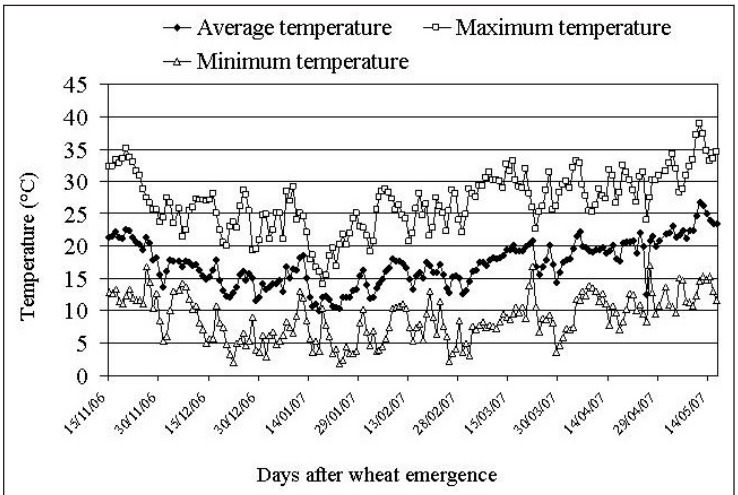

Fig. 6. Daily temperature recorded during the grain yield trial of ten durum wheat advanced lines during the agricultural season 2006–07 at the Yaqui Valley Experimental Station, Sonora, Mexico.

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ITEMS FROM PAKISTAN

NATIONAL AGRICULTURAL RESEARCH CENTER (NARC), ISLAMABAD WHEAT WIDE CROSSES AND CYTOGENETICS AND COLLABORATING NATIONAL PROGRAMS, ISLAMABAD, PAKISTAN.

Pakistan's wheat scenario: The way forward.

A. Mujeeb-Kazi (Project Director, HEC Foreign Faculty Professor at NIBGE and NARC) and Alvina Gul Kazi.

Pakistan's current national wheat yields are 2.6 tons/ha and annual productivity has approached 24 x 10^6 tons. Increasing productivity in the coming years is necessary to keep pace with population increases and food needs. Our production trends have been erratic and significantly influenced by the environment as the production figures show. They were 23.2 x 10^6 tons in 2006–07, dropped to 20.959 in 2007–08, and have now jumped to near 24 x 10^6 tons in 2008–09. These production measures encompass a wide range of factors that integrate several disciplines within Pakistan and across our country boundaries. The way forward research strengthening emphasis stringently focus upon time-bound, multifaceted integrated activities where the prerequisite factors to determine such goals impinge upon using modern technologies, novel genetic diversity, exploiting molecular tools, and managing an integrated practical breeding program that utilizes top-quality national professionals with a similar blend from international alliances. Our production area from 8.29 x 10^6 ha recently surpassed 9.0 x 10^6, which is disconcerting. Thus, the need to adapt to cultivation area limits and address other production aspects requires a vision that recognizes change and addresses it through integrative technologies. Major attention is being given to the key production constraints covering biotic/abiotic stresses. For food security within Pakistan and the region, the foremost factor is the threat from stem rust that has emanated from the spread of the Ug99 pathogen.

Pakistan wheat research and production areas have a long history of sound progress that has been made through volatile international alliances mostly with centers such as CIMMYT and now ICARDA. Well-spaced, timely capacity building has been effective, and the knowledge tank has been kept in balance reasonably well. Changing times, particularly budgetary constraints within Pakistan and internationally, have imposed restrictions that when prolonged allowed negative aspects to surface. Such a downward trend has dominated the agricultural scene over the past decade and confounding this facet has been emerging environmental problems that pose significant production problems threatening regional coverage. Stem rust around Ug99, and its variants, is one such super pathogenic threat for which satisfactory genetic control measures are being sought. Pakistan is in the thick of this pathogen spread. Confounding the issue is the presence within Pakistan of a local virulent race that holds even greater strength to combine with Ug99 and create major epidemic situations. This is not an issue exclusive Pakistan but has regional ramifications requiring serious scientific interventions.

As a immediate measure, Pakistani scientists are combatting the stem rust problem utilizing the international Kenyan screening site, tapping on the international talent that oversees stem rust directly, or through the BGRI network and work with all regional colleagues to circumvent the imminent danger that confronts the country and the region. At present Ug99 is not present in Pakistan.

The Wheat Wide Cross Program at Islamabad encompasses interlinking areas of research and development that are categorized as basic, strategic, and applied, with all operating in tandem but varying in percentage distribution (Maximum share being given to applied aspects).

The overall program will give durable varietal outputs that can withstand the danger from pathogens that limit wheat yields, such as stem rust. Integration means that leaf and yellow rust also are included. Another major threat, Karnal bunt, also will be addressed. The broad vision of the breeders, aided by pathologists, helps in selecting material that has resistance to minor diseases such as powdery mildew, spot blotch, and barley yellow dwarf, which has aphid involvement. Key abiotic stresses such as drought, salinity, sodicity, and heat are integral to our efforts.

Molecular inputs will elucidate the genetic diversity component of the materials and allow monitored varietal and gene deployment options within the country. The generated data base will help the regional professionals.

The scope of our current wheat-improvement effort requires that all provincial partners are on board. Wheat programs are set up in Sindh at Karachi, Tandojam, and Sakrand for quality and stem rust; lower Punjab at RARI for spot blotch, leaf and stem rust; AARI in Faisalabad for all rusts; BARI at Chakwal for rainfed testing; Islamabad for prebreeding, molecular, Karnal bunt and genetic diversity; NWFP at CCRI for yellow rust and BYDV; Kaghan for stem rust and mildew; and Baluchistan for yellow rust and rainfed conditions. These provinces are rich in sites and talent that also can cover salient abiotic stresses that are crucial for giving a holistic wheat-improvement scenario. The entire above structure is in place. The information is being shared here for global awareness.

Some of the salient objectives of our program are:

- the handling of accquired materials that form the 'adaptive' research category,
- executing a recombination breeding program,
- using efficient tools to shorten the breeding cycle,
- using genetic diversity, including conventional and diverse sources,
- using molecular tools to better understand germ plasm and targeted breeding goals,
- disease screening for of all rusts, mildew, Karnal bunt, spot blotch; *in vivo* and *in vitro*
- exposure to field practices and simple data analytical techniques,
- exposure to some upstream and basic techniques, and
- hands-on training of students, provincial support staff, local support personnel, and internationally supported capacity building to cover regional professionals as well.

The winter crop cycle of 2009–10 marks the conclusion of a four-year effort of the wide crosses program that has addressed three major areas of wheat research and development in Pakistan. This time perios has seen the emergence of a modest but quality infrastructure that covers laboratory research, controlled environment investigations, and a field set-up that assists both basic and applied output. We were able to structure a multidisciplinary research team of young professionals that are involved in knowledge generation aspects that embrace wide crossing, cytology, cytogenetics, biochemical genetics, diversity analyses, marker application, biotic stresses, abiotic stresses, prebreeding/breeding, and, through *in vitro* testing, other related areas of interest that relate to wheat productivity.

The focus of our investigations is high on recombination breeding using the novel diversity of the various gene pools that are underutilized globally and scarcely used within Pakistan, thus, no duplication occurs. Here we report on powdery mildew resistance, quality, general biotic stresses, abiotic stresses, and winter synthetics. The program has benefitted from exceptional support from international peers through their sharing of valuable cytogenetic stocks in which germ plasm provided by Dr. B.S. Gill of Kansas State University occupies a significant place.

Evaluation of wheat A- and B-genome-based amphiploids for powdery mildew resistance: morpho-molecular characterization, diversity, and utilization potential for wheat improvement.

Khola Rafique, Farah Naz, Alvina Gul Kazi, Shahzad Asad, Iqbal Ayub Khan, and Abdul Mujeeb-Kazi.

Hexaploid amphiploids (AAAABB) along with their durum parents (AABB) and AABBBB (or SS) were evaluated for their response to *Erysiphe graminis* f. sp. *tritici* at the seedling stage in the greenhouse at Murree, Pakistan, to identify and characterize resistance. Results indicated that 89 (56%) A-genome synthetic hexaploids (SH, AAAABB) along with their nine durum parents (39%) and nine (60%) B-genome synthetic hexaploids (AABBBB) showed seedling resistance against powdery mildew, indicating a valuable source of major resistance genes. The resistant accessions also were subjected to morphological characterization and molecular diversity analysis. Data on morphological traits showed substantial variation and demonstrated that these synthetic hexaploid wheat germ plasm are an important source of genes for desirable traits and can be utilized in wheat breeding programs. Among the A-genome synthetics, 37 genotypes, one durum parent, and among B-genome synthetics, five genotypes were found to be the best morphologically. To evaluate genetic diversity of the resistant genotypes, 12 SSR markers were used for 89 A-genome synthetics and their nine durum parents and 30 SSR markers for nine B-genome synthetics, with scorable bands (Table 1, p. 133). The average polymorphic loci per primer was 4.25 among the A-genome synthetics and their durum parents and 4.3 among the B-genome synthetics. The average similarity matrix was 0.265 (26.5%) in A-genome-based synthetic hexaploids and their durum

parents and 0.433 (43.3%) in B-genome-based synthetic hexaploids. This study suggested that powdery mildew resistance and morpho-molecularly diverse hexaploid amphiploids are important genetic stocks for future utilization in wheat-improvement programs.

Seedling resistance evaluation. Powdery mildew development was good in greenhouse evaluations and readily identifiable variations in disease reactions between resistant and susceptible seedlings were observed (Table 2). The frequency of genotypes among A-genome SHs and their durum parents and among B-genome SHs showing different infection types is presented (Fig 1). Results indicated that 89 accessions (56%) of A-genome-based synthetic hexaploids (AAAABB) or amphiploids along with their nine durum parents (39%) and nine accessions (60%) of B-genome-based synthetic hexaploids (AABBBB) or amphiploids showed seedling resistance against powdery mildew. Among the A-genome SHs, 15 were completely resistant (immune) to powdery mildew; 74 were resistant, 49 were intermediate, and 18 susceptible. Nine durum cultivars were resistant, eight intermediate, and six susceptible. In the B-genome-based SHs, five accessions were completely resistant (immune), four resistant, two intermediate, and four susceptible. The A-genome-based synthetics, along with their durum wheat parents, and the B-genome-based synthetics that gave resistant reactions (IT < 0–3) are listed in Table 3 (p. 134).

Table 1. A list of SSR primers used for the genetic analysis of A- and B-genome-based synthetic hexaploids and their durum parents.

Locus	Primer	Locus	Primer	Locus	Primer
Primers for A-genome-based synthetic hexaploids					
2A	*Xgwm-311*	3A	*Xgwm-666.2*	4A	*Xgwm-397*
4A	*Xgwm-601*	2A	*Xgwm-372*	2A	*Xgwm-473*
2A	*Xgwm-312*	2A	*Xgwm-382*	2A	*Xgwm-515*
4A	*Xgwm-637*	3A	*Xgwm-391*	2A	*Xgwm-558*
Primers for B-genome-based synthetic hexaploids					
5B	*Xgwm-66*	4B	*Xgwm-66*	6B	*Xgwm-88*
5B	*Xgwm-408*	3B	*Xgwm-112*	4B	*Xgwm-113*
6B	*Xgwm-219*	4B	*Xgwm-165*	4B	*Xgwm-149*
5B	*Xgwm-335*	5B	*Xgwm-213*	2B	*Xgwm-191*
2B	*Xgwm-382*	1B	*Xgwm-124*	2B	*Xgwm-210*
2B	*Xgwm-374*	2B	*Xgwm-16*	5B	*Xgwm-234*
5B	*Xgwm-159*	1B	*Xgwm-18*	3B	*Xgwm-340*
6B	*Xgwm-193*	2B	*Xgwm-55.1*	6B	*Xgwm-361*
2B	*Xgwm-257*	5B	*Xgwm-68*	4B	*Xgwm-368*
4B	*Xgwm-6*	3B	*Xgwm-72*	5B	*Xgwm-371*

Table 2. Evaluation of A-genome synthetics, their durum wheat parents, and B-genome synthetics for seedling resistance to powdery mildew.

Seedling infection type range	Reaction	Number of lines tested		
		A-genome synthetics (AAAABB)	Durum (AABB)	B-genome synthetics (AABBBB)
0–3	Resistant	89	9	9
4–6	Intermediate	49	8	2
7–9	Susceptible	18	6	4

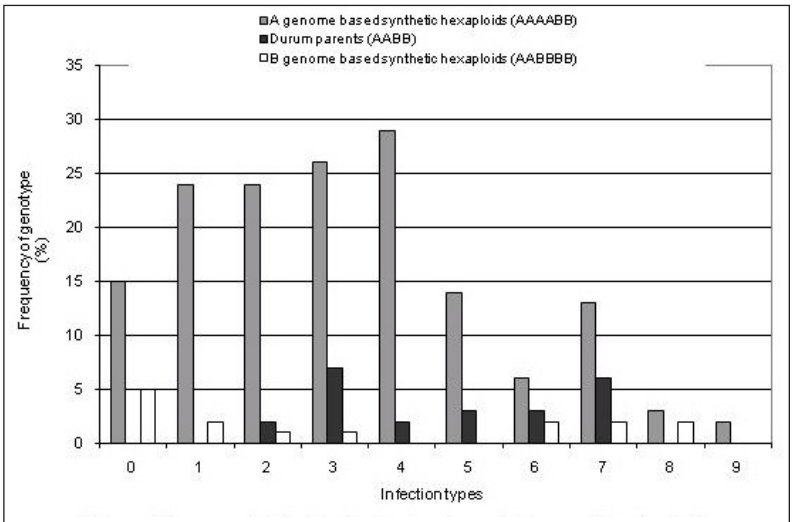

Fig. 1. Frequency distribution of the infection types of powdery mildew resistance of the A-genome-based synthetic hexaploids (AAABB), their durum wheat parents, and the B-genome-based synthetic hexaploids

Phenotypic evaluation. Data on morphological traits of resistant SH wheats, including A-genome-based SHs along with their durum parents and B-genome-based SHs, are given in Table 4 (p. 134-137). On the basis of 1,000-kernel weight and other phenotypic characters, the A-genome-based SH genotypes that were found morphologically good and diverse were 1, 3, 5, 7, 11, 12, 13, 14, 17, 18, 21, 24, 25, 31, 34, 36, 37, 40, 43, 50, 51, 52, 53, 54, 57, 58, 60, 61, 62, 66, 68, 71, 72, 86, and 89, and among durums the genotype D4. Among the B-genome-based SH, genotypes 1, 2, 3, 4, 6, and 7 were found best for the morphological traits.

Table 3. Sources of seedling resistance (IT < 3 on a 0–9 scale) to powdery mildew identified in A-genome-based synthetic hexaploids along with their durum cultivar parents and in B-genome-based synthetic hexaploids

Resistance reaction	Accession numbers		
	AAAABB	AABB	AABBBB
0	27, 30, 31, 39, 40, 49, 51, 52, 53, 54, 56, 59, 69, 86, 89	—	1, 2, 3, 5, 9
1	4, 13, 17, 19, 24, 28, 32, 33, 34, 38, 42, 43, 44, 50, 55, 57, 61, 66, 67, 68, 74, 77, 78, 85	—	4, 7
2	1, 3, 9, 11, 15, 18, 21, 22, 23, 25, 26, 41, 46, 47, 60, 63, 64, 70, 71, 73, 79, 80, 83, 87	D5, D9	6
3	2, 5, 6, 7, 8, 10, 12, 14, 16, 20, 29, 35, 36, 37, 45, 48, 58, 62, 65, 72, 75, 76, 81, 82, 84, 88	D1, D2, D3, D4, D6, D7, D8	8

Table 4. Phenological characterization of 89 powdery mildew resistant, A–genome–based synthetic hexaploids (AAAABB), their nine durum wheat parents (AABB), and nine B–genome–based synthetic hexaploids (AABBBB). * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
AAAABB (A-genome-based synthetic hexaploids)										
1	YUK/T.BOEOTICUM (1)*	–	125	+	104	LB	175	46.0	18	13.5
2	STY–US/CELTA//PALS/3/SRN_5/4/ T.BOEOTICUM (54)	–	127	+	133	LB	176	43.8	6	8.0
3	SCA/T.BOEOTICUM (10)	–	116	+	105	LB	180	60.0	15	13.2
4	GARZA/BOY//T.BOEOTICUM (10)	–	134	+	117	LB	174	40.0	30	12.0
5	GARZA/BOY//T.BOEOTICUM (12)	–	133	–	129	LB	184	60.0	40	10.3
6	ALG86/4/FGO/PALES//MEXI_1/3/ RUFF/FGO/5/ENTE/6/ T.BOEOTICUM (14)	–	135	+	124	LB	181	38.0	7	11.1
7	ALG86/4/FGO/PALES//MEXI_1/3/ RUFF/FGO/5/ENTE/6/ T.BOEOTICUM (15)	–	135	+	127	LB	184	48.0	33	14.1
8	ALG86/4/FGO/PALES//MEXI_1/3/ RUFF/FGO/5/ENTE/6/T.BOEOTICUM (74)	–	135	+	115	LB	193	37.8	13	11.1
9	ALG86/4/FGO/PALES//MEXI_1/3/ RUFF/FGO/5/ENTE/6/T.BOEOTICUM (83)	–	140	–	124	LB	180	40.0	33	9.0
10	BOTNO/T.BOEOTICUM (20)	–	154	+	104	LB	186	32.0	7	12.1
11	DOY1/T.URARTU (543)	–	125	+	120	LB	150	46.0	43	13.1
12	DOY1/T.URARTU (560)	–	127	+	145	LB	175	63.0	11	15.0
13	DOY1/T.URARTU (563)	–	119	+	75	LB	171	49.6	20	14.0
14	DOY1/T.URARTU (552)	–	127	+	100	DB	189	45.3	6	8.0
15	DOY1/T.URARTU (559)	–	131	+	131	LB	173	35.8	20	6.0
16	SHAG_22/T.BOEOTICUM (24)	–	133	+	139	DB	180	41.4	7	12.0
17	SHAG_22/T.BOEOTICUM (56)	–	145	+	121	LB	190	60.0	4	13.5
18	SHAG_22/T.BOEOTICUM (68)	–	116	+	106	LB	178	47.5	4	10.0
19	SHAG_22/T.BOEOTICUM (88)	–	131	+	119	DB	187	32.2	21	11.0
20	SCOOP_1/T.BOEOTICUM (40)	–	135	+	104	LB	186	42.6	12	10.1

Table 4 (continued). Phenological characterization of 89 powdery mildew resistant, A–genome–based synthetic hexaploids (AAAABB), their nine durum wheat parents (AABB), and nine B–genome–based synthetic hexaploids (AABBBB). * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
21	SCOOP_1/T.BOEOTICUM (46)	–	133	+	101	DB	186	48.2	22	10.1
22	SCOOP_1/T.BOEOTICUM (50)	–	147	+	129	LB	190	27.2	29	11.5
23	SCOOP_1/T.BOEOTICUM (59)	–	149	+	104	LB	190	40.6	24	11.0
24	SCOOP_1/T.BOEOTICUM (60)	–	118	+	102	LB	176	54.2	16	10.0
25	SCOOP_1/T.BOEOTICUM (69)	–	125	–	94	LB	175	45.2	24	9.5
26	SCOOP_1/T.BOEOTICUM (79)	–	126	+	110	Y	182	40.0	33	13.5
27	SCOOP_1/T.BOEOTICUM (87)	–	125	+	123	LB	181	44.4	21	10.0
28	SCOOP_1/T.BOEOTICUM (89)	–	146	+	130	DB	193	37.0	16	11.1
29	D67.2/P66.270//T.BOEOTICUM (35)	–	124	+	130	LB	175	13.7	7	18.0
30	D67.2/P66.270//T.MONOCOCCUM (108)	–	127	–	85	LB	182	24.4	18	10.0
31	D67.2/P66.270//T.URARTU (550)	–	122	+	120	LB	173	45.2	7	13.0
32	D67.2/P66.270//T.URARTU (553)	–	135	+	98	LB	177	25.0	4	7.0
33	AJAIA/T.BOEOTICUM (55)	–	135	+	125	LB	181	42.6	9	11.1
34	AJAIA/T.BOEOTICUM (56)	–	127	+	133	LB	179	56.0	18	15.0
35	68.111/RGB–U//WARD/3/ T.MONOCOCCUM (112)	–	121	–	108	LB	158	24.0	6	12.8
36	68.111/RGB–U//WARD/3/ T.URARTU (554)	–	133	+	108	LB	185	46.0	26	14.6
37	AOS/T.MONOCOCCUM (98)	–	127	–	105	LB	150	55.6	21	11.6
38	AOS/T.MONOCOCCUM (111)	–	127	+	103	LB	151	41.6	16	11.1
39	GAN/T.BOEOTICUM (29)	–	120	+	125	LB	175	37.0	35	10.0
40	DEVERD_2/T.BOEOTICUM (37)	–	122	+	125	LB	173	50.0	11	12.0
41	DEVERD_2/T.BOEOTICUM (43)	–	128	+	115	LB	178	38.0	15	11.0
42	DEVERD_2/T.BOEOTICUM (44)	–	131	+	109	LB	172	31.6	5	9.0
43	DEVERD_2/T.BOEOTICUM (45)	–	134	+	119	LB	175	51.8	25	10.0
44	YAV_2/TEZ//T.BOEOTICUM (25)	–	133	+	123	LB	176	31.0	4	13.0
45	YAV_2/TEZ//T.BOEOTICUM (37)	–	125	–	127	LB	178	41.2	15	13.0
46	YAV_2/TEZ//T.BOEOTICUM (43)	–	128	+	104	LB	183	31.0	6	12.0
47	YAV_2/TEZ//T.BOEOTICUM (45)	–	134	+	118	LB	176	40.0	17	11.0
48	YAV_2/TEZ//T.BOEOTICUM (47)	–	139	+	120	LB	180	40.0	13	13.0
49	YAV_2/TEZ//T.BOEOTICUM (62)	–	124	+	118	LB	179	43.4	6	13.0
50	YAV_2/TEZ//T.BOEOTICUM (64)	–	133	+	108	LB	180	65.6	13	7.0
51	YAV_2/TEZ//T.BOEOTICUM (65)	–	134	+	116	LB	183	56.6	38	12.0
52	YAV_2/TEZ//T.BOEOTICUM (67)	–	133	+	89	LB	181	61.6	14	9.8
53	YAV_2/TEZ//T.BOEOTICUM (83)	–	125	+	105	LB	185	48.0	15	13.0
54	YAV_2/TEZ//T.MONOCOCCUM (113)	–	126	–	117	LB	189	48.0	27	12.6
55	YAV_2/TEZ//T.MONOTICUM (121)	–	143	+	124	LB	191	32.4	8	11.0
56	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (38)	–	136	+	112	LB	178	40.0	7	8.0
57	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (41)	–	141	–	110	LB	175	46.0	17	11.0
58	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (48)	–	134	+	123	LB	184	71.0	6	10.0

Table 4 (continued). Phenological characterization of 89 powdery mildew resistant, A–genome–based synthetic hexaploids (AAAABB), their nine durum wheat parents (AABB), and nine B–genome–based synthetic hexaploids (AABBBB). * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
59	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (76)	–	145	+	81	LB	179	30.8	21	9.0
60	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (78)	–	145	+	128	LB	186	44.6	21	11.0
61	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (81)	–	120	+	123	DB	178	46.2	14	10.0
62	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (4)	–	147	+	113	DB	186	45.2	57	14.0
63	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (9)	–	143	–	110	LB	176	35.6	5	10.0
64	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (51)	–	125	+	133	LB	186	42.0	41	12.0
65	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (63)	–	140	+	123	LB	185	40.0	3	17.0
66	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (72)	–	140	+	120	LB	179	58.0	16	11.0
67	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (85)	–	140	+	143	LB	187	41.6	20	13.0
68	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM (53)	–	125	+	108	LB	177	49.6	7	7.0
69	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.MONOCOCCUM (107)	–	137	–	107	LB	182	33.6	12	11.0
70	CPI/GEDIZ/3/GOO//JO//CRA/4/ T. URARTU (548)	–	120	–	86	LB	182	35.6	27	13.0
71	CROC_1/T.URARTU (548)	–	134	+	95	LB	186	59.8	32	14.0
72	ALTAR 84/T.URARTU (558)	–	132	+	100	LB	183	46.2	19	10.0
73	CETA/T.URARTU (558)	–	127	–	120	LB	176	36.6	9	7.0
74	CETA/T.URARTU (562)	–	122	–	119	LB	183	41.8	24	8.0
75	CETA/T.BOEOTICUM((42)	–	140	+	138	LB	185	35.6	9	10.0
76	ARLIN_1/T.BOEOTICUM((32)	–	140	+	137	LB	185	31.6	5	13.0
77	ARLIN_1/T.BOEOTICUM (84)	–	140	+	122	LB	181	27.0	18	12.0
77	ARLIN_1/T.BOEOTICUM (84)	–	140	+	122	LB	181	27.0	18	12.0
78	ARLIN_1/T.BOEOTICUM (86)	–	139	+	135	LB	185	37.6	30	10.1
79	ARLIN_1/T.BOEOTICUM (103)	–	133	–	135	LB	187	30.8	14	10.0
80	ARLIN_1/T.BOEOTICUM (105)	–	141	–	155	Y	188	24.0	13	11.0
81	ARLIN_1/ T.BOEOTICUM (117)	–	128	–	137	LB	185	40.8	29	14.0
82	ARLIN_1/ T.BOEOTICUM (120)	–	127	–	137	LB	187	35.0	24	12.0
83	ARLIN_1/T.MONOCOCCUM (95)	–	141	+	118	LB	183	28.5	4	12.6
84	ARLIN_1/T.MONOCOCCUM (97)	–	140	+	131	LB	180	25.2	34	8.0
85	ARLIN_1/T.MONOCOCCUM (107)	–	129	+	144	LB	187	20.7	25	10.0
86	ARLIN_1/T.MONOCOCCUM (108)	–	136	+	95	LB	180	48.9	12	14.0
87	ARLIN_1/T.MONOCOCCUM (110)	–	133	–	116	LB	186	21.4	52	12.8
88	ARLIN_1T.URARTU (547)	–	141	+	117	LB	187	22.0	29	7.0
89	ARLIN_1/T.URARTU (548)	–	129	+	115	LB	177	44.8	22	8.0

Table 4 (continued). Phenological characterization of 89 powdery mildew resistant, A–genome–based synthetic hexaploids (AAAABB), their nine durum wheat parents (AABB), and nine B–genome–based synthetic hexaploids (AABBBB). * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
Durun wheat parent lines										
D1	ALG86/4/FGO/PALES//MEXI_1/3/ RUFF/FGO/5/ENTE	–	117	–	128	Y	181	32.0	27	13.0
D2	DECOY 1	–	126	–	103	Y	183	28.0	18	8.0
D3	SCOOP_1	–	123	+	124	B	181	37.0	28	9.0
D4	D67.2/P66.270	–	121	+	126	B	180	47.0	34	6.0
D5	LCK59.61	–	122	–	121	Y	184	36.0	15	6.6
D6	FGO/USA2111	–	116	–	128	LB	179	43.0	32	15.0
D7	GAN	–	122	+	144	Y	180	37.0	16	10.0
D8	CPI/GEDIZ/3/GOO//JO/CRA	–	114	+	138	Y	181	40.0	30	7.0
D9	CERCETA	–	115	–	135	B	177	41.0	23	8.0
AABBBB (B-genome-based synthetic hexaploids)										
1	CETA/AE.SPELTOIDES (127)	–	113	–	72	Y	161	52.0	22	10.0
2	CPI/GEDIZ/3/GOO//JO/CRA/4/ AE.SPELTOIDES (133)	–	113	–	75	Y	160	60.3	56	14.0
3	ARLIN_1/AE.SPELTOIDES (134)	–	133	+	90	AW	164	62.7	28	15.0
4	CPI/GEDIZ/3/GOO//JO/CRA/4/ AE.SPELTOIDES (135)	–	112	–	85	AW	163	44.8	60	12.0
5	CETA/AE.SPELTOIDES (135)	–	129	–	98	Y	164	18.0	5	13.0
6	CETA/AE.SPELTOIDES (139)	–	133	+	93	Y	162	44.6	24	14.5
7	ALTAR 84/AE.SPELTOIDES (141)	–	133	+	66	LB	166	60.0	30	13.0
8	ARLIN_1/ AE.SPELTOIDES (130)	–	145	+	74	AW	166	13.2	14	11.0
9	ARLIN_1/ AE.SPELTOIDES (157)	–	118	–	63	AW	161	28.6	46	8.0

Molecular evaluation. ***Genetic diversity estimation and cluster analysis of powdery mildew resistant A- genome based synthetic hexaploids and their durum parents***. Twelve SSR markers produced 51 polymorphic bands in sizes ranging from 50 bp to 400 bp. The average polymorphic loci/primer was 4.25. Primer *Xgwm-558-2A* generated the highest number of polymorphic bands.

The SSR amplification data was used to obtain a similarity matrix and generate a dendrogram. The similarity matrix was calculated using Nei and Li's coefficient analysis and showed genetic distance between individual pairs of all the genotypes. Using the resistant A-genome-based SH accessions along with their resistant durum wheat parents, the genetic diversity ranged from 0 to 100, where 0 represents the minimum genetic distance and 100 represents the maximum genetic distance among the genotypes, thus revealing high variability among accessions. Similarly, the value of the similarity coefficient, based on 12 SSR markers, ranged from 1 (100 percent) to 0. The accessions could be divided into main clusters A and B using UPGMA analysis based on genetic distances (Fig. 2, p. 138).

Cluster A consisted of 38 genotypes (87, 83, 78, D9, D8, 70, 69, 67, 66, 62, 61, 60, 58, 55, 52, 51, 50, 48, 47, 45, 44, 43, D7, 39, 37, 36, 26, 21, 20, 16, 15, 14, 11, 10, 9, 8, 7, and 6). All these genotypes showed the maximum genetic distance of 1 (100%). Cluster B consisted of the remaining 60 genotypes and was subdivided into three groups (1B, 2B, and 3B). Group 1B consisted of six genotypes (13, 79, 59, 68, 42, and 41). Two genotypes (41 and 42) in this group were exactly similar. The most diverse genotype with the highest genetic distance or least similarity in this group was 13, with an average genetic distance of 0.99 (99%) with a group of 59 genotypes. Group 2B consisted of 13 genotypes (89, 30, 74, 73, 53, 77, 72, 3, 57, 46, 71, 28, and 27). The most diverse genotype in this group was 77, with an average genetic distance of 0.633 (63.3%) with a group of two other genotypes. In this group, many genotypes also

showed a minimum genetic distance or 100 % similarity and one grouping included lines 71, 28, and 27. Group 3B was a large group and consisted of the remaining 41 genotypes (23, 40, D6, 88, 76, 56, 75, 12, 65, 64, 63, 54, 80, 49, 38, 33, 84, 85, 82, 86, 81, 29, D4, 32, D3, 22, 25, 24, 35, 34, 31, D1, 18, 17, 19, D2, 4, 2, D5, 5, and 1). Genotype 2 in this group was the most diverse, with an average genetic distance of 0.811 (81.1%) with a group of 16 other genotypes. The dendrogram generated from the SSR data indicated that the most genetically diverse A-genome-based SH wheat genotypes and durum parents were in Cluster A.

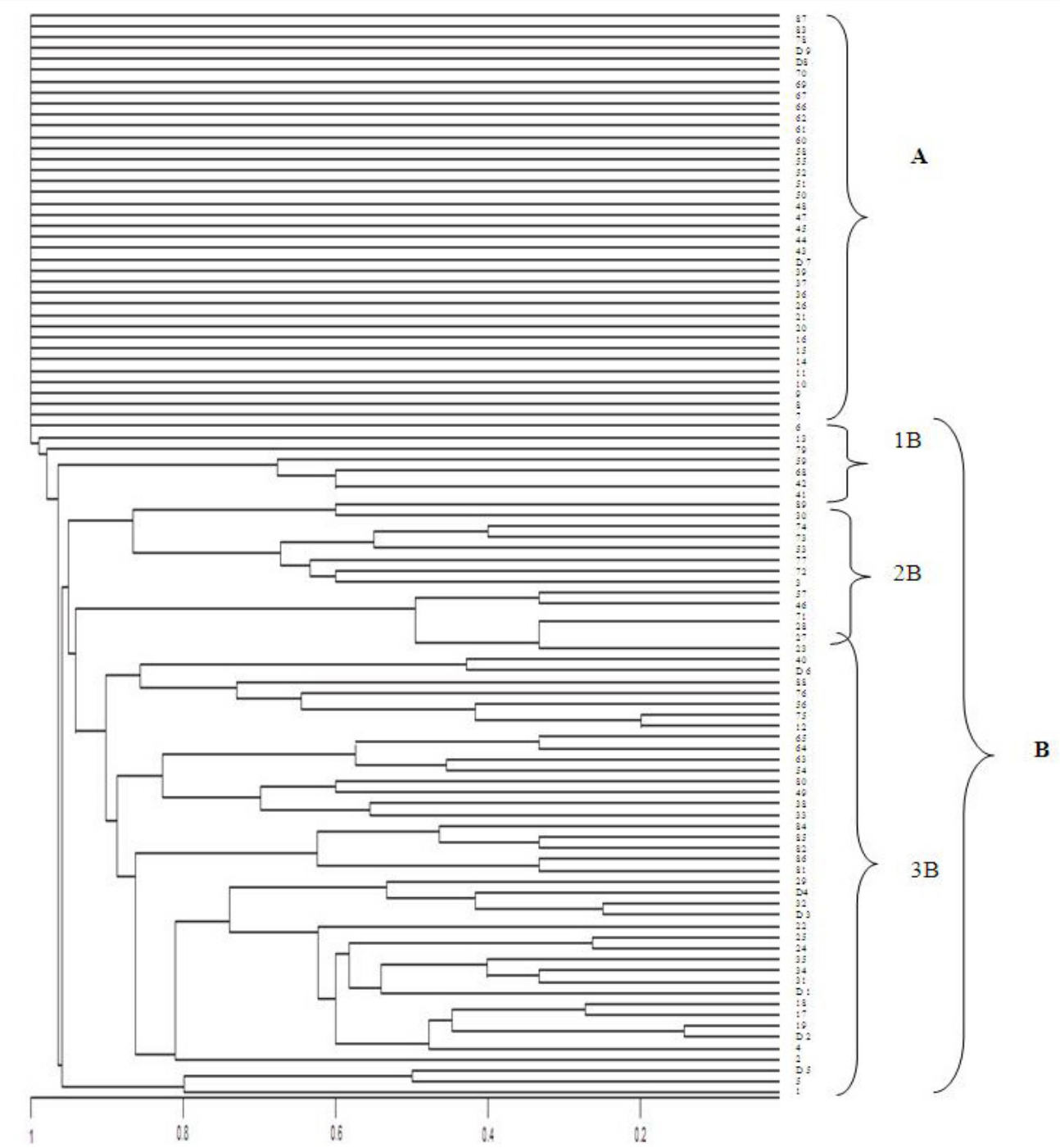

Fig. 2. Grouping of the resistant A-genome-based synthetic hexaploids (2n=6x=42; AAAABB) and their durum wheat parents based on genetic distance

Genetic diversity estimation and cluster analysis of powdery mildew resistant B-genome-based synthetic hexaploids. Thirty SSR markers produced 132 polymorphic bands in size ranging from 50 bp to 1000 bp. The average polymorphic loci/primer were 4.3. Primer *Xgwm-213-5B* generated highest number of polymorphic bands.

The SSR amplification data was used to obtain a similarity matrix and generate a dendrogram. The similarity matrix was calculated using Nei and Li's coefficient analysis and showed genetic distance between individual pairs of all genotypes. Using the resistant B-genome-based SH accessions, the genetic diversity ranged from 0.296 (29.6%) to 0.806 (80.6%), in which 0.296 represents minimum genetic distance and 0.806 represents maximum genetic distance among the genotypes, also revealing considerable variability among the accessions. The value of similarity coefficient based on 30 SSR markers ranged from 0.704 (70.4%) to 0.194 (19.4%). The accessions could be divided into two main clusters A and B using UPGMA analysis based on genetic distances (Fig. 3).

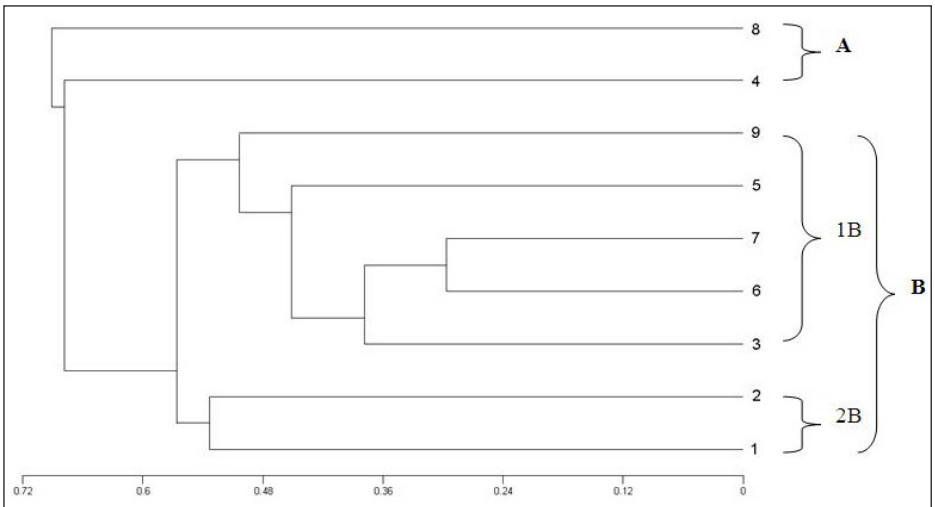

Fig. 3. Grouping of the resistant B-genome-based synthetic hexaploids on the basis of genetic distance.

Cluster A consisted of two genotypes, 8 and 4. These genotypes were found to be highly diverse from all the other genotypes. Compared to all the other gneotypes, the average genetic distance of genotype 8 was 0.691 (69.1%). Similarly, the average genetic distance of genotype 4 with all other genotypes except genotype 8 was 0.679 (67.9%). Cluster B was further subdivided into two groups, 1B and 2B. Group 1B consisted of five genotypes (9, 5, 7, 6 and 3). Among this group, genotype 9 had a maximum genetic distance of 0.503 (50.3%). Group 2B consisted of genotypes 1 and 2, which also were more diverse than the other genotypes in subcluster 1B with an average genetic distance of 0.533 (53.3%). The dendrogram generated from the SSR data indicated that the greatest diversity was observed in genotypes 8 and 4 among B-genome-based SH wheats.

Results. Valuable sources of powdery mildew resistance, good agronomic traits, and novel genetic diversity are available in AAAABB and AABBBB hexaploid amphiploids. The moderate frequency of seedling resistance in the A-genome SHs (56%), the durum wheat parents (39%), and B-genome SHs (60%) could provide diverse sources of resistance. According to seedling resistance evaluations, the A-genome-based genotypes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 87, 86, 88, 89, and 85; durum wheat genotypes D1, D2, D3, D4, D5, D6, D7, D8, and D9 were resistant to powdery mildew. The A-genome-based SHs were resistant due to alien genes received from their durum parents. The resistance in ccessions 6, 7, 8, and 9 was from their durum parent D1; accessions 11, 12, 13, 14, and 15 from parent D2; accessions 20, 21, 22, 23, 24, 25, 26, and 27 from D3; accessions 29, 30, 31, 32 from D4; line 39 from D7; lines 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 6, 69, and 70 from D8; and accessions 73, 74, and 75 from D9. For the B-genome-based SHs, genotypes 1, 2, 3, 4, 5, 6, 7, 8, and 9 were resistant to powdery mildew. These accessions also are a valuable source of major resistance genes to powdery mildew and, therefore, should be used in future breeding programs for incorporation of powdery mildew resistance.

After morphological examination of the resistant synthetics, 35 A-genome synthetics (1, 3, 5, 7, 11, 12, 13, 14, 17, 18, 21, 24, 25, 31, 34, 36, 37, 40, 43, 50, 51, 52, 53, 54, 57, 58, 60, 61, 62, 66, 68, 71, 72, 86, and 89), one durum wheat genotype (D4), and six B-genome synthetics (1, 2, 3, 4, 6, and 7) were morphologically good and diverse based on grain weight and other phenotypic characters. Among the A-genome synthetics, genotype 31 and its durum parent D4 were morphologically good; this genotype inherited these traits from its durum parent. Variation in morphological traits

exists in these respective lines and, therefore, are important sources of genes for desirable traits in plant breeding. These genotypes also should be used by the breeders in wheat improvement programs.

The genetic diversity estimation and cluster analysis revealed a highly diverse relationship between the hexaploid amphiploids (1.0 and 0.691). Kuleung et al. (2006) also reported moderate polymorphic relationships among the Triticale accessions (0.54). Our results indicate that SH wheatsareis very important in broadening of genetic base in hexaploid wheat. This novel diversity residing in SHs is anticipated to add to the durability and give sustainable output. In this study, SSR marker analysis revealed polymorphism between the genotypes indicating that SSR markers are a valuable diagnostic tool showing considerable genetic diversity. According to Röder et al. (1998), microsatellites or SSRs are an important tool for studies on genetic diversity, population structure, genetic mapping, and crop breeding due to their abundance, co-dominance, level of polymorphism, reliability, and ease of assay. Similarly, Parker et al. (2002) compared AFLP and SSR marker systems across 11 and 124 wheat varieties, respectively. Their results suggested that these markers are most effective in detecting polymorphism. Polymorphisms revealed by PCR amplification are due to variation of the number of repeats in a defined region of the genome (Morgante and Olivieri 1993).

The SSR cluster analysis of the A-genome SHs and durum wheats indicated genotypes 87, 83, 78, D9, D8, 70, 69, 67, 66, 62, 61, 60, 58, 55, 52, 51, 50, 48, 47, 45, 44, 43, D7, 39, 37, 36, 26, 21, 20, 16, 15, 14, 11, 10, 9, 8, 7, and 6 were the most diverse with a maximum genetic distance of 100%. The diversity found in A-genome SHs and their durum parents suggested that the durums are the donor of variability in A genome SHs. The diversity found in A-genome SH genotypes 58, 60, 61, 62, 66, 67, 68, 69, and 70 was from durum parent D8 and that in genotype 39 D7. Among B-genome SHs, genotypes 8 and 4 were found to be diverse.

The diversity generated by SSRs is more accurate and reliable, and this information will be helpful for future breeding programs that can utilize the recommended lines with a broad genetic base for incorporating powdery mildew resistance. These results provide an insight to the genetic diversity of these synthetics that should facilitate efficient utilization and management of these germ plasms or genetic stocks. According to Bretting and Widrlechner (1995), knowledge of diversity patterns allows plant breeders to better understand the evolutionary relationships among accessions, to sample germ plasm in a more systematic fashion, and to develop strategies to incorporate useful diversity in their breeding programs. Information about genetic similarity was helpful to avoid any chance of elite germ plasm becoming genetically uniform and endangering long-term productivity gains (Messmer et al. 1992). The data of genetic diversity among closely related lines along with phenotypic evaluation for various parameters proved very effective in selecting powdery mildew resistant lines that are genetically distant and phenotypically excellent. The A-genome synthetic lines 7, 11, 14, 21, 36, 37, 43, 502, 51, 52, 58, 60, 61, 62, and 66, and the B-genome synthetic line 4, exhibited the best seedling resistance against powdery mildew along with good phenotypic characters with a broader genetic base. These lines are recommended for further exploitation by world's breeders in wheat improvement programs.

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Evaluating D-genome-based synthetic hexaploids and their advanced derivatives for powdery mildew resistance: Morpho-molecular characterization, diversity, and utilization potential for wheat improvement.

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We screened the 93 Elite-I and 32 Elite-II synthetic wheat hexaploids and their advanced derivatives at the seedling stage in greenhouses at Murree, Pakistan, and at the adult-plant stage under field conditions at Kaghan, Pakistan, for powdery mildew resistance. In total, 44 Elite-I synthetics (57%), 20 Elite-II synthetics (62%), and 56 D-genome-derived advanced derivatives (93%) showed resistance at the seedling stage. These Elite-I and Elite-II accessions also had adult-plant resistance (APR). Among the advanced derivatives, 11 (18%) accessions showed only seedling resistance. In both the Elite-I and Elite-II synthetics, APR was 100%, and 80% in the D-genome-derived advanced derivatives. Of these lines, 53% of the Elite I, 37% of Elite II, and 5% of the D-genome-derived advanced derivatives had only APR. Most genotypes resistant at seedling stage also were resistant at the adult-plant stage. Forty-four accessions (57%) of tge Elite I, 20 accessions (62%) of the Elite II, and 45 (75%) of the D-genome-derived advanced derivatives were found to be significantly resistant with the resistance being expressed in both seedlings and adult plants. The resistant synthetic germ plasm found in this study has potential for wheat improvement.

A morphological evaluation of the synthetics resistant at adult and at both stages showed that 76 Elite-I genotypes, 13 Elite-II genotypes, and five D-genome-derived advanced derivative genotypes are good and diverse. These synthetic hexaploid wheats are an important source of genes for desirable traits in plant breeding. The resistant 93 Elite-I synthetics were subjected to SSR analysis for molecular diversity evaluation. We used 13 SSR markers (Table 5) that gave clear bands, and the average polymorphic loci/primer was 6.07 and the average similarity matrix was 0.77 (77%). The resistant Elite-II synthetics and D-genome-derived advanced derivatives were checked for the presence of resistance genes *Pm4b*, *Pm9*, *Pm16*, and *Pm30* using SSR markers. The results indicated that SSR marker *Xgwm-382* flanked the resistance gene *Pm4b* in one Elite-II line and five advanced derivatives, *Xgwm-4* detected *Pm9* in one Elite-II line and 27 advanced derivatives, *Xgwm-332* showed the presence of *Pm9* gene in one Elite-II line and in 13 advanced derivatives, and *Pm16* and *Pm30* genes were present in one Elite-II genotype and in two advanced derivatives indicated by *Xgwm-159*. The SSR analysis proved that the resistant Elite-II and D-genome advanced derivative lines with respective genes can be used in wheat breeding programs against powdery mildew. Incorporating and deploying of these powdery mildew resistance genes will be helpful to provide wheat growers with resistant cultivars.

Table 5. A list of the SSR primers used for genetic analysis of Elite-1 synthetic hexaploids.

Locus	Primer	Locus	Primer	Locus	Primer
1D	*Xgwm-106*	3A	*Xgwm-2*	3D	*Xgwm-383*
2B	*Xgwm-210*	4A	*Xgwm-160*	3B	*Xgwm-112*
1B	*Xgwm-140*	6A	*Xgwm-169*	2B	*Xgwm-47*
1A	*Xgwm-136*	4D	*Xgwm-608*		
2A	*Xgwm-71.1*	1D	*Xgwm-458*		

Molecular diagnostics of the *Pm* resistance genes in powdery mildew-resistant the Elite-II synthetic hexaploid set and in D-genome-derived advanced derivatives. Thirty-two Elite-II accessions and 48 D-genome-derived advanced derivatives were tested with SSR markers for the presence of four genes, *Pm4b*, *Pm9*, *Pm16* and *Pm30* (Table 6). The SSR markers use were *Xgwm-382* for powdery mildew resistant gene *Pm4b* (Yi et al. 2008), *Xgwm-4* and *Xgwm-332* linked to *Pm9* (Srnic et al. 2005), and SSR marker *Xgwm-159* linked to genes *Pm16* and *Pm30* (Chen et al. 2005).

Table 6. Sequence and annealing temperature of the molecular markers linked to Pm genes.

Locus	Marker	*Pm* gene	Primer sequence	Annealing temperature
2A	Xgwm-382$_{-125}$	*Pm4b*	F: GTC AGA TAA CGC CGT CCA AT R: CTA CGT GCA CCA CCA TTT TG	60°C
4A	Xgwm-4$_{-253}$	*Pm9*	F: GCT GAT GCA TAT AAT GCT GT R: CAC TGT CTG TAT CAC TCT GCT	55°C
7A	Xgwm-332$_{-212}$	*Pm9*	F: AGC CAG CAA GTC ACC AAA AC R: AGT GCT GGA AAG AGT AGT TTTG	60°C
5B	Xgwm-159$_{-201}$	*Pm16*, *Pm30*	F: GGG CCA ACA CTG GAA CAC R: GCA GAA GCT TGT TGG TAG GC	60°C

Greenhouse evaluation for seedling resistance. Different infection types (ITs) were recorded within the Elite-I, Elite-II, and D genome-derived advanced derivatives at the seedling stage. At the seedling stage, 57% percent of the Elite-I synthetics and 62% of the Elite-II synthetics were resistant. These lines also also had APR, indicating that none were resistant only at seedling stage. Among the D-genome-derived advanced derivatives, 93% of the accessions resistant at the seedling stage also had APR, and 18% were resistant only at the seedling stage. Most of the SHs were found to possess good resistance at seedling stage to powdery mildew.

Field evaluation for adult plant resistance. Synthetic germ plasm also was tested under field conditions at Kaghan, Pakistan, to evaluate APR (Table 7). At the adult-plant stage, 100% of Elite-I synthetics and Elite-II synthetics and 80% of D-genome-derived advanced derivatives were resistant (Fig 4.). Only adult-plant resistance to powdery mildew was found in 53% of the Elite-I, 37% of the Elite-II lines, and 5% of the D-genome-derived advanced derivatives had (Table 8). Most of the lines resistant at seedling stage also had APR. Significant resistance expressed in both seedling and adult-plant stages was found in 57% of the Elite I, 62% of the Elite II, and 75% of the D-genome-derived advanced derivatives (Table 9, p. 143).

Table 7. Powdery mildew evaluation for adult-plant resistance under field condidtions at Kaghan, Pakistan.

Infection type	Reaction	Number of lines tested		
		Elite-I	Elite-II	Advanced derivatives
0–3	Resistant	49	12	3
4–6	Intermediate	—	—	—
7–9	Susceptible	—	—	—

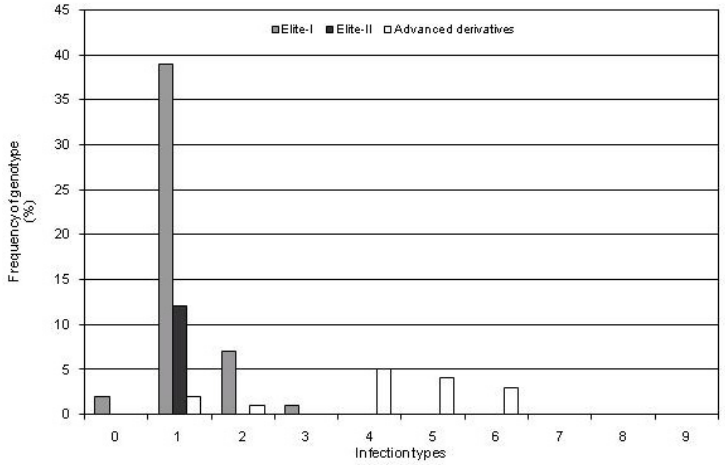

Fig. 4. Frequency distribution for powdery mildew infection type of the Elite-I and Elite-II synthetic hexaploids and the D-genome-derived advanced derivatives at the adult-plant stage.

Phenotypic evaluation. Morphological trait data of the resistant Elite-I and Elite-II SH wheats and the D-genome-derived advanced derivatives are presented in Table 10 (pp. 143-148). On the basis of 1,000-kernel weight and other phenotypic characters, Elite-I SH genotypes 2, 5, 8, 9, 12, 14, 18, 19, 20, 21, 22, 23, 26, 29, 30, 31, 32, 33, 34, 35, 37, 38, 42, 43, 44, 45, 52, 59, 60, 61, 62, 76, 78, 80, 81, 83, 84, 85, 86, 87, 89, and 92; Elite-II SH genotypes 3, 7, 9, 10, 12, 13, 16, 26, 30, 31, and 32; and D-genome-derived advanced derivative genotypes L.R Fusarium-833, M.BCN-7, Dr.MP-2-10, Elite HYDRL-6, and Elite HYDRL-13 were morphologically desirable.

Table 8. Sources of adult-plant resistance (IT < 3 on a 0-9 scale) to powdery mildew identified in Elite-I, Elite-II sets and advanced derivatives tested under field conditions.

Resistant reaction	Accession numbers		
	Elite I	Elite II	Advanced derivatives
0	5, 58	—	—
1	1, 2, 4, 9, 10, 12, 13, 15, 16, 17, 19, 23, 24, 26, 28, 29, 30, 31, 33, 35, 39, 41, 63, 65, 66, 67, 72, 73, 75, 76, 77, 80, 82, 85, 86, 87, 88, 89, 92	1, 4, 13, 14, 15, 20, 21, 23, 24, 25, 27, 28	4, 26
2	3, 20, 21, 22, 46, 61, 74	—	5
3	18	—	—

Molecular evaluation. ***Genetic diversity estimation and cluster analysis of synthetic hexaploid Elite-I set.*** For SSR analysis, 13 primers were used that yielded 79 polymorphic bands, generating 6.07 polymorphic loci/primer. The size range of amplified bands ranged from 50 bp to 1,000 bp. The highest number of polymorphic bands (3) was achieved with primer *Xgwm-383-3D*, 1.96% of the total number of amplified bands.

The SSR amplification data was used to generate similarity matrix and dendrogram. The similarity matrix was calculated using Nei and Li's coefficient analysis and showed genetic distance between individual pairs of all the genotypes. Using all the Elite-I SHs, the genetic diversity using SSR markers ranged from 0.049 (4.9 %) to 0.838 (83.8%), in which 0.049 represents minimum genetic distance and 0.838 represents maximum genetic distance among the genotypes and revealing high variability among the accessions. Similarly, the value of similarity coefficient based on 13 SSR markers ranged from 0.951 (95.1%) to 0.162 (16.2%).

The clustering of the 93 Elite-I SH accessions, based on genetic distances using UPGMA analysis produced, two main clusters A and B (Fig. 5, p. 149). Cluster A was comprised of eight genotypes (80, 75, 76, 44, 31, 18, 17, and 8). Among these genotypes, 80 and 75 were highly diverse, having similarity coefficient of 0.500 (50%). These two genotypes were more diverse than the remaining genotypes with an average genetic distance of 0.68 (68%). The least diverse genotypes in this group were 18 and 17, with a genetic distance of 0.28 (28%). Cluster B was com-

Table 9. Lines of the Elite-I and Elite-II synthetic hexaploids and advanced derivatives resistant (IT = 0–3) to powdery mildew at the seedling and adult-plant stages under field condidtions at Kaghan, Pakistan.

Accession numbers		
Elite-I	**Elite-II**	**Advanced derivatives**
6, 7, 8, 11, 14, 25, 27, 32, 34, 36, 37, 38, 40, 42, 43, 44, 45, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 59, 60, 61, 62, 64, 68, 69, 70, 71, 78, 79, 81, 83, 84, 90, 91, 93	2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18, 19, 22, 26, 29, 30, 31, 32	1, 2, 3, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48

Table 10. Phenological characterization of 93 Elite-I and 32 Elite-II synthetic hexaploid lines and 48 D-genome-derived advanced derivatives. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
Elite-I synthetic hexaploid lines										
1	ALTAR 84/AE.SQUARROSA (188)*	M	120	+	120	LB	148	48.0	22	12.0
2	DOY1/AE.SQUARROSA (188)	M	121	+	130	LB	160	53.2	43	12.0
3	ALTAR 84/AE.SQUARROSA (192)	M	120	+	125	DB	156	48.0	31	12.0
4	ALTAR 84/AE.SQUARROSA (193)	M	121	+	119	LB	152	49.0	23	8.0
5	ALTAR 84/AE.SQUARROSA (198)	M	130	+	130	LB	161	50.3	38	12.0
6	CROC_1/AE.SQUARROSA (205)	+	130	+	103	LB	160	48.2	20	12.2
7	ALTAR 84/AE.SQUARROSA (205)	M	131	+	96	LB	159	49.5	10	10.2
8	CPI/GEDIZ/3/GOO//JO69/CRA/4/ AE.SQUARROSA (208)	M	132	+	85	LB	157	58.3	25	7.2
9	ALTAR 84/AE.SQUARROSA (211)	M	120	+	85	LB	157	59.5	14	8.0
10	D67.2/P66.270//AE.SQUARROSA (211)	M	122	–	102	LB	151	39.4	9	14.0
11	D67.2/P66.270//AE.SQUARROSA (213)	M	128	+	82	LB	157	39.6	13	12.0
12	ROK/KML//AE.SQUARROSA (214)	+	130	+	125	LB	155	58.5	14	11.0
13	D67.2/P66.270//AE.SQUARROSA (217)	M	132	+	80	LB	163	49.0	48	7.0
14	YUK/AE.SQUARROSA (217)	+	131	+	90	LB	171	64.0	42	14.0
15	D67.2/P66.270//AE.SQUARROSA (218)	M	115	+	135	LB	144	39.5	10	11.0
16	ALTAR 84/AE.SQUARROSA (219)	M	132	+	95	LB	164	47.5	9	9.0
17	ALTAR 84/AE.SQUARROSA (220)	–	129	+	106	LB	157	49.3	54	13.7
18	D67.2/P66.270//AE.SQUARROSA (220)	+	115	–	93	LB	157	56.0	10	13.2
19	DVERD_2/AE.SQUARROSA (221)	M	134	–	93	LB	160	54.7	15	12.0
20	ALTAR 84/AE.SQUARROSA (221)	M	133	+	128	LB	162	53.0	14	10.0
21	D67.2/P66.270//AE.SQUARROSA (221)	M	130	–	105	LB	161	50.5	12	10.5
22	D67.2/P66.270//AE.SQUARROSA (222)	M	125	+	139	LB	157	59.2	15	9.0
23	D67.2/P66.270//AE.SQUARROSA (223)	M	111	–	125	LB	155	58.6	18	12.3

Table 10 (continued). Phenological characterization of 93 Elite–I and 32 Elite–II synthetic hexaploid lines and 48 D–genome–derived advanced derivatives. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
24	CROC_1/AE.SQUARROSA (224)	–	120	+	117	LB	127	48.8	16	12.0
25	ALTAR 84/AE.SQUARROSA (224)	+	128	+	112	LB	164	43.0	12	13.0
26	ACO89/AE.SQUARROSA (309)	+	123	+	89	LB	153	51.0	49	9.2
27	GARZA/BOY//AE.SQUARROSA (311)	–	130	–	78	LB	165	46.8	28	7.3
28	68.111/RGB-U//WARD/3/AE. SQUARROSA (316)	M	129	+	108	LB	158	41.0	11	12.5
29	68.111/RGB-U//WARD/3/AE. SQUARROSA (326)	M	120	+	132	LB	158	56.8	6	11.0
30	68112/WARD//AE.SQUARROSA (369)	M	117	+	139	LB	152	61.0	12	14.0
31	68112/WARD//AE.SQUARROSA (369)	+	113	+	109	LB	139	56.0	23	14.2
32	DOY1/AE.SQUARROSA (447)	+	133	+	102	LB	161	55.0	16	14.0
33	YAV_3/SCO//JO69/CRA/3/YAV79/4/AE. SQUARROSA (498)	–	130	+	106	LB	163	55.0	14	13.0
34	DOY1/AE.SQUARROSA (511)	M	116	+	136	LB	158	50.0	10	14.0
35	68.111/RGB-U//WARD/3/AE. SQUARROSA (511)	M	117	+	109	LB	148	60.3	17	14.3
36	DOY1/AE.SQUARROSA (515)	M	113	–	125	LB	151	49.6	13	14.5
37	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE. SQUARROSA (629)	+	128	+	132	LB	162	53.9	15	12.0
38	FGO/USA2111//AE.SQUARROSA (658)	–	120	+	132	LB	154	54.2	23	14.0
39	CROC_1/AE.SQUARROSA (725)	–	120	–	135	DB	151	49.0	38	14.0
40	68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (781)	–	130	+	139	LB	173	49.5	10	15.5
41	68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (783)	M	129	+	129	LB	160	44.5	16	14.2
42	YAR/AE.SQUARROSA (783)	M	132	+	121	LB	176	57.9	9	14.8
43	YUK/AE.SQUARROSA (864)	M	132	+	119	LB	167	52.3	13	11.0
44	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	M	123	+	88	LB	159	54.0	17	12.0
45	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	M	136	+	97	LB	173	53.0	28	9.0
46	CROC_1/AE.SQUARROSA (879)	M	134	–	103	LB	161	49.4	18	12.0
47	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (882)	M	131	+	86	LB	161	46.0	20	12.0
48	SORA/AE.SQUARROSA (884)	–	130	–	140	DB	166	39.4	22	12.0
49	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE. SQUARROSA (890)	–	130	+	135	LB	156	46.9	5	10.0
50	CROC_1/AE.SQUARROSA (518)	+	138	+	92	LB	165	49.0	20	10.0
51	PBW114/AE.SQ	+	136	+	104	LB	165	45.9	6	12.3
52	ALTAR 84/AE.SQUARROSA (JBANGOR)	+	113	–	142	LB	139	53.1	12	14.0
53	YAV_2/TEZ//AE.SQUARROSA (249)	M	130	–	145	LB	155	39.6	8	14.2
54	CETA/AE.SQUARROSA (895)	–	133	+	138	LB	156	43.5	23	14.0
55	D67.2/P66.270//AE.SQUARROSA (257)	M	133	–	99	LB	168	49.0	9	10.0
56	LCK59.61/AE.SQUARROSA (313)	M	135	+	99	LB	164	40.7	5	12.0
57	LCK59.61/AE.SQUARROSA (324)	M	127	+	112	LB	159	44.0	8	12.0

Table 10 (continued). Phenological characterization of 93 Elite-I and 32 Elite-II synthetic hexaploid lines and 48 D-genome-derived advanced derivatives. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
58	SRN/AE.SQUARROSA (358)	+	127	+	132	LB	156	45.0	11	10.2
59	SCOOP_1/AE.SQUARROSA (358)	M	131	+	135	LB	171	54.2	16	14.0
60	GAN/AE.SQUARROSA (408)	M	134	–	126	LB	179	52.6	61	14.2
61	SCA/AE.SQUARROSA (518)	M	134	+	97	LB	179	56.8	46	13.0
62	YAR/AE.SQUARROSA (518)	M	131	–	114	LB	157	52.0	8	11.0
63	BOTNO/AE.SQUARROSA (617)	M	131	+	140	LB	169	46.0	58	9.3
64	BOTNO/AE.SQUARROSA (620)	M	131	+	142	LB	161	49.8	22	15.2
65	BOTNO/AE.SQUARROSA (625)	M	132	–	99	LB	159	41.0	15	14.0
66	SNIPE/YAV79//DACK/TEAL/3/ AE.SQUARROSA (629)	M	134	+	139	LB	158	48.8	14	12.0
67	D67.2/P66.270//AE.SQUARROSA (633)	M	126	+	96	LB	149	49.0	4	8.0
68	D67.2/P66.270//AE.SQUARROSA (659)	M	132	+	98	LB	156	48.0	10	14.0
69	SNIPE/YAV79//DACK/TEAL/3/ AE.SQUARROSA (700)	M	131	+	140	LB	155	47.0	15	10.2
70	TRN/AE.SQUARROSA (700)	M	130	+	132	LB	157	49.0	30	12.0
71	SNIPE/YAV79//DACK/TEAL/3/ AE.SQUARROSA (877)	–	128	+	138	LB	156	48.0	21	14.3
72	GAN/AE.SQUARROSA (897)	M	129	+	98	LB	161	39.3	9	13.3
73	YAV_2/TEZ//AE.SQUARROSA (895)	M	135	+	112	LB	165	48.6	18	11.2
74	ARLIN/AE.SQUARROSA (283)	M	138	+	119	LB	169	47.9	17	14.3
75	FALCIN/AE.SQUARROSA (312)	+	136	+	140	LB	164	45.2	18	14.3
76	RASCON/AE.SQUARROSA (312)	+	136	+	138	LB	165	55.0	5	12.0
77	SCOT/MEXI_1//AE.SQUARROSA (314)	M	133	+	120	LB	166	45.5	15	14.0
78	DOY1/AE.SQUARROSA (333)	M	132	–	115	LB	164	56.5	12	16.0
79	68.111/RGB-U//WARD/3/AE.SQUARROSA (452)	M	131	+	120	LB	160	38.3	18	16.0
80	68.111/RGB-U//WARD/3/AE.SQUARROSA (454)	M	128	+	130	LB	158	52.0	20	16.0
81	DOY1/AE.SQUARROSA (458)	M	130	+	130	LB	161	54.0	14	15.2
82	GREEN/AE.SQUARROSA (458)	M	135	–	130	LB	171	44.4	13	16.0
83	CETA/AE.SQUARROSA (174)	M	135	+	131	LB	174	61.0	19	15.0
84	DOY1/AE.SQUARROSA (372)	M	134	+	123	LB	165	58.4	15	15.0
85	SCA/AE.SQUARROSA (409)	M	134	+	128	LB	166	50.9	16	15.0
86	CPI/GEDIZ/3/GOO//JO69/CRA/4/AE. SQUARROSA (409)	+	134	+	132	LB	163	54.0	18	14.0
87	STY-US/CELTA//PALS/3/SRN_5/4/ AE.SQUARROSA (502)	–	133	+	122	LB	158	52.0	15	14.0
88	ALTAR 84/AE.SQUARROSA (502)	+	132	+	109	LB	164	44.0	16	16.0
89	CROC/AE.SQUARROSA (517)	M	115	+	128	LB	153	55.0	13	15.2
90	CETA/AE.SQUARROSA (1024)	M	115	+	118	LB	152	48.4	14	15.0
91	DVERD_2/AE.SQUARROSA (1027)	+	133	+	127	LB	162	42.0	16	15.0
92	CETA/AE.SQUARROSA (1027)	+	140	+	118	LB	165	55.4	30	15.0
93	DOY1/AE.SQUARROSA (1030)	+	128	+	112	LB	160	49.9	28	15.0

Table 10 (continued). Phenological characterization of 93 Elite-I and 32 Elite-II synthetic hexaploid lines and 48 D-genome-derived advanced derivatives. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
Elite-II synthetic hexaploid lines										
1	SORA/AE.SQUARROSA (192)	–	135	+	131	LB	192	38.0	20	11.5
2	CROC_1/AE.SQUARROSA (210)	M	135	–	120	Y	191	30.8	15	14.6
3	DVERD_2/AE.SQUARROSA (214)	M	128	–	120	B	187	57.4	10	10.5
4	ARLIN_1/AE.SQUARROSA (218)	M	128	+	130	LB	179	31.6	29	10.6
5	GAN/AE.SQUARROSA (236)	M	140	+	140	DB	184	41.6	17	10.6
6	SORA/AE.SQUARROSA (323)	M	135	–	123	DB	178	34.2	28	15.1
7	D67.2/P66.270//AE.SQUARROSA (308)	M	144	–	130	Y	180	50.0	26	15.0
8	STY-US/CELTA//PALS/3/SRN_5/4/ AE.SQUARROSA (431)	+	141	–	128	DB	182	48.0	13	10.3
9	LCK59.61/AE.SQUARROSA (693)	M	139	+	127	LB	178	51.5	25	13.1
10	SKARV_2/AE.SQUARROSA (304)	–	133	–	143	Y	183	54.0	33	12.6
11	CETA/AE.SQUARROSA (1025)	–	124	+	117	DB	184	43.0	30	10.3
12	DOY1/AE.SQUARROSA (1027)	–	126	+	112	LB	183	57.8	26	12.0
13	CETA/AE.SQUARROSA (386)	–	146	+	143	Y	178	56.0	22	12.0
14	CETA/AE.SQUARROSA (392)	–	123	+	116	LB	180	33.3	42	12.0
15	CETA/AE.SQUARROSA (533)	M	129	+	119	LB	182	24.3	30	12.0
16	CPI/GEDIZ/3/GOO//JO/CRA/4/ AE.SQUARROSA (1018)	M	146	+	136	DB	192	58.2	11	10.6
17	CETA/AE.SQUARROSA (1031)	–	133	+	113	Y	195	33.0	20	11.0
18	CETA/AE.SQUARROSA (1038)	M	135	+	138	DB	192	40.0	21	10.0
19	CETA/AE.SQUARROSA (1046)	–	124	+	136	LB	183	43.5	25	10.0
20	CETA/AE.SQUARROSA (1053)	M	143	–	110	B	182	34.0	11	11.5
21	CROC_1/AE.SQUARROSA (212)	M	143	–	110	Y	189	49.2	27	13.0
22	CETA/AE.SQUARROSA (368)	M	139	+	132	LB	195	36.0	18	11.5
23	ARLIN_1/AE.SQUARROSA (430)	M	124	+	115	DB	185	14.0	16	11.0
24	D67.2/P66.270// AE.SQUARROSA (497)	M	126	+	80	DB	182	27.0	9	13.0
25	D67.2/P66.270// AE.SQUARROSA (1015)	M	128	+	115	DB	184	40.4	21	12.8
26	GAN/AE.SQUARROSA (206)	M	146	+	124	LB	194	50.2	16	10.0
27	ARLIN_1/AE.SQUARROSA (335)	M	150	+	102	LB	196	40.2	11	12.5
28	GAN/AE.SQUARROSA (335)	–	143	+	141	DB	181	27.8	20	11.6
29	68.111/RGB-U//WARD RESEL/3/STIL/4/ AE.SQUARROSA (385)	–	143	+	132	LB	182	34.0	14	9.6
30	CETA/AE.SQUARROSA (417)	–	146	–	128	DB	196	57.6	18	11.5
31	68.111/RGB-U//WARD RESEL/3/STIL/4/ AE.SQUARROSA (431)	M	146	–	134	B	185	64.0	31	14.0
32	DOY1/ AE.SQUARROSA (534)	M	146	+	131	DB	179	50.0	23	11.0
D-genome-derived advanced lines										
1	BCN//CETA/AE. SQUARROSA (895)	–	107	–	101	DB	146	26.6	57	12.0
2	CPI/GEDIZ/3/GOO//JO69/CRA/4/AE. SQUARROSA (409) CIGM93.388	–	120	+	106	DB	153	34.0	13	14.0
3	ALTAR 84/ AE. SQUARROSA (224)	–	120	–	82	DB	152	31.8	27	11.0
4	68.111/RGB-U//WARD/3/FGO/4/RABI/5/ AE. SQUARROSA (809)	–	95	+	112	AW	149	26.8	19	10.0

Table 10 (continued). Phenological characterization of 93 Elite-I and 32 Elite-II synthetic hexaploid lines and 48 D-genome-derived advanced derivatives. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
5	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE. SQUARROSA (878)	–	114	+	92	LB	152	32.6	57	11.0
6	BOTNO	–	124	+	121	LB	152	24.0	32	11.0
7	AJAIA_9	–	114	+	82	LB	155	43.3	45	10.0
8	-	–	107	–	102	AW	148	45.0	62	13.0
9	CETA/AE.SQUARROSA (533)	–	119	+	115	LB	151	20.1	15	14.0
10	CETA/AE.SQUARROSA (1038)	–	111	+	109	AW	151	23.0	21	12.0
11	YS/PASTOR	–	112	+	104	AW	149	26.6	46	13.0
12	YS/PASTOR	–	105	–	109	AW	149	28.0	65	12.0
13	YS/PASTOR	–	107	–	113	AW	150	40.4	63	13.0
14	YS/PASTOR	–	108	–	113	AW	150	33.4	49	14.0
15	YS/PASTOR	–	111	+	113	AW	144	40.9	40	13.0
16	YS/PASTOR	–	110	+	105	AW	151	40.2	59	13.5
17	YS/PASTOR	–	110	–	109	Y	151	32.6	66	12.8
18	MAYOOR//TK SN1081/AE. SQUARROSA (222)/3/FCT	–	119	–	101	LB	154	33.8	36	14.3
19	MAYOOR//TK SN1081/AE. SQUARROSA (222)/3/BCN	–	105	–	111	LB	151	34.8	56	12.0
20	MAYOOR//TK SN1081/AE. SQUARROSA (222)/3/BCN	–	113	–	99	LB	150	44.9	40	13.3
21	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE. SQUARROSA (205)/3/3*BUC/6/OPATA	–	108	–	95	AW	150	38.8	74	13.3
22	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE. SQUARROSA (205)/3/3*BUC/6/CNO	–	108	–	90	AW	151	35.8	72	13.0
23	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE. SQUARROSA (205)/3/3*BUC/6/BCN	–	109	–	96	AW	151	36.6	47	12.1
24	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE. SQUARROSA (205)/3/3*BUC/6/BCN	–	109	–	89	AW	152	41.8	58	13.5
25	SABUF/3/BCN//CETA/AE. SQUARROSA (895)/4/BCN	–	106	–	99	LB	154	37.4	29	14.6
26	SABUF/3/BCN//CETA/AE. SQUARROSA (895)/4/BCN	–	110	–	100	LB	152	35.8	65	11.3
27	SABUF/3/BCN//CETA/AE. SQUARROSA (895)/4/FCT	–	112	–	82	Y	151	39.2	65	12.4
28	SABUF/3/BCN//CETA/AE. SQUARROSA (895)/4/FCT	–	110	–	104	LB	154	23.7	29	12.6
29	YAV_3/SCO//JO69/CRA/3/YAV79/4/AE. SQUARROSA (498)/5/OPATA	–	90	+	74	Y	152	53.0	24	12.0
30	GAN/AE. SQUARROSA (897)//OPATA	–	90	–	107	Y	152	30.4	22	11.6
31	Not Available	–	100	–	90	Y	149	31.8	52	11.0
32	Not Available	–	110	–	108	LB	149	39.0	64	12.9
33	Not Available	–	113	–	109	Y	156	29.4	77	15.3
34	Not Available	–	111	–	94	Y	156	43.6	62	14.0
35	Not Available	–	110	–	93	LB	154	33.2	58	12.6
36	Not Available	–	107	–	102	AW	155	34.6	42	12.3

Table 10 (continued). Phenological characterization of 93 Elite-I and 32 Elite-II synthetic hexaploid lines and 48 D-genome-derived advanced derivatives. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prostrate (+), erect (–), or medium (M); FLOW = days–to–flowering; PUB = pubescence, absence (–) or prescence (+); HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm).

No.	Parentage/Pedigree	GH	FLOW	PUB	HT	AWN	PMA	TKW	G/S	SL
37	Not Available	–	108	–	94	AW	154	36.0	64	11.6
38	Not Available	–	109	–	94	AW	154	24.4	42	13.0
39	Not Available	–	110	–	95	AW	152	18.2	49	13.0
40	Not Available	–	112	–	94	AW	156	41.8	67	13.0
41	Not Available	–	109	+	90	Y	156	36.6	62	12.0
42	Not Available	–	110	–	93	AW	156	26.4	51	12.6
43	Not Available	–	112	–	89	Y	155	36.4	50	11.6
44	Not Available	–	112	–	94	Y	154	40.8	80	13.0
45	Not Available	–	116	–	100	Y	154	36.4	77	12.0
46	Not Available	–	109	–	96	AW	154	40.2	60	13.6
47	Not Available	–	101	–	104	Y	153	52.2	51	12.0
48	Not Available	–	105	–	98	Y	150	47.2	56	11.0

posed of remaining 85 genotypes and was subdivided into three groups, 1B, 2B, and 3B. Group 1B consisted of seven genotypes (45, 28, 93, 74, 73, 72, and 43). The most diverse genotype with the highest genetic distance or least similarity in this group was 45, with a genetic distance of 0.479 (47.9%) with genotype 28. The least diverse group included 73 and 74 with a genetic distance of 0.102 (10.2%). Group 2B consisted of 56 genotypes (89, 92, 90, 88, 87, 91, 84, 82, 81, 79, 78, 77, 30, 85, 83, 56, 53, 38, 37, 36, 35, 20, 71, 64, 60, 59, 68, 70, 65, 67, 66, 62, 61, 32, 86, 19, 16, 63, 69, 58, 57, 55, 49, 54, 52, 51, 39, 6, 50, 47, 46, 42, 41, 40, 48, and 21). Among this group, the most diverse genotype was 30, having a genetic distance of 0.334 (33.4%) with a group of 35 genotypes. Genotype 20 also was diverse with respect to the others, having a genetic distance of 0.319 (31.9%) with four other genotypes. Genotype 16 had a genetic distance of 0.247 (24.7%) with genotypes 19 and 86. Group 3B consisted of the remaining 23 genotypes (3, 33, 29, 27, 25, 26, 24, 23, 22, 34, 14, 5, 12, 15, 9, 13, 11, 10, 7, 4, 2, and 1). Among this group, the most diverse genotype was 3, with a genetic distance of 0.289 (28.9%) with a group of 21 genotypes. The least diverse genotypes, 10 and 11, also fall in this group, which have a genetic distance of 0.049 (4.9%). By analyzing dendrogram generated on SSR data, the most genetically diverse Elite-1 SH wheat genotypes were 80 and 75.

Molecular diagnostics of Pm resistant genes using SSR markers. A number of genes are responsible for powdery mildew resistance in wheat. In this study, four SSR markers were used to detect the presence of *Pm* genes *Pm4b*, *Pm9*, *Pm16*, and *Pm30* in the Elite-II accessions and the D-genome-derived advanced derivatives. The gene *Pm9* is linked to *Xgwm-4* with a fragment size of 253 bp in the D-genome-derived advanced derivatives (Fig. 6, Tables 11 and 12, p. 150). These results demonstrate that novel sources of powdery mildew resistance are available in the Elite-I and Elite-II sets and D-genome-derived advanced derivatives. Lines resistant at the seedling stage also gave a good level of field or APR in 57% of the Elite-I, 62% of the Elite-II, and 75% of the derivatives. All these lines had excellent resistance to powdery mildew at both stages. Most genes that confer mildew resistance at seedling stage also confer a good level of APR.

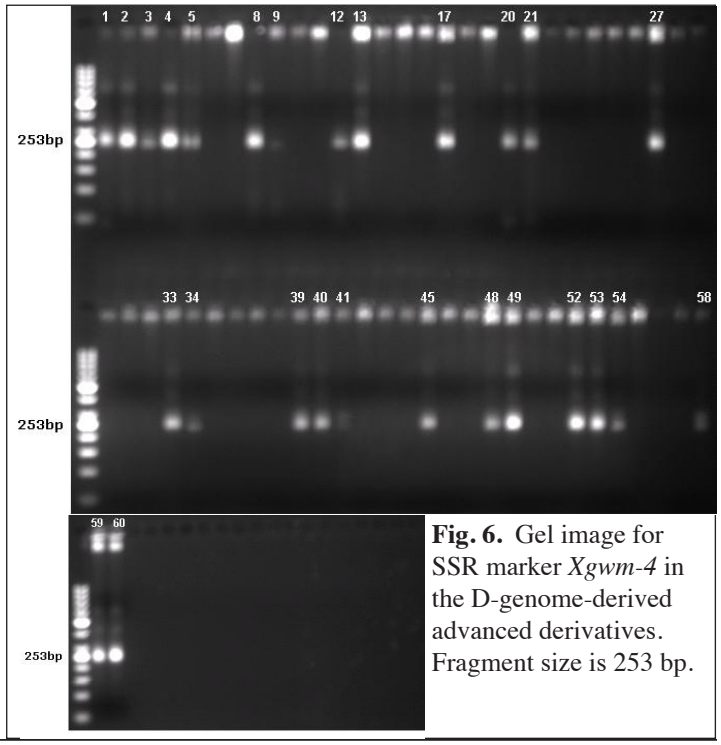

Fig. 6. Gel image for SSR marker *Xgwm-4* in the D-genome-derived advanced derivatives. Fragment size is 253 bp.

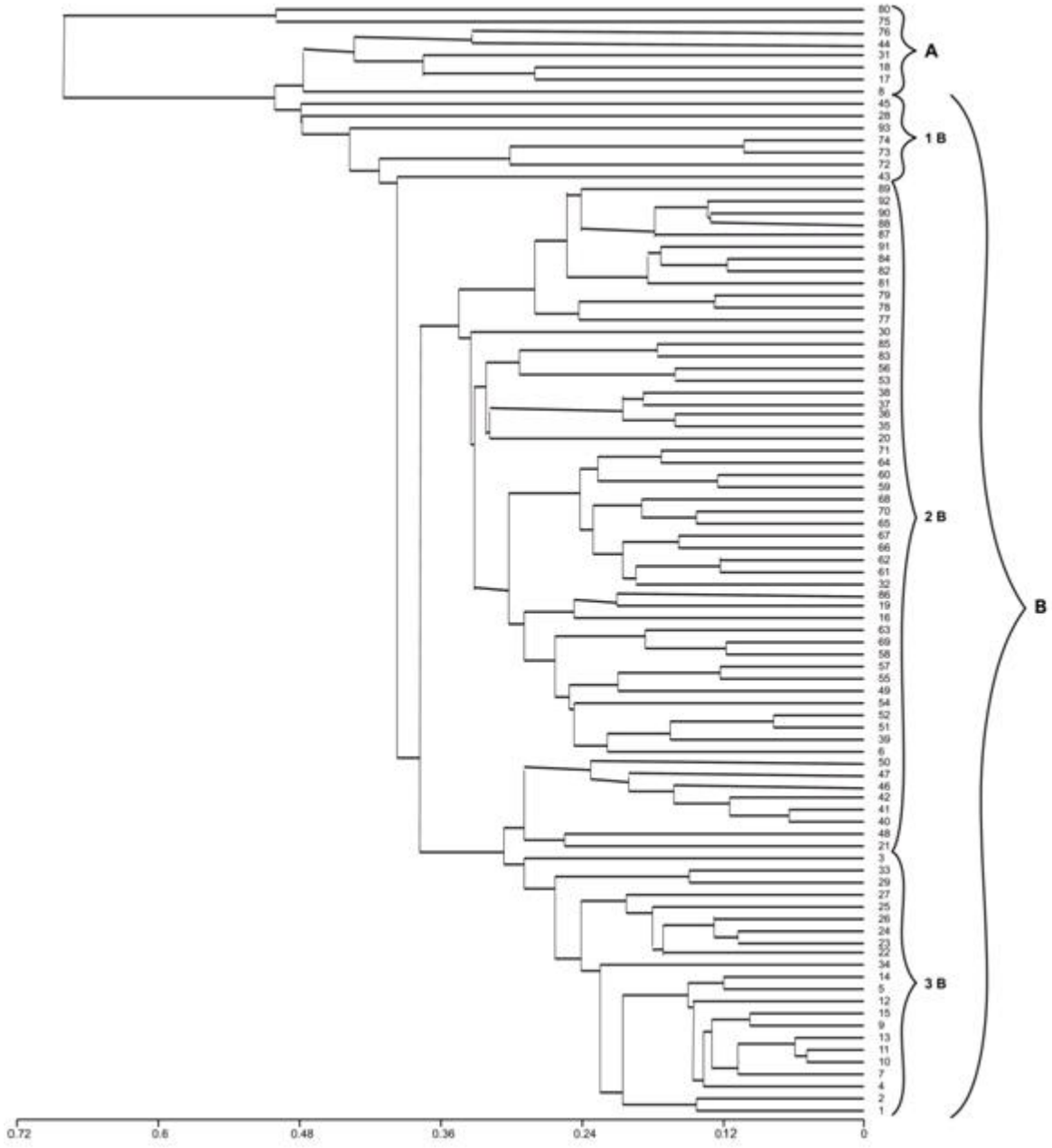

Fig. 5. Grouping of the resistant Elite-I synthetic hexaploids (2n=6x=42; AABBDD) on the basis of genetic distance.

Thus, identifying APR in these lines provides new sources of resistance that could be durable. Synthetics with both seedling and APR are preferred for utilization in wheat breeding programs. These lines can be used in direct crossing with elite commercial cultivars of wheat for further exploitation as source of resistance against powdery mildew.

The morphological trait data showed that the resistant synthetic lines possessed good phenotypic characters that will be an important source of genes for plant breeding. For 1,000-kermel weight and other phenotypic characters, Elite-I SH genotypes 2, 5, 8, 9, 12, 14, 18, 19, 20, 21, 22, 23, 26, 29, 30, 31, 32, 33, 34, 35, 37, 38, 42, 43, 44, 45, 52, 59, 60, 61, 62, 76, 78, 80, 81, 83, 84, 85, 86, 87, 89, and 92; Elite-II SH genotypes 3, 7, 9, 10, 12, 13, 16, 26, 30, 31, and 32; and D-genome-derived advanced derivatives 8, 20, 29, 47, and 48 were found to be morphologically good and desirable. The SH wheats have a considerable variability for these morphological characteristics that can be utilized in wheat improvement programs. Similar results were found by Villareal et al. (1994) among the synthetic hexaploid wheats derived from the cross '*T. turgidum*/*Ae. tauschii*', and they proposed that these synthetic lines possess substantial variation among their morphological traits can be utilized in hexaploid wheat for broadening of genetic base.

Table 11. Powdery mildew genes detected in the 32 resistant Elite-II synthetic hexaploid lines. **+** indicates presence and – absence of the *Pm* gene.

Sample No.	*Pm* Gene			
	Pm4b	*Pm9*	*Pm16*	*Pm30*
1	–	–	–	–
2	–	–	–	–
3	–	–	–	–
4	–	–	–	–
5	–	–	–	–
6	–	–	–	–
7	–	–	–	–
8	–	–	–	–
9	–	–	–	–
10	–	–	–	–
11	–	–	–	–
12	–	–	–	–
13	–	–	–	–
14	+	+	+	+
15	–	–	–	–
16	–	–	–	–
17	–	–	–	–
18	–	–	–	–
19	–	–	–	–
20	–	–	–	–
21	–	–	–	–
22	–	–	–	–
23	–	–	–	–
24	–	–	–	–
25	–	–	–	–
26	–	–	–	–
27	–	–	–	–
28	–	–	–	–
29	–	–	–	–
30	–	–	–	–
31	–	–	–	–
32	–	–	–	–

Evaluating genetic diversity and cluster analysis of the Elite-I SH revealed a diverse relationship between accessions. The molecular diversity generated in the present study would be useful in future breeding programs that can employ the recommended synthetic lines with powdery mildew resistance incorporation and a broad genetic base. The novel diversity residing in SH lines is anticipated to add the durability and give sustainable outputs (Mujeeb-Kazi and Rajaram 2002). These results indicated that SSR analysis could be successfully used to estimate genetic diversity among wheat cultivars. Thus, it could serve as an efficient tool for the selection of genetically diverse genotypes. The polymorphism revealed by SSR primers between the genotypes clearly

Table 12. Powdery mildew genes detected in the 48 resistant D-genome-derived advanced derivative. **+** indicates presence and – absence of the *Pm* gene.

Sample No.	*Pm* Gene			
	Pm4b	*Pm9*	*Pm16*	*Pm30*
1	–	+	–	–
2	–	+	–	–
3	–	+	–	–
4	–	+	–	–
5	–	–	–	–
6	–	–	–	–
7	–	+	–	–
8	–	+	–	–
9	–	–	–	–
10	–	–	–	–
11	+	+	–	–
12	–	+	–	–
13	–	–	–	–
14	–	–	–	–
15	–	–	–	–
16	–	+	–	–
17	–	–	–	–
18	–	+	–	–
19	–	+	+	+
20	–	–	–	–
21	–	–	–	–
22	–	–	–	–
23	–	–	–	–
24	–	–	–	–
25	–	+	–	–
26	–	–	–	–
27	–	–	–	–
28	–	–	–	–
29	–	–	–	–
30	–	–	–	–
31	–	+	–	–
32	–	+	–	–
33	–	–	–	–
34	–	–	–	–
35	–	–	–	–
36	–	–	–	–
37	–	+	–	–
38	–	+	–	–
39	–	+	–	–
40	–	–	–	–
41	–	–	–	–
42	–	–	–	–
43	–	+	+	+
44	–	–	–	–
45	–	+	–	–
46	–	+	–	–
47	+	+	–	–
48	–	+	–	–

demonstrated that SSRs are a valuable diagnostic tool showing considerable genetic diversity. According to Röder et al. (1998), microsatellites or SSRs represent an important tool for genetic diversity studies, population structure, genetic mapping, and crop breeding because of their abundance, co-dominance nature, polymorphism level, reliability, and ease of assay. Information on genetic similarity helped avoid any chance of elite germ plasm becoming genetically uniform and endangering long-term productivity gains (Messmer et al. 1992). The data on genetic diversity among closely related lines, along with the morphological evaluation for various parameters, proved very effective in the selection of powdery mildew resistant lines that are genetically distant and morphologically excellent. Among the Elite-1 SHs, genotypes 80 and 75 were found most genetically variable and also exhibit best resistance against powdery mildew and good phenotypic characters and are recommended for future breeding efforts.

Molecular markers are powerful tools to identify gene of interest and have been used to genetically and physically locate *Pm* genes in the wheat genome. Using the Elite II and D-genome-derived advanced derivatives, four powdery mildew resistance genes (*Pm4b*, *Pm9*, *Pm16*, and *Pm30*) were found to be present and linked to four SSR markers and were used to identify powdery mildew resistant lines carrying these *Pm* genes. In our study, the SSR marker *Xgwm-382* amplified the PCR fragment in one Elite II and five D-genome-derived advanced derivatives with a size of 125 bp for *Pm4b*. Yi et al. (2008) confirmed that a 125-bp allele indicates the presence of *Pm4b* gene located on the chromosome 2AL . Two SSR markers were employed to detect the presence of *Pm9* resistance gene located on the long arm of chromosome 7AL. Polymorphism between the Elite II and the advanced derivatives were observed at the *Xgwm-4* and *Xgwm-332* SSR loci. A 253-bp fragment was observed at the *Xgwm-4* locus in only one Elite-II genotype but in 27 of the D-genome-derived advanced derivatives. A 212-bp fragment was observed at the *Xgwm-332* locus in one Elite-II genotype of and in 13 of the D-genome-derived advanced derivatives. Srnic et al. (2005) reported that *Pm9* was linked with the SSR locus *Xgwm-4* at 253 bp and *Xgwm-332* at 212 bp on chromosome 4AL and 7AL, respectively. Powdery mildew resistance genes *Pm16* and *Pm30* share common origin and chromosome location, short arm of chromosome 5B linked to SSR locus *Xgwm-159* at 201 bp (Chen et al. 2005). The result indicates that both genes were present in one Elite-II and two advanced derivative genotypes at 201 bp. We assume that the presence of these *Pm* genes in these respective genotypes that were resistant at both seedling and adult-plant stages indicates that all these genes are major genes.

Powdery mildew resistance conferred by the synthetic germ plasm lines utilized in this study with desirable morphological traits and molecular diversity should have utility in cultivar-development programs. The powdery mildew resistant genes with tightly linked and flanking markers identified and reported in this manuscript should aid in the incorporation of these powdery mildew resistance genes into future cultivars.

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Genetic diversity for some yield and quality traits in selected lines of the 4th Early Bread Wheat Yield Trial (4EBWYT).

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A randomized complete block design with three replications was used to characterize 20 4EBWYT genotypes for yield and quality characteristics. Plot size was 5 x 1.2 m^2. The end-use quality and utilization of wheat is highly dependent on the traits such as kernel texture, protein content, ash content, wet gluten content, and α-amylase activity. A significant genotypic effect was shown for all the characters studied except days-to-heading, plant height, and test weight.

Plant height ranged from 99.27 to 110.27 cm with an average of 105.70 cm. Days-to-heading ranged from 116.67 to 128 days with an average of 121.78. Most of the genotypes were not significantly different from the mean. Grain yield ranged from 1,034 to 3,025 g/plot. The genotypic effect was significant at $F_{0.05}$. Ten genotypes were significantly different from the mean, and the rest were non-significantly different (Table 13, p. 153).

Moisture content ranged from 8.57–9.9% with an average of 9.34%. The co-efficient of variation for moisture content was 3.36%, indicating lower variability among genotypes for this trait compared to other traits. Moisture content is greatly influenced by variation in the processing of the grain, the method of grinding, and variation in the climatic conditions and temperature during harvest (FAO 1999).

The maximum protein content was in 4EBWYT-520 (12.57%) and the minimum in 4EBWYT-527 (10.63%). All genotypes were significantly different at $CD_{0.05}$ except 4EBWYT-503. Mean protein content was 11.72% with a CV of 5.87%, indicating better variability among genotypes for this character. The protein content in Pakistani wheat cultivars ranged from 10.32–15.42% (Ahmad et al. 2001). Finney and Bolte (1985) recorded protein in the range of 9.0–14.6% in different wheat cultivars. The strong negative association between protein content and grain yield makes it difficult to breed for both traits. However, finding lines with high yield and high protein is of prime importance, and the nurseries consisting of higher-yielding genotypes can be used to identify lines to screen for higher protein content.

Ash content of these genotypes ranged from 2.77% (4EBWYT-506) to 1.50% (4EBWYT-512, 513, 514) with an average of 1.81%. All the genotypes were significantly different from the mean at $CD_{0.05}$. Ash content is the inorganic material left after flour is burned and is an important determinant of extraction rate and influences flour color and quality. None of these genotypes meet the criteria for good ash content, which ideally should be 0.39–0.42% (Li and Posner 1987). Zahoor (2003) reported that the ash content ranged from 0.30–0.53% in Pakistani wheat cultivars. The higher ash content found in these genotypes indicates the presence of a higher proportion of bran than for endosperm flour.

Maximum wet gluten was observed in 4EBWYT-507 (29.46%) and the minimum in 4EBWYT-525. The average wet gluten was 24.66%. Both replications and genotypes were significantly different (P = 0.05). Wet gluten has a strong effect on dough rheology and baking performance. Wet forms are more quickly incorporated into low protein flour than dry form (Czuchajowska and Paszczynska 1996) and also affects dough strength, gas retention and controlled expansion, structural enhancement, water absorption and retention, and natural flavor (Grausgruber et al. 2000; William 1997).

Thousand-kernel weight ranged from 29.80 (4EBWYT-504) to 47.17 g (4EBWYT-506) with an average of 39.79 g. The coefficient of variation (12.74%) was sufficient for this trait among genotypes. All genotypes were significantly different from the mean at $CD_{0.05}$. Both the replication and genotypic effects were significant at 0.05. This trait is a function of grain size and density. Wheat kernels can be classified according to grain weight; 15–25 g (very small), 26–35 g (small), 36–45 g (medium), 46–55 g (large), and over 55 g (very large) (Williams et al. 1986). According to this scale, most of the genotypes are of medium grain. Zanetti et al. (2001) reported 1,000-kernel weight in the range of 42.4–48.7 g in 128 wheat cultivars, whereas Anjum et al. (2002) reported a range of 31.43–37.28 g in Pakistani wheat cultivars.

The test weight (kg/hl) of these genotypes ranged from 49.92–77.43 kg/hl with an average of 72.60 kg/hl. Both replications and genotypes were not significantly different, however, genotype 4EBWYT-503 was significantly different from the mean at $CD_{0.05}$. Test weight is an important criterion in all wheat grading systems because it is a rough index of flour yield. Milling yield decreases rapidly with decreasing test weight. Previous studies indicated that this trait is

Table 13. Means and ANOVA for quality traits of 20 4th Early Bread Wheat Yield Trial genotypes. Numbers with an * are significant at CD $_{0.05}$; ** at 0.01 probability level, and NS indicates not significant.

Name	Pedigree	Days-to-heading	Plant height (cm)	Grain yield (g/plot)	Moisture (%)	Protein (%)	Ash content (%)	Wet gluten (%)	1,000-kernel weight (gm)	Test weight (kg/hl)	Falling number (Sec)	Hardness score
4EBWYT-502	WAXWING*2/KIRITATI	121.67	106.73	1,749.97*	9.20	12.17*	2.12*	25.52*	35.40*	73.33	334.33*	51.33*
4EBWYT-503	KIRITATI/4/2*SERI.1B*2/3/ KAUZ*2/BOW//KAUZ	120.33	110.27*	3,025.84*	9.60*	11.77	1.70*	24.22*	39.67*	49.92*	452.00*	52.33
4EBWYT-504	SERI/RAYON*2//PFAU/WEAVER	118.00	108.80	1,268.86*	9.10*	12.33*	2.13*	26.29*	29.80*	70.42	419.67*	54.33*
4EBWYT-505	SAAR/2*WAXWING	121.33	102.27	1,924.83	9.13*	11.93*	2.19*	25.57*	31.90*	72.62	326.67*	49.33*
4EBWYT-506	SERI.1B*2/3/KAUZ*2/BOW// KAUZ*2/5/CNO79//…	116.67*	113.67*	2,186.68	9.90*	11.33*	2.77*	23.24*	47.17*	76.18	303.33*	52.67
4EBWYT-507	PBW343*2/KUKUNA/3/PASTOR// CHIL/PRL/4/…	121.00	102.33	2,747.28*	9.40	12.33*	2.29*	29.46*	44.82*	74.03	430.00*	52.33
4EBWYT-508	WHEAR//INQLAB91*2/TUKURU	119.33	105.47	3,373.96*	9.20	12.37*	2.51*	27.45*	43.03*	77.18	478.67*	55.67*
4EBWYT-509	PBW343*2/KUKUNA//PBW343*2/ KUKUNA	123.00	98.60*	2,651.82*	9.40	11.53*	1.61*	25.29*	43.00*	69.68	483.00*	52.33
4EBWYT-512	CNDO/R134//ENTE/MEXI_2/3/…..	121.67	106.33	2,360.51	9.60*	11.30*	1.50*	23.07*	41.03*	74.60	417.00*	54.33*
4EBWYT-513	MINO/898.97	123.33	107.00	1,888.64	9.47	11.30*	1.50*	24.12*	44.60*	74.75	399.67	54.00*
4EBWYT-514	KIRITATI//SERI/RAYON	124.67	99.27*	1,589.59*	9.27	11.67	1.50*	23.20*	42.80*	77.43	399.00	50.33*
4EBWYT-515	WBLL1*2/BRAMBLING	128.00*	107.67	2,496.25	9.30	10.77*	1.48*	24.54	45.27*	74.42	395.00	51.67
4EBWYT-517	WBLL1*2/KIRITATI	121.33	108.87	2,091.83	8.87*	11.63*	1.62*	23.49*	36.00*	70.53	398.00	52.00
4EBWYT-518	WBLL1*2/KIRITATI	122.00	109.40	2,374.90	9.27	10.87*	1.60*	22.37*	42.40*	73.62	393.33	51.67
4EBWYT-519	PRL/2*PASTOR//PBW343*2/ KUKUNA	121.00	101.47*	2,563.86	9.20	12.37*	1.58*	26.22*	47.00*	73.92	356.00*	55.33*
4EBWYT-520	PBW343/HUITES/4/YAR/ AE.SQUAROSSA(783)//	121.00	107.13	2,048.26	9.87*	12.57*	1.54*	24.58	40.59*	74.63	376.00*	51.33*
4EBWYT-524	PFAU/SERI.1B//AMAD*2/3/ PBW343*2/KUKUNA	123.67	103.20	1,034.39*	9.87*	12.53*	1.67*	28.18*	31.60*	69.47	366.67*	52.00
4EBWYT-525	PFAU/SERI.1B//AMAD*2/3/ PBW343*2/KUKUNA	121.00	107.33	2,341.16	9.27	11.20*	1.70*	28.96*	37.23*	73.13	448.67*	53.33
4EBWYT-527	WAXWING*2//PBW343*2/KUKU-NA	124.33	105.20	1,299.60*	8.57*	10.63*	1.49*	20.57*	34.20*	74.13	425.33*	54.67*
4EBWYT-530	WHEAR//2*PRL/2*PASTOR	122.33	103.07	2,966.33*	9.13*	12.03*	1.71*	23.60*	42.37*	72.10	384.00	51.00*
	Mean	121.78	105.70	2,199.23	9.33	11.73	1.81	25.00	39.99	72.22	399.32	52.60
	SED	2.84	2.73	303.6	0.11	0.08	0.03	0.18	0.05	7.96	11.00	0.68
	CV (%)	2.85	3.16	16.88	1.45	0.81	2.20	0.87	0.16	13.50	3.37	1.57
	ANOVA											
	Replication	NS	NS	NS	**	**	**	**	**	NS	NS	NS
	Genotype	NS	NS	**	**	**	**	**	**	NS	**	**
	C.D $_{0.05}$	5.70	5.48	609.16	0.26	0.16	0.07	0.36	0.11	16.00	22.11	1.37

controlled not only genetically, but environmental conditions also affect this trait (Halverson and Zeleny 1988). Pushman and Bingham (1975) reported that test weight provides a useful guide to flour yield but is likely to be misleading for comparison between cultivars.

Falling number of the genotypes ranged from 303.33–483 sec with an average of 397.71. Replications were not significant, whereas genotypes were significant at $P_{0.05}$. Fourteen genotypes were found significant at $CD_{0.05}$. Falling number is an important determinant of α-amylase activity and an indicator of sprout damage and set up ability of the flour. Mailhott and Patton (1988) reported that all types of bread flour should have falling number values in between 200–300. Wheat flour with a falling number higher than 400 has very low or no α-amylase activity. In this study, nine genotypes have a falling number greater than 400; 4EBWYT-506 has the lowest value for this trait at 303.3 sec.

Grain texture is the most important trait which determines hardness or softness of wheat. Hardness scores ranged from 49.33–55.67 with an average of 52.54. Replications were not significant, whereas genotypes were statistically significant. Eleven genotypes were significantly different from mean, and the others were not significant at $CD_{0.05}$. Grain hardness is the key determinant for the classification and end -product quality in wheat (Campbell et al. 1999). Grain hardness primarily influences rheological properties of dough (Martinant et al. 1998). The most important physical difference between the endosperm of hard and soft wheat lies in the adhesion between the starch granules and the surrounding protein matrix (Simmonds et al. 1973). All these wheat genotypes fall into the category of soft wheat according to NIR hardness scale of Williams et al. (1986). Some authors also report that kernel size exerts an effect on grain hardness, however, differ in their opinion about the extent of the effect. Williams et al. (1987) emphasized that kernel size exert a small effect, whereas Pomeranz et al. (1988) reported direct effect of kernel size on grain hardness.

These genotypes were found promising for better yield in Pakistan. Most had good characteristics for useful quality traits and offered good variability. A detailed analysis of quality traits is required in order to exploit these genotypes further via use in recombination breeding programs.

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Physio-chemical characterization in relation to bread-making quality of some candidate wheat genotypes.

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Eight candidate genotypes and the cultivar C-591 were characterized for different physio-chemical characteristics, test weight, wet gluten, dry gluten, falling number, protein content, 1,000-kernel weight, and grain hardness score, at the Grain Quality Testing Laboratory, Karachi. The allelic variations at the *Glu-1* and *Glu-3* loci were determined by SDS–PAGE at the Wheat Wide Crosses and Cytogenetics, Laboratory, NARC, Islamabad. C-591 is cultivar of the pre-Green Revolution Era and is considered excellent for bread-making quality in Pakistan.

High-molecular-weight glutenins subunits (HMW–GS) resolved by SDS–PAGE determined that at locus *Glu-A1*, all the genotypes possessed either allele *Glu-A1a* or *Glu-A1b* encoding subunits 1Dx1 and 1Dx2*, respectively (Table 14). The null allele at this locus was absent. The two subunits found at this locus impart better quality characteristics in terms of bread-making qual (Liang et al. 2010). At the Glu-B1 locus, Kazi-1, and Kazi-2 had allele Glu-B1i encoding subunits 1Bx17+1By18. All other candidate lines had the Glu-B1b allele encoding subunit 1Bx7+1By18. These two subunits at the Glu-B1 locus impart better quality characteristics than do other other subunits at this locus (Payne et al. 1980). At the Glu-D1 locus, all the candidate lines possessed the alleles for Glu-D1d encoding subunits 1Dx5+1Dy10. Gupta and MacRitchie (1994) ity established that 1Dx5+1Dy10 had a stronger effect on dough strength by producing a greater proportion of larger-size glutenin polymers.

Low-molecular-weight glutenin subunits (LMW–GS) were determined by SDS–PAGE and revealed that at the *Glu-A3* locus, the two candidate lines Kazi-1 and Kazi-2 possessed *Glu-A3b*; three lines Kazi-6, Kazi-7, and Kazi-8 had *Glu-A3d*; and the remaining three lines had *Glu-A3e*. Genotypes with *Glu-A3b* are known to possess better quality parameters, such as sedimentation volume, mixing time, and dough development time (Luo et al. 2001; Liang et al. 2010). At the *Glu-B3* locus, Kazi-3 possessed *Glu-B3b*, Kazi-1 and Kazi-4 had *Glu-B3g*, and the remaining lines possessed *Glu-B3d*. *Glu-B3j*, associated with the T1BL·1RS translocation, was absent in these genotypes predicting the absence of a rye chromosome arm in these candidate lines. Previous studies indicated that *Glu-B3b* and *Glu-B3g* are the desirable alleles and gave high quality values (Luo et al. 2001).

Characteristics such as test weight, moisture content, and protein contents were more consistent than other characteristics (Table 14, p. 156). Test weight is measure of the bulk density of grains, expresses soundness and maturity of the grains (Donelson et al. 2002), and is positively correlated with milling yield (Halverson and Zeleny 1988). The test weight ranged from 72.6 to 74.9 kg/hl and is within the desired range reported by Paliwal and Singh (1985). The cultivar C-591 showed the maximum test weight and was significantly different from all the other genotypes (Table 14, p. 156).

Thousand-kernel weight is an important character determining grain yield and grain quality and also reflects soundness of the grains. This trait ranged from 34.4–42.8 g. C-591 had a very low 1,000-kernel weight (36.4g). Improvement in 1,000-kernel weight not only improves yield but also improves milling yield. The grain weight of these candidate lines is higher than average, which is desirable.

The moisture content of these candidate lines ranged from 10.5–11.0% and for C-591 was 9.9%. All candidate lines did not differ significantly from each other or from C-591 (Table 14, p. 156). Many genetic and nongenetic factors

are known to influence moisture content but is mainly influenced by the environmental factors and storage conditions due to hygroscopic nature of the grain (Whiteley 1970). These findings agree with the range of reported by the Anjum and Walker (2000) and Ijaz et al. (2001), indicating that these genotypes can be stored easily due to low moisture content and will be less prone to microbial attack (Zeleny 1991).

Wet gluten ranged from 18.4 to 22.8% with the maximum exhibited by Kazi-1 (Table 14). C-591 had 27.1% more wet gluten than all the candidate lines and was significantly different from all the other genotypes. Gluten content has a significant impact on bread-baking potential of wheat flour (Kent and Evers 1994). Wheat cultivars with higher wet gluten content are suitable for breadmaking, and those with low gluten content can be exploited for other bakery products. Crop year and other environmental factors also influence wet gluten content (Anjum and Walker 2000; Ijaz et al. 2001). The wet gluten content of these lines fell into the desirable category.

Falling number is an indirect method to determine α-amylase activity. The enzyme α-amylase degrades starch to a mixture of glucose and maltose. Screening for α-amylase activity has a high priority in most wheat breeding programs, because the great majority of wheat products are adversely affected by this enzyme (Blackman and Payne 1990). The falling number of our candidate lines ranged from 316–422 sec. The cultivar C-591 had a value of 344 sec. This character varied significantly compared to all other characters (Table 14). A falling number value range from 200–400 sec is considered ideal for bread-making quality (Mailhot and Patton 1988) and values ranging from 350–400 possess a very low α-amylase activity. From these results, these candidate lines have desirable a-amylase activity values.

The protein content of these lines ranged from 9.9–11.0% and did not vary significantly (Table 14). C-591 had a protein content of 12.5%. Protein content is considered to be an important quality criterion governing end-use quality. Protein content not only is an inherited character but also depends on environmental factors (Bushuk et al. 1969). Kent (1983) reported that a protein content between 6–21% among different wheat genotypes is mainly influenced by edaphic factors such as soil, climatic conditions, and fertilizer use.

The grain hardness of the candidate lines ranged from 45–48, and C-591 had a hardness score of 45. Genotypes with grain hardness ranging from 40–50 have ideal bread-making quality. Hard wheat flour is suitable for bread and pasta products use very hard flour. Grain hardness also is negatively correlated with cookie diameter, because damaged starch increases water absorption capacity and viscosity, which hinders cookie spread (Monsalve-Gonzalez and Pomeranz 1993) . These candidate lines had the desirable allelic variation at the *Glu-1* and *Glu-3* loci, and their other physio-chemical characteristics make them acceptable for bread and chapatti making.

Table 14. Physio-chemcial characteristics of candidate wheat lines and C-591 (P = 0.05).

Line	*Glu-1* subunits	*Glu-3* (*Glu-A3*, *Glu-B3* alleles)	Test weight (kg/hl)	1,000-kernel weight (gm)	Moisture content (%)	Wet gluten (%)	Dry gluten (%)	Water binding in wet gluten (%)	Falling number (sec)	Protein (%)	Hardness score
KAZI-1	2*, 17+18, 5+10	b, g	73.9 abc	41.4 ab	10.5 a	22.8 b	10.2 abc	12.6 ab	377 e	10.6 ab	45 bc
KAZI-2	2*, 17+18, 5+10	b, d	73.9 bc	43.0 a	10.7 a	20.2 bcd	8.5 bc	11.7 b	372 f	10.7 ab	45 bc
KAZI-3	1, 7+8, 5+10	e, b	73.8 bc	42.2 a	11.0 a	19.6 cd	8.2 c	11.4 b	362 g	11 ab	45 c
KAZI-4	1, 7+8, 5+10	e, g	72.6 c	39.6 b	10.8 a	21.1 bc	9.5 bc	11.6 b	422 a	10.5 b	47 ab
KAZI-5	2*, 7+8, 5+10	e, d	74.7 ab	43.0 a	10.8 a	21.8 b	12.1 ab	9.7 b	401 c	10.6 b	47 ab
KAZI-6	2*, 7+8, 5+10	d, d	74.9 ab	42.4 a	11.0 a	22.0 b	10.6 abc	11.4 b	419 b	9.9 b	46 bc
KAZI-7	2*, 7+8, 5+10	d, d	74.9 ab	42.8 a	10.6 a	18.4 d	9.7 bc	8.7 b	394 d	9.9 b	45 c
KAZI-8	2*, 7+8, 5+10	d, d	72.6 bc	34.4 d	10.7 a	22.6 b	12.6 a	10.0 b	316 i	10.9 ab	48 a
C-591	1, 13+16, 5+10	b, b	76.6 a	36.4 c	9.9 a	27.1 a	10.8 abc	16.3 a	344 h	12.5 a	45 c

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Allelic variation and composition of HMW–GS in bread wheat/synthetic derivatives.

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Improving the bread-making quality of wheat by utilizing allelic variation and composition of the high-molecular-weight glutenin subunit *Glu-1* (HMW–GS) loci in novel genetic resources is actively going on in the Wheat Wide Crosses Laboratories in Islamabad, Pakistan. The HMW–GS composition of 202 F_7 advanced lines obtained by crosses between 135 different types of bread wheat with synthetic hexaploid wheats was studied using SDS–PAGE. A total of 23 allelic variants and 61 HMW–GS combinations were observed at the *Glu-A1*, *Glu-B1*, and *Glu-D1* loci. In breadwheat, the *Glu-D1* locus usually is characterized by subunits 1Dx2+1Dy12 and 1Dx5+1Dy10 with the latter having a stronger effect on bread-making quality and is observed predominantly in these advanced lines. The inferior subunit 1Dx2+1Dy12 was successfully replaced by other, better allelic variants at the *Glu-D1* locus inherited by these SH wheats from *Ae. tauschii*.

The HMW–GS were analyzed through horizontal SDS–PAGE following the Laemmli (1970) using Pavon, Chinese Spring, and Pak-17951 wheat as standards for identifying and comparing generated bands. The allelic classification at the *Glu-A1* and *Glu-B1* loci and the numbering of HMW–GS were based on the classification of Payne and Lawrence (1983). Alleles at the *Glu-D^{t}1* locus were identified according to William et. al. (1993). The quality score was calculated according to Payne et. al (1980) by adding together the scores of individual subunits.

The genetic diversity at each locus was calculated using Nei's index (Nei 1973), $H=1-\Sigma Pi^2$, with H and Pi denoting the genetic variation index and the frequency of the number of alleles at the locus, respectively. Allelic frequencies were determined by summing the frequencies of alleles in the individual accessions, irrespective of whether the HMW–GS composition was homogeneous or heterogeneous, and then dividing this total by the number of accessions.

Distribution of HMW–GS. Twenty-three HMW-GS allelic variants were detected in the 202 F_7 advanced lines (Table 15). At the *Glu-A1* locus, the composition of alleles were only contributed by x-type subunits, 1Ax1, 1Ax2*, and null, which are controlled by alleles *Glu-A1a*, *Glu-A1b*, and *Glu-A1c*, respectively. The null allele the most frequent, in oOver

62% of the F_7 advanced lines, followed by 1Ax2* (24.26%) and 1Ax1 (12.87%) (Table 16). The predominance of the null allele at this locus was previously reported by several workers. A higher proportion of the null allele in SHs was reported by Pena et. al (1995) and in the world collection of wheat cultivars by Payne and Lawrence (1983) supports the predominant presence of the null allele in these F_7 advanced lines derived from the 'synthetic/bread wheat' crosses. Recently, Fang et. al (2009) and Li et. al (2009) also reported a higher frequency of null alleles in Chinese genotypes. However, the frequency in the European spelt wheat genotypes was reported as minimal (An et al. 2005). Apart from the null allele, 75 (37.13%) of the 202 advanced lines had either 1Ax1 or 1Ax2*, which impart better quality to wheat flour and are associated with higher extensibility plus better dough strength (Branlard and Dardevet 1985; Khan et al. 1989).

Table 15. Number of alleles and combinations of *Glu-1* loci in F_7 advanced lines from 'bread wheat/ synthetic hexaploid' crosses

Locus	Number of alleles	x-type	y-type
Glu-A1	3	3	—
Glu-B1	8	5	5
Glu-D1	12	5	4
Glu-1 combinations	61	—	—

At the *Glu-B1* locus, five x-type subunits, 7, 6, 20, 13, and 17; five y-type subunits, 8, 9, 16, 18, and 15; and their eight combinations were detected (Table 15). Subunit 1Bx7 was found in 18 (8.91%) advanced lines and its combination with 1By8, 1By9, and 1By8 were found in 49 (24.25%) advanced lines (Table 16). The most frequent subunit, 1Bx17+1By18, encoded by *Glu-B1i*, was found in 75 (37.13%) advanced lines followed by 1Bx13+1By16, encoded by *Glu-B1f* in 36 (18.81%) genotypes. The other subunits found at this locus are 1Bx7+1By8 (8.91%), 1Bx7+1By9 (17.82%), 1Bx6+1By8 (4.45%), 1Bx20 (6.43%), and 1Bx7+1By15 (0.99%) encoded by alleles *GluB1b, Glu-B1c, Glu-B1d, GLu-B1e*, and *Glu-B1z*, respectively. The genetic diversity calculated by Nei's index at this locus was the maximum at 0.78. The durum parents of synthetic hexaploids (Pena et al. 1994) and SHs (Pena et al. 1995; Hsam et al. 2001) were known to possess subunits 1Bx7+1By8, 1Bx20, and 1Bx6+1By8 at this locus. Rashid et al. (2003), Masood et al. (2004), and Tayyaba et al. (2007) reported a higher proportion of 1Bx17+1By18 and 1Bx7+1By9 in land races and locally adapted cultivars of Pakistan. Because the studied genotypes consisted of derivatives from SHs and locally adapted germ plasm, a higher proportion (71.28%) of these subunits was observed in these advanced lines. The comparatively higher level of allelic diversity (H) at this locus is attributed in part to the allelic richness and to the diverse parental lines from different genetic backgrounds. Earlier, An et al. (2005), Li et al. (2009), Fang et al. (2009), and Moragues et al. (2006) also reported higher H at the *Glu-B1* locus.

Table 16. Allelic frequency and diversity at the *Glu-1* locus in F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses.

Locus	Allele	Subunit	Number of accessions	Frequency (%)	H (Nei's index)
Glu-A1	a	1	26	12.87	0.53
	b	2*	49	24.26	
	c	null	127	62.87	
Glu-B1	a	7	18	8.91	0.78
	b	7+8	11	5.44	
	c	7+9	36	17.82	
	d	6+8	9	4.45	
	e	20	13	6.43	
	f	13+16	38	18.81	
	i	17+18	75	37.13	
	z	7+15	2	0.99	
Glu-D1	a	2+12	54	26.73	0.70
	b	3+12	4	1.98	
	d	5+10	95	47.02	
	e	2+10	6	2.97	
	h	5+12	3	1.48	
	n	2.1+10	2	0.99	
	x	2+T2	5	2.47	
	z	3+10	3	1.48	
	ae	2.1+T2	4	1.98	
	ah	1.5+10	13	6.43	
	ai	2.1+10.5	7	3.46	
	aj	1.5+12	6	2.97	

The *Glu-D1* locus in these advanced lines contributed 12 alleles having the combination of five x-type and four y-type subunits (Tables 15 and 16). The x-type subunits include 2, 3, 5, 1.5, and 2.1 and y-type subunits include 10, 12, 10.5, and T_2. The most frequent subunit 1Dx5+1Dy10, encoded by allele *Glu-D1d*, was observed in 95 (47.02%) advanced lines followed by 1Dx2+1Dy12, encoded by allele *Glu-D1a*, in 54 (26.73%) advanced lines. The frequency of the other alleles at this locus was less than 3%, except for 1Dx1.5+1Dy10, which had a frequency of 6.43%. The genetic diversity according to Nei's index (H) was 0.70. The cultivars characterized by subunit pair 5+10, a superior and favorable allele imparting greater viscoelasticity and dough characteristics

(Popineau et al. 1994; Redaelli et al. 1997) are considered to be the best. This subunit combinationwas correlated with good bread-making quality characteristics in commercial wheat cultivars grown in Canada (Bushuk 1998), Germany (Wieser and Zimmermann 2000), the U.K. (Payne et al. 1987), Norway (Ulhen 1990), Syria (Mir ali et al. 1999), the United States (Dong et al. 1991), and New Zealand (Luo et al. 2001), and also in SH wheats (Peña et al. 1995). The allelic richness at *Glu-D1* is higher than *Glu-B1* but genetic diversity is slightly lower because two subunit pairs, 2+12 and 5+10, have a greater proportion in these advanced lines. The *Glu-D1* alleles h, n, x, ae, ah, ai, and aj, encoding subunits 1Dx5+1Dy12, 1Dx2.1+1Dy10, 1Dx2+1DyT2, 1Dx2.1+1DyT2, 1Dx1.5+1Dy10, 1Dx2.1+1Dy10.5, and 1Dx1.5+1Dy12, respectively, were incorporated into SHs from *Ae. tauschii* during the course of wide hybridization. These subunit pairs also were observed in these advanced lines, and their association with bread-making quality parameters was previously determined by Pena et al. (1995).

Composition of HMW-GS and *Glu-1* quality score. The HMW–GS compositionsand *Glu-1* quality scores are given in Table 17 (p. 159-165). The HMW-GS allelic composition found most frequently is null, 17+18, 5+10 in 19 out of 202 advanced lines. The other allelic compositions are 1, 17+18, 5+10 (15); null, 7+9, 2+12 (11); null, 7, 5+10; null, 13+16, 5+10; and null, 17+18, 2+12 (9). Twenty-five combinations appeared once in these lines. The *Glu-1* quality score ranged from 4–10 with an average of 7.4. The quality score of these lines is higher than those in German (Rogers et al. 1989) U.K. (Lukow et al. 1989), Danish (Payne et al. 1987), Chinese (Zhong-Hu et al. 1992), and Spanish wheats (Payne et al. 1988) and very close to those of Canadian, Australian, U.S, and Russian cultivars (Graybosch et al. 1990; Khan et al. 1989; Lawrence 1986; Lukow et al. 1989; Morgunov et al. 1990; Ng et al. 1989). The quality score of 54 advanced lines could not be determined because of the presence of rare alleles from *Ae. tauschi*i. However, Pena et al. (1995) determined the different quality characteristics of SHs having these subunits. They reported that groups with subunit pairs 2.1+10 or 1.5+10 had higher flour protein than groups with 2.1+T2. Groups with subunit pairs 1.5+10, 2.1+T2, 5+12, and 3+10 had larger bread loaf volume than those with pair 2+12, and no differences among these subunit pairs were observed in relation to sedimentation volume.

Table 17. High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/ synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
1	GAN/AE.SQUARROSA (897)//OPATA x D67.2/P66.270//AE.SQUARROSA (223)*	N	7	2+12
2	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)/6/CETA/… x 68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (783)	N	7	2+12
3	Opata x DOY1/AE.SQUARROSA (458)	N	7	2+12
4	MAYOOR/TK SN1081/AE.SQUARROSA (222)/3/PASTOR x CROC_1/ AE.SQUARROSA (444)	N	7	5+10
5	Opata x CROC_1/ AE.SQUARROSA (886)	N	7	5+10
6	Opata x GAN/ AE.SQUARROSA (408)	N	7	5+10
7	Opata x DOY1/AE.SQUARROSA (458)	N	7	5+10
8	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (629)	N	7	5+10
9	Not Available	N	7	5+10
10	Not Available	N	7	5+10
11	Not Available	N	7	5+10
12	GAN/AE.SQUARROSA(236)//CETA/AE.SQUARROSA (895)/3/MAIZ/4/IN-QALAB 91 x BKH-94	N	7	5+10
13	M. OPATA-108 x CETA/AE.SQUARROSA (895)	N	7	1.5+10
14	Opata x CETA/AE.SQUARROSA) (895)	N	7+8	2+12
15	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x ARLIN_1/T. MONOCOCCUM (95)	N	7+8	2+12
16	Opata x ALTAR 84.AE.SQUARROSA (J BANGOR)	N	7+8	2+12
17	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	7+8	1.5+10
18	M.Opata 164 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	7+8	1.5+10

Table 17 (continued). High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
19	Opata x DOY 1/AE.SQUARROSA (517)	N	7+8	2.1+10.5
20	Opata x 68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (783)	N	7+8	1.5+12
21	Not Available	N	7+8	1.5+12
22	Opata x DOY1/AE.SQUARROSA (372)	N	7+9	2+12
23	ALTAR 84/AE.SQUARROSA (221)//YACO x 68.111/RGB-U//WARD/3/ FGO/4/RABI/5/AE.SQUARROSA (878)	N	7+9	2+12
24	Opata x CETA/AE.SQUARROSA (1031)	N	7+9	2+12
25	Opata x DOY1/AE.SQUARROSA (372)	N	7+9	2+12
26	Opata x CPI/GEDIZ/3/GOO//JO/CRA/4/AE.SQUARROSA (227)	N	7+9	2+12
27	CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA x 68.111/ RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (783)	N	7+9	2+12
28	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	7+9	2+12
29	CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA x 68.111/ RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (783)	N	7+9	2+12
30	MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/PASTOR x SARSABZ	N	7+9	2+12
31	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC/6/ FCT x Opata	N	7+9	2+12
32	Opata x 68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (1038)	N	7+9	2+12
33	Opata x 68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (1038)	N	7+9	5+10
34	ALTAR 84/AE.SQUARROSA (224)//2*YACO/3/MAYOOR/TK SN1081/ AE.SQUARROSA/) (222)/4/KUKUN x GAN/AE.SQUARROSA (248)	N	7+9	5+10
35	CNDO/R143//ENTE/MEXI_2/3/AE.SQUARROSA (TAUS)/4/ WEAVER/5/2*KAUZ x DOY1/AE.SQUARROSA (458)	N	7+9	5+10
36	Opata x ALTAR 84.AE.SQUARROSA (J BANGOR)	N	7+9	5+10
37	Opata x ALTAR 84/AE.SQUARROSA (205)	N	7+9	5+10
38	Opata x 74 INQALAB 91/TSAPKI	N	7+9	5+10
39	URES/PRL//BAV92 x YAV_2/TEZ//AE.SQUARROSA (249)	N	7+9	2+10
40	GAN/AE.SQUARROSA(236)//CETA/AE.SQUARROSA (895)/3/MAIZ/4/IN-QALAB 91 x BKH-94	N	7+9	5+12
41	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)/6/CETA/… x CETA/AE.SQUARROSA (895)	N	7+9	2+T2
42	Opata x CPI/GEDIZ/3/GOO//JO/CRA/4/AE.SQUARROSA (273)	N	7+9	2.1+T2
43	CROC-1/AE.SQUARROSA) (224)//KAUZ x CETA/AE.SQUARROSA (895)	N	7+9	2.1+10.5
44	Not Available	N	7+9	1.5+12
45	MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/PASTOR x GAN/ AE.SQUARROSA (259)	N	6+8	2+12
46	162 CHAPIO/ INQALAB 91 x 68.111/RGB-U//WARD/3/AE.SQUARROSA (452)	N	6+8	2+12
47	Opata x CETA/AE.SQUARROSA (1027)	N	6+8	2+T2
48	Opata x CETA/AE.SQUARROSA) (895)	N	6+8	2+10.5
49	Opata x DOY1/AE.SQUARROSA (1024)	N	6+8	2.1+10.5
50	MAYOOR//TK SN1081/AE.SQUARROSA)(222)/3/FCT x	N	20	2+12
51	Not Available	N	20	5+10
52	CHIR3/CBRD x GAN/AE.SQUARROSA (897)//OPATA	N	20	5+10
53	Opata x BORLOUG M95	N	20	5+10
54	SERI x 68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (392)	N	20	5+10

Table 17 (continued). High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
55	Opata x SCA/AE.SQUARROSA (518)	N	20	5+10
56	139 CHAPIO/INQALAB 91 x PICUS/3/KAUZ*2/BOW//KAUZ	N	13+16	2+12
57	182 SAAR/INQALAB 91 x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/ CBRD	N	13+16	2+12
58	CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA x 68.111/ RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (783)	N	13+16	2+12
59	Not Available	N	13+16	2+12
60	Not Available	N	13+16	2+12
61	Not Available	N	13+16	2+12
62	Not Available	N	13+16	2+12
63	ALTAR 84/AE.SQUARROSA (193) x PASTOR	N	13+16	2+12
64	MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/PASTOR x SARSABZ	N	13+16	3+12
65	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x KAMBARA	N	13+16	3+12
66	182 SAAR/INQALAB 91 x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/ CBRD	N	13+16	5+10
67	Not Available	N	13+16	5+10
68	BAV x (MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD	N	13+16	5+10
69	Opata x D67.2//P66.270//AE.SQUARROSA (257)/3/OPATA	N	13+16	5+10
70	CROC-1/AE.SQUARROSA) (205)//BORL95 x	N	13+16	5+10
71	KAMBARA x Opata	N	13+16	5+10
72	Not Available	N	13+16	5+10
73	ALTAR 84/AE.SQUARROSA (193) x PASTOR	N	13+16	5+10
74	GAN/AE.SQUARROSA (236)//CETA/AE.SQUARROSA (895)/3/MAIZ/4/IN-QALAB 91 x BKH-94	N	13+16	5+10
75	M.Opata 164 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	13+16	2.1+10
76	D67.2/P66.270//AE.SQUARROSA (223) x ARLIN_1/T.MONOCOCCUM (95)	N	13+16	1.5+10
77	149 CHAPIO/INQALAB 91 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/ AE.SQUARROSA (878)	N	13+16	1.5+10
78	M.Opata 164 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	13+16	1.5+10
79	M. OPATA-164 x /4/RABI/5/AE.SQUARROSA (878) 68.111/RGB U//WARD/3/ FGO	N	13+16	1.5+10
80	CHIR3/CBRD x Opata	N	13+16	1.5+10
81	M.Opata 164 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	13+16	1.5+12
82	SARSABZ x CHIR3/CBRD	N	13+16	1.5+12
83	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	17+18	2+12
84	MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/PASTOR x GAN/ AE.SQUARROSA (259)	N	17+18	2+12
85	BAKHTAWAR 94 x 68.111/RGB-U//WARD RESEL/3/STIL/4/ AE.SQUARROSA (431)	N	17+18	2+12
86	162 CHAPIO/ INQALAB 91 x 68.111/RGB-U//WARD/3/AE.SQUARROSA (452)	N	17+18	2+12
87	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (629)	N	17+18	2+12
88	MAYOOR//TK SN1081/AE.SQUARROSA)(222)/3/FCT x YAV_3/SCO//JO69/ CRA/3/YAV/79/4/AE.SQUARROSA (498)/5/OPATA	N	17+18	2+12
89	Not Available	N	17+18	2+12

Table 17 (continued). High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
90	Not Available	N	17+18	2+12
91	Opata x DVERD_2/AE.SQUARROSA (333)	N	17+18	2+12
92	Not Available	N	17+18	3+12
93	Opata x CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA	N	17+18	5+10
94	Opata x YAV_3/SCO//JO69/CRA/3/YAV/79/4/AE.SQUARROSA (498)/5/ OPATA	N	17+18	5+10
95	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x	N	17+18	5+10
96	Opata x CPI/GEDIZ/3/GOO//JO/CRA/4/AE.SQUARROSA (227)	N	17+18	5+10
97	Opata x CETA/AE.SQUARROSA (895)	N	17+18	5+10
98	Opata x 0 INQALAB 91/AC8528	N	17+18	5+10
99	Opata x ALTAR 84/AE.SQUARROSA (205)	N	17+18	5+10
100	Opata x 74 INQALAB 91/TSAPKI	N	17+18	5+10
101	Opata x DOY 1/AE.SQUARROSA (1026)	N	17+18	5+10
102	MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/PASTOR x MH-97	N	17+18	5+10
103	Not Available	N	17+18	5+10
104	Not Available	N	17+18	5+10
105	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	N	17+18	5+10
106	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	N	17+18	5+10
107	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	N	17+18	5+10
108	Opata x YAV_3/SCO//JO69/CRA/3/YAV/79/4/AE.SQUARROSA (498)/5/ OPATA	N	17+18	5+10
109	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	N	17+18	5+10
110	Not Available	N	17+18	5+10
111	INQILAB 91 (RABI) x	N	17+18	5+10
112	Not Available	N	17+18	2+10
113	Opata x CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA	N	17+18	2+10
114	Opata x D67.2/P66.270//T.BOEOTICUM (66)	N	17+18	5+12
115	MAYOOR//TK SN1081/AE.SQUARROSA (222)/4/SABUF/3/BCN//CETA/ AE.SQUARROSA (895) x GAN/AE.SQUARROSA (897)//OPATA	N	17+18	2.1+10
116	Opata x YAV_3/SCO//JO69/CRA/3/YAV/79/4/AE.SQUARROSA (498)/5/ OPATA	N	17+18	2+T2
117	M. OPATA-108 x DOY1/AE.SQUARROSA (372)	N	17+18	3+10
118	Opata x ALTAR 84.AE.SQUARROSA (J BANGOR)	N	17+18	3+10
119	KAUZ x MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD	N	17+18	1.5+10
120	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x CPI/GEDIZ/3/ GOO//JO/CRA/4/T.MONOCOCCUM (101)	N	17+18	1.5+10
121	DOYI/AE.SQUARROSA (1018) x CPI/GEDIZ/3/GOO//JO69/CRA/4/ AE.SQUARROSA (208)/5/OAPTA	N	17+18	1.5+10
122	Not Available	N	17+18	1.5+10
123	Not Available	N	17+18	1.5+10
124	M.Opata 164 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	17+18	2.1+10.5
125	D67.2/P66.270//AE.SQUARROSA (223) x ARLIN_1/T.MONOCOCCUM (95)	N	17+18	2.1+10.5
126	D67.2//P66.270//AE.SQUARROSA (257)/3/OPATA x STY-US/CELTA//PALS/3/ SRN_5/4/AE.SQUARROSA (418)	N	7+15	2+12
127	CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA x 68.111/ RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	N	7+15	2+12

Table 17 (continued). High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
128	BACANORA x 68.111/RGB-U//WARD	1	7	5+10
129	Not Available	1	7	5+10
130	Not Available	1	7	5+10
131	Inqilab x BORLOUG M95	1	7+9	5+10
132	144 ALTAR 84/ AE.SQUARROSA) (221)//YACO/3/ INQALAB 91 x D67.2/ P66.270//T.BOEOTICUM (66)	1	7+9	5+10
133	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC/6/ FCT x DOY1/AE.SQUARROSA (458)	1	7+9	3+10
134	Opata x BORLOUG M95	1	20	5+10
135	PBW-343*2/CHAPIO x D67.2/P66.270//T.BOEOTICUM (66)	1	20	5+10
136	CHIR3/CBRD x GAN/AE.SQUARROSA (897)//OPATA	1	20	5+T2
137	MAYOOR//TK SN1081/AE.SQUARROSA (222)/4/SABUF/3/BCN//CETA/ AE.SQUARROSA (895) x GAN/AE.SQUARROSA (897)//OPATA	1	20	5+T2
138	Not Available	1	20	2+10.5
139	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC/6/ FCT x DOY1/AE.SQUARROSA (458)	1	17+18	5+10
140	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
141	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
142	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
143	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
144	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
145	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
146	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
147	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
148	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
149	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
150	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
151	PASTOR x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	1	17+18	5+10
152	139 CHAPIO/INQALAB 91 x PICUS/3/KAUZ*2/BOW//KAUZ	1	17+18	5+10
153	TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC/6/ FCT x Opata	1	17+18	5+10
154	ALTAR 84/AE.SQUARROSA (224)//2*YACO/3/MAYOOR/TK SN1081/ AE.SQUARROSA/) (222)/4/KUKUN x GAN/AE.SQUARROSA (248)	2*	7	5+10
155	Not Available	2*	7	5+10
156	Opata x SCA/AE.SQUARROSA (518)	2*	7+8	2+12
157	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	2*	7+8	5+10
158	DOYI/AE.SQUARROSA (1018) x Opata CPI/GEDIZ/3/GOO//JO69/CRA/4/ AE.SQUARROSA (208)/5/OAPTA	2*	7+8	5+10
159	Opata x GAN/AE.SQUARROSA (248)	2*	7+9	2+12
160	RABE/2*MO88 x Opata	2*	7+9	2+12
161	Opata x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)	2*	7+9	2+12
162	KAUZ x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	2*	7+9	2+12
163	Opata x CETA/AE.SQUARROSA) (895)	2*	7+9	5+10
164	MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD x CPI/GEDIZ/3/ GOO//JO/CRA/4/T.MONOCOCCUM (101)	2*	7+9	5+10
165	Not Available	2*	7+9	5+10
166	Opata x DOY1/AE.SQUARROSA (1024)	2*	7+9	2+10

Table 17 (continued). High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
167	Opata x DOY1/AE.SQUARROSA (515)	2*	7+9	2+10
168	DOYI/AE.SQUARROSA (1018) x Opata CPI/GEDIZ/3/GOO//JO69/CRA/4/ AE.SQUARROSA (208)/5/OAPTA	2*	7+9	2+10
169	Opata x CPI/GEDIZ/3/GOO//JO69/CRA/4/AE.SQUARROSA (208)/5/OAPTA	2*	6+8	5+10
170	Not Available	2*	6+8	5+10
171	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x CPI/GEDIZ/3/ GOO//JO/CRA/4/T.MONOCOCCUM (101)	2*	6+8	5+10
172	ALTAR 84/AE.SQUARROSA (224)//2*YACO/7/OPATA/6/68.111RGB-U// WARD/3/FGO/4/… x 162 SAAR/INQALAB 91	2*	20	5+10
173	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x	2*	20	5+T2
174	Opata x DOY1/AE.SQUARROSA (458)	2*	13+16	2+12
175	CNDO/R143//ENTE/MEXI_2/3/AE.SQUARROSA (TAUS)/4/ WEAVER/5/2*KAUZ x DOY1/AE.SQUARROSA (458)	2*	13+16	2+12
176	SAT-5/PBW-343 x DOY1/AE.SQUARROSA (188)	2*	13+16	2+12
177	Not Available	2*	13+16	2+12
178	Opata x DOY 1/AE.SQUARROSA (255)	2*	13+16	5+10
179	Opata x 0 INQALAB 91/FISCAL	2*	13+16	5+10
180	Opata x CETA/AE.SQUARROSA (1031)	2*	13+16	5+10
181	Opata x ROK/KML// AE.SQUARROSA (214)	2*	13+16	5+10
182	182 SAAR/INQALAB 91 x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/ CBRD	2*	13+16	5+10
183	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x KAMBARA	2*	13+16	5+10
184	ALTAR 84/AE.SQUARROSA (224)//2*YACO/3/MAYOOR//TK SN1081/ AE.SQUARROSA (222)/4/KUKUN x ALTAR 84/AE.SQUARROSA (221)// YACO	2*	13+16	5+10
185	Opata x AE.SQUARROSA (1026)/DOY 1	2*	17+18	2+12
186	87 INQALAB 91/TSAPKI x SCA/AE.SQUARROSA (518)	2*	17+18	2+12
187	MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD x ARLIN_1/T. MONOCOCCUM (95)	2*	17+18	2+12
188	DOYI/AE.SQUARROSA (1018) x CPI/GEDIZ/3/GOO//JO69/CRA/4/ AE.SQUARROSA (208)/5/OAPTA	2*	17+18	2+12
189	KAUZ x MAYOOR//TK SN1081/AE.SQUARROSA (222)/3/CBRD	2*	17+18	2+12
190	SARSABZ x CHIR3/CBRD	2*	17+18	2+12
191	MAYOOR//TK SN1081/AE.SQUARROSA)(222)/3/FCT x Opata	2*	17+18	3+12
192	Opata x CROC_1/AE.SQUARROSA (444)	2*	17+18	5+10
193	M. OPATA-108 x DOY1/AE.SQUARROSA (372)	2*	17+18	5+10
194	Opata x 68.112/WARD//AE.SQUARROSA (369)	2*	17+18	5+10
195	ALTAR 84/AE.SQUARROSA (224)//2*YACO/7/OPATA/6/68.111RGB-U// WARD/3/FGO/4/… x 162 SAAR/INQALAB 91	2*	17+18	5+10
196	Opata x 68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA (1038)	2*	17+18	5+10
197	139 CHAPIO/INQALAB 91 x PICUS/3/KAUZ*2/BOW//KAUZ	2*	17+18	5+10
198	GAN/AE.SQUARROSA (236)//CETA/AE.SQUARROSA (895)/3/MAIZ/4/IN-QALAB 91 x PBW-343	2*	17+18	5+10
199	MAYOOR//TK SN1081/AE.SQUARROSA)(222)/3/FCT x Opata YAV_3/SCO// JO69/CRA/3/YAV/79/4/AE.SQUARROSA (498)/5/OPATA	2*	17+18	5+12
200	D67.2/P66.270//AE.SQUARROSA (223) x ARLIN_1/T.MONOCOCCUM (95)	2*	17+18	2+T2
201	139 CHAPIO/INQALAB 91 x PICUS/3/KAUZ*2/BOW//KAUZ	2*	17+18	1.5+12

Table 17 (continued). High-molecular-weight glutenin subunit allele composition of F_7 advanced lines derived from 'bread wheat/synthetic hexaploid' crosses (* indicates the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico).

S. No.	Pedigree	*Glu-1* subunits		
		Glu-A1	*Glu-B1*	*Glu-D1*
202	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)/6/CETA/… x CETA/AE.SQUARROSA (895)	2*	6+9	5+T2

After establishing the importance of *Glu-D^{1}1* encoded proteins, many attempts have been made to improve bread-making quality by increasing their genetic variability (Lagudah et al. 1987; William et al. 1993). Our data describes the end-use quality of the newly developed breeding material by combining the HMW–GS from different genetic backgrounds and selecting superior combinations. Most of this material has superior HMW–GS from *Glu-B1* (7+8, 7+9 17+18 and 13+16) and *Glu-D^{1}1* (5+10). In the conventional existing germ plasm, the *Glu-D1* locus is usually present as 1Dx5+1Dy10 or 1Dx2+1Dy12, however, the proportion of 1Dx2+1Dy12 is comparatively very high.

Our most important finding is that the subunit pair 1Dx2+1Dy12 from the *Glu-D1* locus, which has the most negative association with protein quality, weak gluten, and low sedimentation value (Ulhen 1990) is replaced by other variants at this locus using the D-genome SHs, and these subunits are inherited from *Ae. tauschii*. Hsam et al. (2001) also reported while conducting a microbaking test that rheological properties of the gluten as well as bread volume in synthetic wheats depends on the inherent properties of *Ae. tauschii* accessions.

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Potential of A-genome amphiploids (2n=6x=42, AAAABB) to improve bread-making quality: allelic variation at the Glu-1 and Glu-3 loci.

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In durum and common wheat, the HMW-GS *1Ay* is always absent but may be expressed in wild diploid and tetraploid wheats (Waines and Payne 1987). Ciaffi et al. (1995) indicated that the presence of active *Ay* genes could have a clear effect on bread-making quality. The evolution and domestication hexaploid wheat yielded a high degree of genetic erosion, assessed by studing these proteins, which might result in a reduced potential for successful breeding for wheat quality. Consequently, the search for new alleles, especially the active *Ay* gene, is very important. The diploid wild wheat species could be interesting candidates (Caballero et al. 2008). At the diploid level, the three main species *T. monococcum* subsp. *monococcum*, *T. monococcum* subsp. *aegilopoides*, and *T. urartu* (2n=2x=14) (Johnson 1975; Miller 1987) may be important sources of seed-storage proteins for enlarging the gene pool of cultivated wheats. Later studies at molecular level suggested that *T. monococcum* subsp. *aegilopoides* was the species from which einkorn wheat (*T.*

monococcum L. subsp. *monococum*) was domesticated with the A-genome of the polyploid wheats (durum and common wheat) being derived from *T. urartu* (Dvorak et al. 1988).

Accessions of these wild diploids were utilized by bridge crosses, where AAAABB amphiploids produced by '*T. turgidum*/A-genome diploid species' accession hybridization were exploited. Allelic variation exhibited by 193 AAAABB amphiploids at various *Glu-1* and *Glu-3* loci were studied using SDS–PAGE method with the objective of exploring their potential for use as a novel genetic resource to improve durum wheat quality.

In these A-genome amphiploids, 120 out of 193 were derived from *T. monococcum* subsp. *aegilopoides* utilizing 93 different accessions in combination with 20 durum wheat genotypes. At the *Glu-A^b1* locus, 14 allelic variants were observed (Table 18). *Glu-A^b1-I* was found most frequent; in 22 (18.33%) genotypes. Out of these 14 alleles, six have an active *Ay* gene at the *Glu-A^b1* locus. The presence of an active *Ay* gene is very important, because it always is absent in hexaploid bread wheat. The impact of this active *Ay* gene on bread-making quality needs to be explored, and these A-genome amphiploids or their derivatives will be important resources for such studies. Previously, Xu et al. (2009) identified five *Ay* alleles while analyzing 113 diploid wheat accessions. At *Glu-B1*, six allelic variants were observed (Table 18). *Glu-B1b, Glu-B1i*, and *Glu-B1f* were the most common. These alleles were inherited in these genotypes directly from the durum parents. In ours and previous studies, the most frequent alleles at the *Glu-B1* locus were mainly *Glu-B1b*, *Glu-B1d*, and *Glu-B1e* (Branlard et al. 1989; Vallega 1988; Moregues et al. 2006). At the *Glu-3* locus, 18 alleles at *Glu-A^b3* and six alleles at *Glu-B3* locus were observed (Table 18). Allelic variation at *Glu-A^b3* was more than that at *Glu-A^b1*. At the *Glu-B3* locus, allele *Glu-B3g* was most frequent and was identified in 31 genotypes. At this locus five alleles were rare and two alleles were extremely rare.

Table 18. Allelic frequencies at the *Glu-1* and *Glu-3* loci in A-genome amphiploids (2n=6x=42; AAAABB) derived from *Triticum monococcum* subsp. *aegilopoides*.

Allele (*Glu-1*)	Frequency (%)	Population (N)	Allele (*Glu-3*)	Frequency (%)	Population (N)
Glu-A^b1-I	18.33	22	*Glu-$A3^b$-I*	16.67	20
Glu-A^b1-II	15.83	19	*Glu-$A3^b$-II*	14.17	17
Glu-A^b1-III	12.50	15	*Glu-$A3^b$-III*	12.50	15
Glu-A^b1-IV	10.00	12	*Glu-$A3^b$-IV*	12.50	15
Glu-A^b1-V	7.50	9	*Glu-$A3^b$-V*	10.00	12
Glu-A^b1-VI	5.83	7	*Glu-$A3^b$-VI*	5.83	7
Glu-A^b1-VII	5.83	7	*Glu-$A3^b$-VII*	4.17	5
Glu-A^b1-VIII	5.00	6	*Glu-$A3^b$-VIII*	4.17	5
Glu-A^b1-IX	5.00	6	*Glu-$A3^b$-IX*	4.17	5
Glu-A^b1-X	5.00	6	*Glu-$A3^b$-X*	2.50	3
Glu-A^b1-XI	4.17	5	*Glu-$A3^b$-XI*	2.50	3
Glu-A^b1-XII	1.67	2	*Glu-$A3^b$-XII*	2.50	3
Glu-A^b1-XIII	1.67	2	*Glu-$A3^b$-XIII*	1.67	2
Glu-A^b1-XIV	1.67	2	*Glu-$A3^b$-XIV*	1.67	2
			Glu-$A3^b$-XV	1.67	2
Glu-B1a	9.17	11	*Glu-$A3^b$-XVI*	1.67	2
Glu-B1b	29.17	35	*Glu-$A3^b$-XVII*	0.83	1
Glu-B1f	20.00	24	*Glu-$A3^b$-XVIII*	0.83	1
Glu-B1d	7.50	9			
Glu-B1e	10.83	13	*Glu-B3b*	18.33	22
Glu-B1i	23.33	28	*Glu-B3c*	23.33	28
			Glu-B3d	25.83	31
			Glu-B3g	10	12
			Glu-B3h	8.33	10
			Glu-B3i	14.17	17

Of the 193 amphiploids, 35 were derived from *T. urartu* utilizing 20 different accessions. In these genotypes, allelic variation was less compared to genotypes derived from *T. monococcum* subsp. *aegilopoides*. Eight alleles were found at the *Glu-A^u1* locus and five alleles at *Glu-B1* (Table 19, p. 168). At the *Glu-3* locus, nine alleles were found at *Glu-A^u3* and five alleles at *Glu-B3*. Three alleles at the *Glu-B^u3* locus were very rare; three alleles were rare at *Glu-Au1* (Table 19). Caballero et al. (2008) found 17 alleles at the *Glu-A^u1* locus and 24 alleles at the *Glu-A^u3* locus while analyzing 169 different accessions of *T. urartu*. At the *Glu-A^u1* locus, all the alleles expressed the *Ax* subunit and four expressed the *Ay* subunit. These findings agreed with that of Caballero et al. (2008) who found eight *Ay* active subunits

in *T. urartu* accessions. The variability found at this locus was comparatively greater than described for the homologous locus in durum wheat, where only 10 allelic variants are described (McIntosh et al 1998; 2007). The *Glu-B3* locus is traditionally associated with gluten strength in durum wheat. Previously, Dvorak et al. (1988) reported the equivalence of the A genome of polyploid wheat to that of *T. urartu*, thus strengthening the use of these amphiploids to improve end-use quality in durum wheat.

Table 19. Allelic frequencies at the *Glu-1* and *Glu-3* loci in A-genome amphiploids (2n=6x=42; AAAABB) derived from *Triticum urart*u.

Allele (Glu-1)	Frequency (%)	Population (N)	Allele (*Glu-3*)	Frequency (%)	Population (N)
Glu-A^{u}1-I	25.71	9	*Glu-A3^u-I*	28.57	10
Glu-A^{u}1-II	20.00	7	*Glu-A3^u-II*	17.14	6
Glu-A^{u}1-III	14.29	5	*Glu-A3^u-III*	14.29	5
Glu-A^{u}1-IV	11.43	4	*Glu-A3^u-IV*	14.29	5
Glu-A^{u}1-V	11.43	4	*Glu-A3^u-V*	8.57	3
Glu-A^{u}1-VI	5.71	2	*Glu-A3^u-VI*	8.57	3
Glu-A^{u}1-VII	5.71	2	*Glu-A3^u-VII*	2.86	1
Glu-A^{u}1-VIII	5.71	2	*Glu-A3^u-VIII*	2.86	1
			Glu-A3^u-IX	2.86	1
Glu-B1b	34.29	12			
Glu-B1c	14.29	5	*Glu-B3b*	14.29	5
Glu-B1d	17.14	5	*Glu-B3c*	28.57	10
Glu-B1f	14.29	6	*Glu-B3d*	34.29	12
Glu-B1i	20.00	7	*Glu-B3g*	14.13	4
			Glu-B3h	14.13	4

Table 20. Allelic frequencies at the *Glu-1* and *Glu-3* loci in A-genome amphiploids (2n=6x=42; AAAABB) derived from *Triticum monococcum* subsp. *monococcum*.

Allele (Glu-1)	Frequency (%)	Population (N)	Allele (Glu-3)	Frequency (%)	Population (N)
Glu-A^{m}1-I	31.58	12	*Glu-A3^m-I*	23.68	9
Glu-A^{m}1-II	13.16	5	*Glu-A3^m-II*	15.79	6
Glu-A^{m}1-III	13.16	5	*Glu-A3^m-III*	15.79	6
Glu-A^{m}1-IV	10.53	4	*Glu-A3^m-IV*	13.16	5
Glu-A^{m}1-V	10.53	4	*Glu-A3^m-V*	10.53	4
Glu-A^{m}1-VI	10.53	4	*Glu-A3^m-VI*	5.26	2
Glu-A^{m}1-VII	5.26	2	*Glu-A3^m-VII*	5.26	2
Glu-A^{m}1-VIII	5.26	2	*Glu-A3^m-VIII*	5.26	2
			Glu-A3^m-IX	2.63	1
Glu-B1b	21.05	8	*Glu-A3^m-X*	2.63	1
Glu-B1c	26.31	10			
Glu-B1d	15.78	6	*Glu-B3b*	10.53	4
Glu-B1f	26.31	10	*Glu-B3c*	18.42	7
Glu-B1i	10.52	4	*Glu-B3d*	28.95	11
			Glu-B3g	13.16	5
			Glu-B3h	15.79	6
			Glu-B3i	13.16	5

The 38 genotypes of *T. monococcum* subsp. *monococcum* were derived from 28 different accessions and 12 durum wheat genotypes. Eight allelic variants at the *Glu-A^{m}1* and five variants at the *Glu-B1* locus were identified (Table 20). *Glu-A^{m}1-I* was most frequent and two alleles were very rare. At the *Glu-B1* locus, *Glu-B1c* and *Glu-B1f* were most frequent. Saponaro et al. (1995) analyzed 56 accessions of *T. monococcum* subsp. *monococcum* and found 30 *Glu-A^{m}1* allelic variants at the *Glu-A^{m}1* locus. Most of the genotypes contained both x- and y-type subunits, but two accessions were null for both. In our study, five alleles encoded both x- and y-type subunits. These A-genome amphiploids are rich in allelic variation at the *Glu-1* and *Glu-3* loci and most important is their active *Ay* subunit, which can be introduced into durum wheat genotypes to enhance end-use quality.

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Characterization of the HMW–GS in synthetic hexaploid wheats and their durum parents.

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High-molecular-weight glutenin subunit composition and variation in 93 synthetic hexaploid (SH) wheats of an Elite-1 SH subset (Mujeeb-Kazi 2003) and their 31 durum wheat parents were determined by SDS–PAGE. Eighteen different alleles at the *Glu-1* locus in the SHs and nine alleles in durum wheat lines were observed. Forty-nine different patterns of HMW–GS in the SHs and 15 different subunit compositions in durum wheats were found. Genetic variability at the *Glu-D^{t}1* locus was greater than that at other loci. The relatively high frequency of superior alleles, *Glu-B1b* and *Glu-D^{t}1d*, indicated the superior bread-making quality attributes in these SH wheats.

Allelic variation at the *Glu-1* locus for HMW–GS in synthetic hexaploid wheats. The results obtained from this study categorized the HMW–GS composition and allelic frequencies in 93 synthetic hexaploid wheats (Table 21, p. 170, and Table 22, p. 171). Eighteen different *Glu-1* alleles were found, three at *Glu-A1*, six at *Glu-B1*, and nine at *Glu-D^{t}1* (Table 22, p. 171). At the *Glu-A1* locus, three x-type subunits were found, 1, 2*, and null, encoded by alleles *Glu-A1a, Glu-A1b*, and *Glu-A1c*, respectively. The null allele was the most frequent, in 65 (69.89%) of the genotypes, followed by subunit 2* in 27 (17.20%), and subunit 1 was observed in 16 (12.90%). These results are different from those of Peña et al. (1995), who reported the presence of null allele in all SH wheats studied. An et al. (2005) reported the genetic diversity at this locus depicted by different codominant alleles at *Glu-A1* locus to be 0.19, which was very low compared to our findings, i.e., 0.47. The frequency of allele *Glu-A1a* encoding subunit 1 in Chinese, Japanese, and a world collection of 300 cultivars was 5.2%, 12.2%, and 28%, respectively. The frequency of the null allele in Chinese (70%), Japanese (80.4%), and in the world collection (74.1%) also was higher than other subunits at this locus (Payne and Lawrance 1983). The quality characteristics of cultivars with subunit 1 are better than those with 2* and the null allele (Li et al. 2009). However, the quality characteristics of cultivars with subunit 2* and null were not significant.

Six different codominant alleles were found at the *Glu-B1* locus. The *Glu-B1g* allele controlling the subunit 13+19 was less frequent (2.15%) among all the subunits at this locus. The most frequent allele was *Glu-B1i* controlling subunit 17+18 found in 26 (27.95%) genotypes followed by *Glu-B1b* and *Glu-B1f* controlling the subunits 7+8 and 13+16 in 24 (25.80%) and 20 (21.50%) genotypes, respectively. The other HMW-GS alleles found at this locus, *Glu-B1c* encoding 7+9 subunit and *Glu-B1d* encoding subunit 6+8, were observed in 15 (16.12%) and six (6.45%) accessions, respectively. The genetic diversity at this locus by these alleles was 0.78. Peña et al. (1995) reported that subunit 7+8 was most frequent in a studied group of SHs. Chinese (71.9%) and Japanese cultivars (83.2%), in which the subunit 7+8 was most frequent, are similar (Nakamura 2000). For 60 (64.51%) of the synthetics in our study, subunits 7+8, 13+16,

or 17+18 are found, which have a superior impact on bread-making quality. These subunits were considered to have the same quality score at *Glu-B1* locus (Gianibelli et al. 2002). The effect of subunit 7 on quality characteristics was found to be the lowest at this locus (Li et al. 2009), and this subunit was not found alone in these accessions. The frequent subunit 7+8 also is associated with extensibility in bread wheat doughs (Uhlen 1990; Peña et al. 1995). So the higher the frequency of the important alleles *Glu-1Bb, Glu-1Bf*, and *Glu-b1i* increases the inherent potential of these SHs for bread-making quality.

Table 21. Allelic composition, frequency, and quality score of 93 accessions of synthetic hexaploid wheats.

Line No.	Subunit combination	Alleles	No. of accessions	Accessions
1	1, 17+18, 2.1+10	a, i, n	1	E-52
2	1, 17+18, 5+10	a, i, d	2	E-11, E-55
3	1, 7+8, 2+12	a, b, a	2	E-35, E-85
4	1, 7+9, 1.5+10	a, c, ah	1	E-93
5	1, 7+9, 5+10	a, c, d	2	E-53, E-69
6	1, 13+16, 1.5+10	a, f, ah	1	E-71
7	1, 13+16, 2+12	a, f, a	2	E-37, E-82
8	1, 13+16, 5+10	a, f, d	1	E-41
9	2*, 17+18, 1.5+12	b, i, aj	1	E-46
10	2*, 17+18, 2.1+10	b, i, n	2	E-50, E-66
11	2*, 17+18, 2+12	b, i, a	1	E-74
12	2*, 17+18, 5+10	b, i, d	1	E-1
13	2*, 7+8, 2.1+10	b, b, n	1	E-26
14	2*, 7+8, 2.1+12	b, b	1	E-28
15	2*, 7+8, 2+12	b, b, a	1	E-44
16	2*, 7+8, 5+10	b, b, d	1	E-57
17	2*, 13+16, 2.1+12	b, f	2	E-21, E-24
18	2*, 13+16, 2+12	b, f, a	3	E-27, E-33, E-45
19	2*, 13+16, 1.5+T1T2	b, f, ag	1	E-59
20	2*, 6+8, 1.5+12	b, d, aj	1	E-43
21	null, 17+18, 1.5+T1T2	c, I, ag	4	E-16, E-23, E-70, E-84
22	null, 17+18, 2.1+10	c, I, n	3	E-39, E-60, E-83
23	null, 17+18, 2.1+12	c, I,	2	E-54, E-58
24	null 17+18, 2+12	c, I, a	2	E-47, E-87
25	null, 17+18, 2+T1T2	c, I, x	2	E-31, E-79
26	null, 17+18, 5+10	c, I, d	5	E-14, E-15, E-40, E-42, E-81
27	null, 7+8, 1.5+10	c, b, ah	4	E-61, E-62, E-64, E-65
28	null, 7+8, 1.5+12	c, b, aj	3	E-18, E-89, E-9
29	null, 7+8, 1.5+T1T2	c, b, ag	2	E-72, E-77
30	null, 7+8, 2.1+10	c, b, n	2	E-6, E-80
31	null, 7+8, 2.1+12	c, b	3	E-19, E-67, E-92
32	null, 7+8, 2+12	c, b, a	4	E-2, E-4, E-29, E-25
33	null, 7+8, 3+10	c, b, z	1	E-7
34	null, 7+9, 1.5+10	c, c, ah	1	E-34
35	null, 7+9, 1.5+12	c, c, aj	2	E-3, E-5
36	null, 7+9, 1.5+T1T2	c, c, ag	2	E-32, E-78
37	null, 7+9, 2.1+10	c, c, n	1	E-76
38	null, 7+9, 2.1+12	c, c	3	E-30, E-88, E-90
39	null, 7+9, 2+12	c, c, a	2	E-10, E-73
40	null, 13+16, 1.5+T1T2	c, f, ag	1	E-22
41	null, 13+16, 2.1+10	c, f, n	1	E-12
42	null, 13+16, 2.1+12	c	1	E-63
43	null, 13+16, 2+12	c, f, a	1	E-20
44	null, 13+16, 5+10	c, f, d	6	E-13, E-36, E-56, E-68, E-86, E-91
45	null, 13+19, 1.5+12	c, g, aj	1	E-38
46	null, 13+19, 1.5+T1T2	c, g, ag	1	E-17
47	null, 6+8, 2.1+10	c, d, n	1	E-51
48	null, 6+8, 2+12	c, d, a	1	E-49
49	null, 6+8, 5+10	c, d, d	3	E-8, E-48, E-75

Valuable genetic variability (0.85) was found at the *Glu-D^{1}1* locus in these synthetics and also justifies their development. The allelic variation of the HMW–GS strongly influences the variability in bread-making quality and the D-genome strongly influences bread-making quality (Pfluger et al. 2001; William et al. 1993). A higher level of genetic variability at this locus is a valuable genetic reservoir to improve bread-making quality. At the *Glu-D^{1}1* locus, five x-type subunits, 1.5, 2, 2.1, 5, and 3, three y-type subunits, 10, 12, and T2, constituting nine different co-dominant allelic combinations were found. The *Glu-D1d* allele, controlling the subunit 5+10, is the most important and superior bread-making quality subunit, was most frequent (22.58%) among all the subunits at this locus. Li et al. (2009) reported the superiority of this allele among all the other alleles at *Glu-1* loci. Luo et al. (2001) reported the association of the 5+10 subunit with sedimentation volume

Table 22. Allelic frequencies of the high-molecular-weight glutenin subunits at the *Glu-1* loci in 93 synthetic hexaploid wheats.

Locus	Allele	Subunit	Number of accessions	Frequency (%)	H (Nei's index)
Glu-A1	a	1	12	0.13	0.47
	b	2*	16	0.17	
	c	null	65	0.70	
Glu-B1	b	7+8	24	0.26	0.78
	c	7+9	15	0.16	
	f	13+16	20	0.22	
	i	17+18	26	0.28	
	d	6+8	6	0.06	
	g	13+19	2	0.02	
Glu-D1	ah	1.5+10	7	0.07	0.85
	aj	1.5+12	8	0.08	
	ag	1.5+T1T2	11	0.12	
	n	2.1+10	12	0.13	
		2.1+12	12	0.13	
	a	2+12	19	0.20	
	d	5+10	21	0.23	
	x	2+T1T2	2	0.02	
	z	3+10	1	0.01	

and longer Pelshenke time. They also reported that the 5+10 subunit in a genotype also results in greater whole-meal flour protein. Payne et al. (1981) established that the 5+10 subunit has a superior quality affect over 2+12 and all other alleles at *Glu-D1*. Other subunit at this locus included 2+12, encoded by allele *Glu-D1a* and found in 19 (20.43%) genotypes. Some rare subunits, 2+T2 and 1.5+T2, also were observed. The allele *Glu-D^{t}1-2l*, which controls subunit T1+T2, was first reported by William et al. (1993) in *Ae. tauschii*, and they concluded that T1 and T2 occur together and their presence is usually designated as T2. The occurrence of these rare combinations in synthetic wheats is due to the utilization of *Ae. tauschii* accessions with diverse subunit combinations, which also was reported by Peña et al. (1995). Other important subunits at this locus were 2.1+10 and 2.1+12 found in 12 (12.90%) accessions. The subunit pair 3+10 was found in only one genotype. This subunit is associated with extensible gluten type and had larger bread loaf volume than 2+10 (Peña et al. 1995). The subunit 1.5+10 was present in seven of the 93 synthetics, and this subunit had better overall quality characteristics than genotypes with other subunits. Peña et al. (1995) concluded that genotypes with the 1.5+10 subunit possess the best bread-making quality.

HMW–GS composition in synthetic hexaploid wheats. Forty-nine different HMW–GS compositions were observed in synthetic wheats (Table 21, p. 170). Peña et al. (1995) reported 36 different allelic compositions in SH wheats. Six (6.45%) genotypes had the subunit combination null, 13+16, 5+10. Five (5.37%) genotypes had subunit composition of null, 17+18, 5+10. Thirteen synthetics had the rare allele 1DyT2 at *Glu-D^{t}1* with either subunit 1.5 or 2. The quality effects of genotypes with 1DyT2 subunits were not determined, because these are rare and their quality effects are yet to be determined. Durum cultivars with either subunit 1 or 2* at *Glu-A1*, along with *Glu-B1*-encoding subunits 7+8, 17+18, or 13+16, can enhance the bread-making quality of these genotypes. Twenty-four synthetics have either subunit 1 or 2* at the *Glu-A1* locus along with superior (7+8, 17+18, or 13+16) subunits at the *Glu-B1* locus. The variation in the patterns of HMW–GS among the different SH accessions described here is nearly similar to those of Peña et al. (1995), Galili and Feldman (1983), and Lawrence and Shepherd (1980), although there are some discrepancies. From these results, it is evident that synthetics have good potential towards bread-making quality and their exploitation in breeding programs becomes important to the breeder when using SH wheats as diversity sources for wheat improvement.

Allelic variation at the *Glu-1* loci for HMW–GS in durum parental lines. In the durum wheat parents, nine different codominant alleles were found at the *Glu-A1 and Glu-B1* loci (Tables 23 and 24, p. 172). At the *Glu-A1* locus, the x-type subunits 1, 2* and null are encoded by the alleles *Glu-A1a, Glu-A1b*, and *Glu-A1c*, respectively. The null allele was the most frequent, appearing in 14 (45%) lines, followed by subunit 2* in nine (32%) and subunit 1 in seven (23%) genotypes. Branlard et al. (1989) reported the frequency of the *Glu-A1c* (null) allele in 83% of the 502 durum wheat cultivars. The extent of variability exhibited by the *Glu-A1* alleles was 66%, which is higher compared to that at this locus in the synthetics.

At the *Glu-B1* locus, six alleles were found, *Glu-B1b, Glu-B1c, Glu-B1f, Glu-B1i, Glu-B1g*, and *Glu-B1d*, control the subunits 7+8, 7+9, 13+16, 17+18, 13+19, and 6+8, respectively. Aghai et al. (1996) reported seven alleles at this locus in landraces from Turkey, Trucheta et al. (1995) reported ten in landraces from Iran, and Branlard et al. (1989) and Kaan et al. (1993) described 12 alleles in a world collection of durum wheats. The frequency of subunit 7+8 and 13+16

was highest, found in nine (29%) genotypes. The results agree with Pfluger et al. (2000). Kaan et al. (1993), Branlard et al. (1989), and Carrillo (1995) also determined that the most frequent subunit was 7+8. Subunit 17+18 was found in six (6.45%) genotypes. The diversity of alleles at this locus was recorded 77% according to Nei's index. Moragues et al. (2006) reported genetic diversity of 80% at this locus in a study of 63 durum land races from diverse geographic origins. Alleles *Glu-B1c* and *Glu-B1i*, encoding the subunits 7+9 and 13+16 and generally absent in tetraploid wheats, were found in these durums. The same alleles were also reported by Xu et al. (2009). Some subunits, such as 6+8 (10%), 7+9 (10%), and 13+19 (3%), were found with very less frequency.

Table 23. Allelic composition, frequency, and quality score of 31 durum parents of D-genome synthetic hexaploid wheats.

Line No.	Subunit combination	Alleles	No. of accessions	Quality score	Accessions
1	1, 7+8	a, b	1	6	D-16
2	1, 17+18	a, i	1	6	D-22
3	1, 7+9	a, c	1	5	D-27
4	1, 13+16	a, f	3	6	D-20, D-28, D-30
5	1, 6+8	a, d	1	5	D-24
6	2* 7+8	b, b	4	6	D-2, D-19, D-23, D-25
7	2*, 17+18	b, i	3	6	D-11, D-18, D-26
8	2*, 13+16	b, f	2	6	D-4, D-31
9	2*, 6+8	b, d	1	5	D-29
10	null, 7+8	c, b	4	4	D-1, D-3, D-5, D-7
11	null, 17+18	c, i	2	4	D-9, D-17
12	null, 7+9	c, c	2	3	D-13, D-21
13	null, 13+16	c, f	4	4	D-6, D-8, D-10, D-12
14	null, 13+19	c, g	1	4	D-14
15	null, 6+8	c, d	1	3	D-15

HMW–GS composition and quality score in durum parental lines of synthetic wheats. Fifteen different combinations of HMW–GS were found at the *Glu-1* loci in the durum wheat genotypes. Three combinations, 2*, 7+8; null, 7+8; and null, 13+16; were found in four (12.90%) lines (Table 24). Branlard and Le Blanc (1985) and Ponga et al. (1985) reported that commercial durum cultivars generally possess subunits 7+8 and 13+16. The quality score ranged from 3–6, and 14 genotypes exhibited the quality score of 6, which was considered the best.

Table 24. Allelic frequencies of the high-molecular-weight glutenin subunits at the *Glu-1* loci in 31 durum wheat parental lines.

Locus	Allele	Subunit	Number of accessions	Frequency (%)	H (Nei's index)
Glu-A1	a	1	7	0.23	0.47
	b	2*	9	0.32	
	c	null	14	0.45	
Glu-B1	b	7+8	24	0.29	0.78
	c	7+9	9	0.10	
	i	17+18	3	0.19	
	f	13+16	9	0.29	
	g	13+19	1	0.03	
	d	6+8	3	0.10	

These results reveal that higher variability at the *Glu-1* loci is associated with SH wheats. This variability could be effectively utilized as a source for the improvement of bread-making quality in breeding programs. The higher crossability of SH wheats with bread wheat will increase their utilization for introducing new *Glu-D*^{t}*1* allelic variations into bread wheat. Undesirable, qualitative effects associated with the *Glu-B1* locus can be avoided by utilizing satisfactory quality durum cultivars in SH wheat production.

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A comprehensive report on the attack of foliar blight on wheat in Pakistan in the 2008–09 wheat crop.

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The 2008–09 crop season was different. Early on, a shortage of urea and the high price of DAP fertilizer remained a burning problem for the farming community of Pakistan. Temperature fluctuations also were unpredictable for the wheat crop. Timely rain and normal sowing were good signs for a bumper wheat crop. Up to mid February, 2009, farmers expected a good harvest, but some unexpected problems changed the situation in the Sindh and Southern Punjab. The spread of a new disease in the region became a new threat to the wheat crop in Pakistan, especially in the upper Sindh and Southern Punjab, which account for nearly 50% of the wheat production area in Pakistan.

Favorable environmental conditions increase the chances of disease in any field. For the first time in the history of Pakistan, a foliar disease had covered such a vast area of million acres in Sindh and Punjab. The disease spread in Sindh at early stages of growth caused a significant loss in wheat production. The crop was found to be susceptible

in the Kacha and Pucca areas of the Khairpur District of Sindh, Rahim Yar Khan, Rajan Pur, Bahawalpur District, Dera Ghazi Khan, Multan, Khanewal District, Lodhran District, Bahawalnagar, and Vehari district.

Spot blotch or Helminthosporium leaf blight (HLB, Fig. 7) is a major disease of wheat, particularly in warmer growing areas where the average temperature is above 17°C in the coolest months. In past 20 years, HLB has been recognized as a major disease in plains of south Asia and is a major problem in India, Bangladesh, and Nepal. This disease is seed and soil borne.

Fig. 7. Spot blotch or Helminthosporium leaf blight cused by *Cochiobolus sativus*.

Varietal resistance. The disease was found with different intensity in fields on all wheat cultivars. Bhakkar-02, covering more than 50% area in the Upper Sindh and Southern Punjab, was badly affected. Mehran 89/ Pak 81 was also found to be susceptible in Sindh. TJ-83 and TD-1 of Sindh were resistant. Two wheat cultivars of Punjab, Seher-06 and Fareed-06, were resistant both in Punjab and Sindh. A new wheat strain 032862 was found to be resistant under high pressure at P.S.C Khanewal. The resistant sources can be used as good sources for breeding purposes in the future.

Direction of disease spread. The disease epidemic was first thought to have begun in the river-side area of Moro, Dadu, and then spread south. The direction of spread from south to north indicated its southern origin. The spread near the Indus River shows greater prevalence in hot and humid areas. The temperature of South Punjab and Sindh remained high during the 2008–09 wheat crop season. Although spot blotch is seed borne, the spread also shows an airborne trend. If airborne, spore shift is expected from the coastal areas of Southern India and Bangladesh.

Estimating losses. Losses in Kacha area of the Upper Sindh may range between 15–20%, whereas 10–15% losses were found in the Pucca area of Sindh. In Punjab, losses in crops near the Indus River ranged from 10–15%. Losses may be 5–10% in areas away from the river. Crop yield was expected to be 26 x 10^6 tons with losses close to 8% (2 x 10^6 tons). Expected losses in monitory terms may reach up to one-billion rupees (1 USD = Rs. 85 Pak).

Control of disease. Genetic control is cheap, easy, and effective. Recommended chemicals can be used at the proper growth stage to control the disease but are expensive. Susceptible wheat cultivars such as Bhakkar-02 should be banned in the Upper Sindh and Southern Punjab. Seed of two Punjabi wheat cultivars, Seher-06 and Fareed-06, should be allowed for sowing in the Upper Sindh. Two new wheat cultivars, Mairaj-08 and Faisalabad-08, which may have better resistance, can be spread in Punjab. Awareness in this respect should be created in the farming community and extension workers through the press and electronic media.

Future threat. The susceptible wheat Bhakkar-02 covers about 50% of the area and will be too difficult to replace in one year because of the lack of seed availability. In the case of disease reoccurrence, 5–10% losses are expected in wheat production during 2009–10 due to HLB. A three-year, continuous, high disease pressure in the field can create an uncontrollable disease complex, thus, it is important to control it at the proper time.

Stripe rust resistance and genetic diversity of some A-genome, diploid progenitor resources of wheat.

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Resistance to stripe rust in 194 A-genome-based SH lines (2n=6x=42; AAAABB) was evaluated at the seedling stage in the greenhouse using bulk inoculum. Twenty-four (15%) A-genome amphiploids were found resistant at the seedling stage. The remaining accessions were either moderately resistant (IT 4-6) or susceptible (IT 7–9). Seventeen (12.93%) genotypes resistant at the seedling stage were also resistant as adult plants, indicating the presence of major resistance genes. Sixty-two (54.31%) genotypes that were susceptible as seedlings were resistant as adult plants indicated the presence of minor resistance genes. The resistant A-genome-based SHs also were molecularly evaluated for DNA-based diversity using RAPD and SSR primers. Five hundred twenty RAPD primers of the Operon series were screened; 107 generated bands and only 50 of these were subsequently selected for further analysis. Ninty-two A-genome-specific SSR primers also were tested. Only 35 primers generated bands, and 13 of these were subsequently selected for further analysis. The 13 SSR primers produced a total of 58 polymorphic bands, whereas 216 polymorphic bands were generated using the 50 RAPD primers. Genetic similarities among the entries were estimated using Nei and Li's coefficient and cluster analysis was performed using the UPGMA clustering method. The average similarity matrix for RAPDs and SSRa were 7.05 and 1.39, respectively. Two known markers for *Yr* resistance genes, namely *Yr* 155 and *Yr* 501, were also applied on resistant entries. The A-genome-based SHs found resistant in this study provide a useful genetic resource for stripe rust resistance, which can be transferred to *T. turgidum* and also be used for bread wheat improvement.

Phenotypic evaluation. The evaluation was across the following categories: pubescence, days-to-heading, plant height, awn color, days-to-physiological maturity, 1,000-kernel weight, number of grains/spike, and spike length. Resistant genotypes that showed good agronomic traits were 2, 29, 35, 36, 39, 40, 49, and 53 (Table 25, pp. 175-177).

Table 25. Phenotypic evaluation and stripe rust infection-type data of A-genome-based synthetic hexaploids. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm); S IT = seedling infection type; and AP IT = adult-plant infection type.

Line No.	PEDIGREE	PUB	FLOW	HT (cm)	AWN	PMA	TKW (g)	G/S	SL (cm)	S IT	AP IT
1	YUK/T.BOEOTICUM(1)*	+	125	104	LB	175	46	18	14	9	0
2	GARZA/BOY// T.BOEOTICUM(12)	–	133	129	LB	184	60	40	10	6	0
3	SCA/ T.BOEOTICUM(14)	+	125	125	LB	185	38	5	14	7	0
4	ALG86/4/FGO/PALES//MEXI_1/3/ RUFF/FGO/5/ENTE/6/T.BOEOTICUM(14)	+	135	124	LB	181	38	7	11	9	0
5	BOTNO/ T.BOEOTICUM(20)	+	124	104	LB	176	32	7	12	8	0
6	GARZA/BOY// T.BOEOTICUM(21)	–	143	104	LB	186	23	24	12	1	0
7	DOY1/ T.BOEOTICUM(23)	+	131	128	LB	187	14	2	12	9	0
8	DOY1/ T.BOEOTICUM(26)	+	133	125	LB	186	41	13	12	0	0
9	DOY1/ T.BOEOTICUM(27)	+	135	135	LB	186	16	4	12	1	0
10	SCA// T.BOEOTICUM(28)	+	143	125	LB	185	44	18	13	9	0
11	SCA/ T.BOEOTICUM(31)	–	142	92	LB	181	50	11	11	0	0
12	SCA/ T.BOEOTICUM(33)	+	140	121	LB	187	50	5	12	4	0
13	SCOOP_1/ T.BOEOTICUM(33)	+	135	133	LB	187	44	9	13	8	0
14	SCA/ T.BOEOTICUM(39)	+	108	119	LB	176	43	9	12	0	0
15	SCA/ T.BOEOTICUM(40)	+	133	100	LB	181	44	2	11	8	0
16	SCOOP_1/ T.BOEOTICUM(40)	+	135	104	LB	186	43	12	10	0	0
17	SCOOP_1/ T.BOEOTICUM(46)	+	133	101	DB	186	48	22	10	8	0
18	SCOOP_1/ T.BOEOTICUM(50)	+	147	129	LB	190	27	29	12	9	0
19	LCK59.61/ T.BOEOTICUM(52)	+	135	118	LB	187	48	6	10	2	0
20	AJAIA/ T.BOEOTICUM(55)	+	135	125	LB	181	43	9	11	9	0

Table 25. Phenotypic evaluation and stripe rust infection-type data of A-genome-based synthetic hexaploids. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm); S IT = seedling infection type; and AP IT = adult-plant infection type.

Line No.	PEDIGREE	PUB	FLOW	HT (cm)	AWN	PMA	TKW (g)	G/S	SL (cm)	S IT	AP IT
21	SHAG_22/ T.BOEOTICUM(56)	+	145	121	LB	190	60	4	14	9	0
22	SCOOP_1/ T.BOEOTICUM(59)	+	149	104	LB	190	41	24	11	8	0
23	SCOOP_1/ T.BOEOTICUM(69)	–	125	94	LB	175	45	24	9	9	0
24	SCOOP_1/ T.BOEOTICUM(71)	–	133	102	AW	189	33	4	13	9	0
25	BOTNO/ T.BOEOTICUM(75)	+	145	80	LB	191	29	32	12	9	0
26	D67.2/P66.270// T.BOEOTICUM(75)	+	126	110	AW	182	40	33	14	9	0
27	SCOOP_1/ T.BOEOTICUM(79)	+	146	130	DB	193	37	16	11	89	0
28	SCOOP_1/ T.BOEOTICUM(89)	–	136	116	LB	189	56	27	11	1	0
29	SCOOP_1/ T.BOEOTICUM(91)	–	131	117	LB	171	56	37	12	1	0
30	SCOOP_1/ T.MONOCOCCUM(98)	–	127	105	LB	150	56	21	12	0	0
31	AOS/ T.MONOCOCCUM(98)	+	127	103	LB	151	42	16	11	0	0
32	AOS/ T.MONOCOCCUM(111)	–	121	108	LB	158	24	6	13	9	0
33	68.111/RGB-U//WARD/3/ T.MONOCOCCUM(112)	+	125	120	LB	150	42	43	12	9	2R
34	DOY1/ T. URARTU (550)	+	126	144	LB	179	46	31	13	2	3R
35	DOY1/ T. URARTU (560)	+	127	145	LB	175	63	11	15	9	2R
36	DOY1/ T. URARTU (563)	+	119	75	LB	171	59	20	14	9	5R
37	DOY1/ T. URARTU (543)	+	128	104	LB	183	31	6	12	9	5R
38	YAV_2/TEZ// T.BOEOTICUM(44)	+	131	114	LB	180	52	19	11	9	8R
39	YAV_2/TEZ// T.BOEOTICUM(43)	+	148	114	LB	191	59	6	13	6	0
40	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(49)	+	134	116	LB	183	57	38	12	9	4R
41	YAV_2/TEZ// T.BOEOTICUM(65)	+	133	89	LB	181	62	14	9	9	0
42	YAV_2/TEZ// T.BOEOTICUM(67)	–	133	85	LB	179	50	51	10	9	0
43	YAV_2/TEZ// T.BOEOTICUM(73)	–	135	79	LB	178	72	36	9	1	0
44	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(77)	+	145	128	LB	186	45	21	11	0	0
45	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(78)	–	135	100	LB	187	48	20	13	9	0
46	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(93)	+	135	102	LB	187	44	9	11	9	0
47	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.MONOCOCCUM (99)	+	145	114	LB	188	45	26	8	9	0
48	STN/ T.MONOCOCCUM (111)	+	143	107	LB	188	38	7	14	9	0
49	STN/ T.MONOCOCCUM (112)	–	141	117	LB	189	33	34	12	2	0
50	YAV_2/TEZ// T.MONOTICUM (112)	–	126	117	LB	189	54	27	13	9	0
51	YAV_2/TEZ// T.MONOCOCCUM (113)	+	139	87	LB	187	48	7	13	9	0
52	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.MONOCOCCUM (114)	–	143	137	LB	191	44	10	12	9	0
53	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.MONOCOCCUM (115)	+	143	124	LB	191	46	8	11	9	0
54	YAV_2/TEZ// T.MONOCOCCUM(121)	+	127	100	DB	189	60	6	8	9	0
55	DOY1/T. URARTU (552)	+	132	100	LB	183	45	19	10	9	0
56	ALTAR 84/T. URARTU (558)	–	127	120	LB	176	46	9	7	8	4R
57	CETA/T. URARTU (558)	+	131	131	LB	173	36	20	6	1	5R
58	DOY1/T. URARTU (559)	–	140	115	LB	175	36	9	13	9	0
59	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(30)	+	140	137	LB	185	32	5	13	9	0
60	ARLIN_1/T.BOEOTICUM((32)	+	140	138	LB	185	36	9	10	9	5R

Table 25 (continued). Phenotypic evaluation and stripe rust infection-type data of A-genome-based synthetic hexaploids. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; HT = plant height at maturity; AWN = awn color, LB = light brown, DB = dark brown, B = black, AW = amery white, and Y = yellow; PMA = days–to–physiological maturity; TKW = 1,000–kernel weight; G/S = number of grains/spike; and SL = spike length (cm); S IT = seedling infection type; and AP IT = adult-plant infection type.

Line No.	PEDIGREE	PUB	FLOW	HT (cm)	AWN	PMA	TKW (g)	G/S	SL (cm)	S IT	AP IT
61	CETA/T.BOEOTICUM((42)	+	125	133	LB	186	42	41	12	8	0
62	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(51)	+	140	122	LB	181	27	18	12	9	6R
63	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(63)	+	140	143	LB	187	48	20	13	9	8R
64	ARLIN_1/T.BOEOTICUM(84)	+	139	135	LB	185	38	30	10	7	0
65	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(100)	+	140	135	LB	180	25	6	11	7	0
66	CPI/GEDIZ/3/GOO//JO//CRA/4/ T.BOEOTICUM(85)	–	133	135	LB	187	31	14	10	7	0
67	ARLIN_1/T.BOEOTICUM(86)	–	135	111	LB	186	38	11	8	9	5R
68	ARLIN_1/T.BOEOTICUM(103)	–	144	130	LB	187	30	28	12	9	0
69	ARLIN_1/ T.BOEOTICUM(109)	+	141	131	LB	186	20	19	12	9	0
70	ARLIN_1/T.BOEOTICUM(11)	+	141	117	LB	187	22	29	7	9	0
71	ARLIN_1T. URARTU (547)	+	133	119	LB	181	40	33	12	9	0
72	ARLIN_1/T.BOEOTICUM(66	+	133	100	LB	182	33	9	14	9	0
73	D67.2/P66.270//T.BOEOTICUM(66)	+	128	108	LB	182	34	16	13	9	0
74	ARLIN_1/T.MONOCOCCUM(97)	+	140	131	LB	180	35	34	8	9	5 R
75	ARLIN_1/T.MONOCOCCUM(110)	–	133	116	LB	186	21	52	13	8	0
76	D67.2/P66.270//T. URARTU (542)	+	128	112	LB	176	42	32	13	8	5 R
77	D67.2/P66.270//T. URARTU(543)	+	124	113	LB	175	43	25	10	8	5 R
78	ARLIN_1/T. URARTU (548)	+	129	115	LB	177	44	22	8	9	5R
79	D67.2/P66.270//T. URARTU(550)	+	122	120	LB	173	46	7	13	9	0

Rust resistance. ***Greenhouse evaluation for seedling resistance.*** Different infection types were recorded in A-genome amphiploids. Among the 194 SHs tested at the seedling stage, 25 (20.83%) were classified as resistant (IT 0–3), nine (5.42%) as intermediate (IT 4-6), and 132 (79%) as susceptible (IT 7-9) (Table 26). Those showing consistently low ITs are listed in Table 25 (pp. 175-177).

Table 26. Seedling stripe rust resistance evaluation of the A-genome-based synthetic hexaploids under greenhouse conditions.

Infection type	Rating	Number of A-genome synthetic hexaploids
0–3	Resistant	25
4–6	Moderately resistant	9
7–9	Susceptible	132

Adult-plant screening. Of the 194 A-genome-based synthetic hexaploids, only 17 (12.93%) genotypes resistant at seedling stage were resistant at the adult-plant stage. These genotypes are 6, 8, 9, 11, 12, 14, 16, 19, 28, 29, 30, 31, 34, 43, 44, 49, and 57. Sixty-two (54.31%) genotypes susceptible at seedling stage were resistant at the adult-plant stage. These genotypes have the high APR needed by breeders and agronomists. Disease control is most efficient using different minor genes working independently or a group of genes working together, so that overcomming the resistance by new races of the pathogen will be difficult. Genotypes in this group are 1, 2, 3, 4, 5, 7, 10, 13, 15, 17, 18, 20, 21, 22, 23, 24, 25, 26, 27,32, 33, 34, 35, 36, 37, 38, 40,41, 42, 45, 46, 47, 18, 50,51, 52, 53, 54, 55, 56, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 77, 78, and 79. These APR in these accessions was either from their durum parents or the A-genome accessions (Table 27). These accessions provide novel durable resistance genes against new emerging races of stripe rust. They can be screened separately and used in direct crosses to enrich the A-genome of durum in bread wheat cultivars.

Table 27. Evaluation of adult-plant resistance in the A-genome-based synthetic hexaploids and their durum parents under field conditions.

Rating	Number of A-genome synthetic hexaploids
Resistant	79
Moderately resistant	11
Susceptible	31

Molecular fingerprinting. Fifty RAPD primers amplified a total of 216 polymorphic bands and 13 SSR primers produced a total of 58 polymorphic bands (Table 28). Genetic similarity calculated using Nei and Li's coefficient gave comparable values. Both similarity matrices, when clustered by UPGMA, produced major clustering differences among the genotypes.

Table 28. RAPD and SSR primers used for genetic analysis of A-genome-based synthetic hexaploid lines.

RAPD primers				
OPA-07	OP E-14	OP F-20	OP H-04	OP I-06
OPD-20	OP E-15	OP G-02	OP H-05	OP I-07
OPE-01	OP E-16	OP G-03	OP H-11	OP I-09
OPE-02	OP E-19	OP G-08	OP H-12	OP I-10
OP E-03	OP F-10	OP G-10	OP H-13	OP I-12
OP E-04	OP F-12	OP G-17	OP H-15	OP I-14
OP E-05	OP F-13	OP G-18	OP H-17	OP I-16
OP E-06	OP F-14	OP G-19	OP H-19	OP I-17
OP E-07	OP F-15	OP H-01	OP I-02	OP I-18
OP E-12	OP F-16	OP H-02	OP I-04	OP I-20
SSR primers				
Xgwm5-3A	*Xgwm47.1-2A*	*Xgwm71.2-2A*	*Xgwm162-3A*	*Xgwm249-2A*
Xgwm10-2A	*Xgwm47.2-2A*	*Xgwm95-2A*	*Xgwm265-2A*	*Xgwm501-1B*
Xgwm30-3A	*Xgwm71.1-2A*	*Xgwm122-2A*	*Xgwm296-2A*	*Xgwm155-3A*

From the RAPD and SSR analyses, the minimum genetic distance shown by genotypes was 0.3 for the RAPDs and 0 for the SSRs. The maximum genetic distance for both was 1. The average similarity matrix for the RAPDs and SSRs was 1.39 and 7.05, respectively. The two dendrograms showed clustering differences (Fig. 8, p. 179, and Fig. 9, p. 180). In the RAPDs, 79 A-genome-based SHs were clustered in three clusters, A, B, and C (Fig. 8, p. 179). Cluster A consists of five genotypes with a maximum genetic distance with each other of 15. These genotypes are 48, 63, 67, 77, and 79. Cluster B consists of 29 genotypes. Genotype 78 is highly diverse with an average genetic distance of 98% with 73 other genotypes. Genotypes 71 and 41 are exactly similar. Genotype 71 has an average genetic distance of 76% with 72 other genotypes and genotype 41 has an average genetic distance of 97% with 71 other genotypes. Genotype 26 is highly diverse with an average genetic distance of 89%. In this cluster, genotypes 23 and 39 appear to be the least diverse with genetic distance of 41% with between them. Cluster C consists of 45 genotypes. In this cluster, genotype 5 and 25 are highly diverse with an average genetic distance of 60%, and genotypes 33 and 34 appear to be the least diverse with average genetic distance of 23%

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In the SSRs (Fig. 9, p. 180), cluster A consists of 20 genotypes with a maximum genetic distance of 1. These genotypes are 2, 6, 9, 13, 17, 27, 26, 35, 40, 41, 47, 48, 51, 63, 64, 66, 73, 74, and 78. Cluster B consists of 27 genotypes. Genotype 42 is highly diverse and has an average genetic distance of 96%with two other genotypes. Highly diverse genotypes in this group are 52 and 127. Cluster C consists of 32 genotypes in which genotype 50 is highly diverse and has a genetic distance of 84% with three other genotypes. The level of genetic diversity is high among the genotypes. A few genotypes amplified bands for stripe rust resistance marker *Xgwm-501* at 195 bp/160 bp. Genotypes 11, 13, and 77 generated bands of 195 bp and genotypes 34, 35, and 36 generated bands of 160 bp. Genotypes that amplified the bands for marker *Xgwm-155* at 147 bp are 38, 65, 69, 74, and 75 (Table 29).

Table 29. Application of simple sequence repeat markers for stripe rust genes *Yr5* and *YrSp* (+ = present; – = absent).

Accession	***Yr5***	***YrSp***	**Accession**	***Yr5***	***YrSp***
11	+	–	65	–	+
13	+	–	69	–	+
34	+	–	74	–	+
35	+	–	75	–	+
36	+	–	77	+	–
38	–	+			

Resistance to rust diseases may comprise genes effective at both the seedling and adult-pant stages. The germ plasm showed a wide range of variability for disease response in both greenhouse and field tests, indicating the presence of major and minor genes. Seventeen genotypes with seedling resistance were found to be resistant at the adult-plant stage, whereas 62 genotypes, which were susceptible or intermediate as seedlings, were found to be resistant at adult plants.

We also studied different morphological parameters to select the best agronomic types. Eight genotypes proved to be best for spike length, grains/spike, and 1,000-kernel weight and can be used in wheat yield improvement programs in Pakistan.

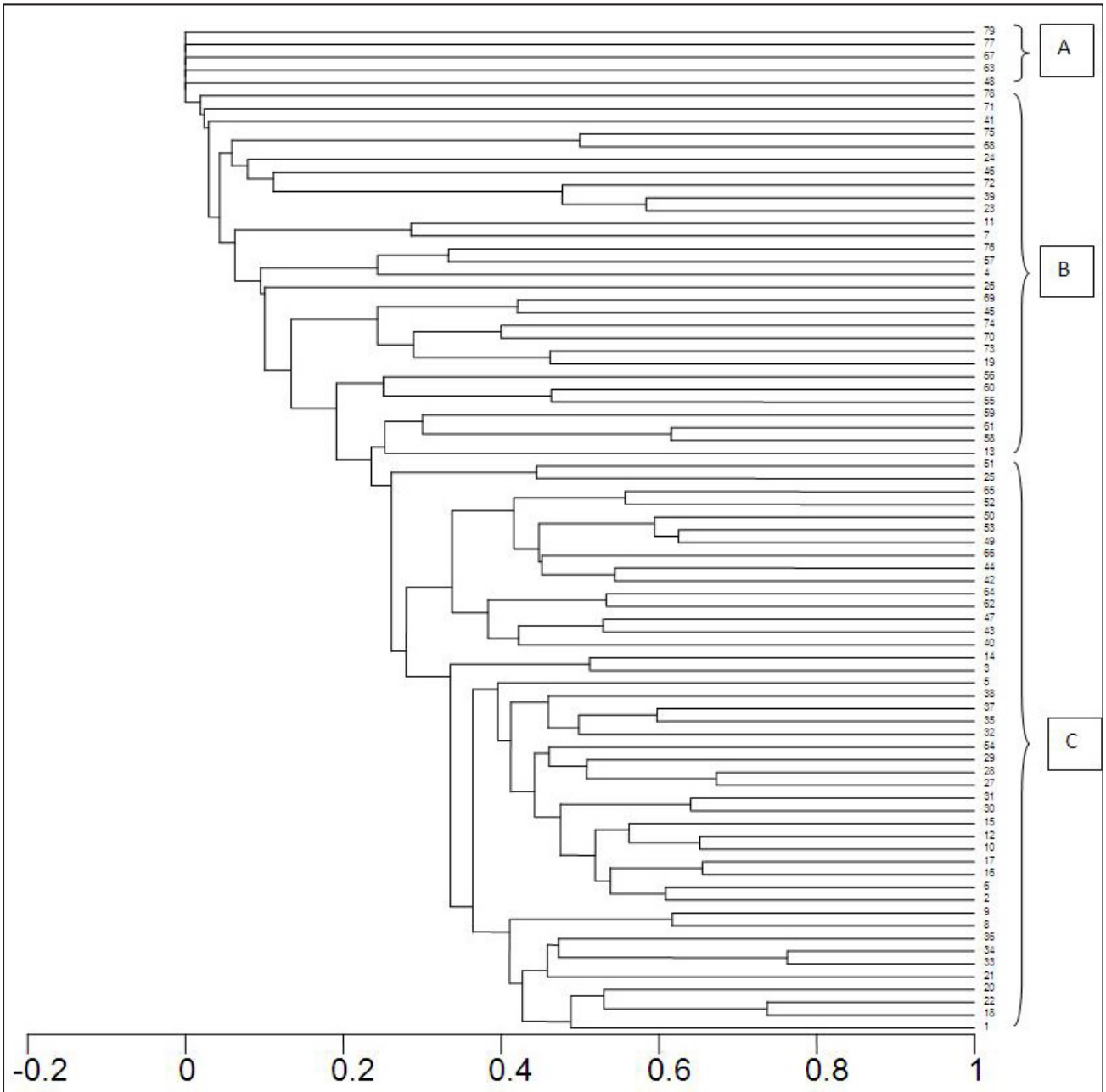

Fig. 8. Grouping of A-genome-based synthetic hexaploids (2n=6x=42; AAAABB) on the basis of genetic distance.

DNA marker technology is a powerful tool to study the genetic diversity among genotypes. In RAPD markers, the maximum number of polymorphic loci were produced by primers OPE-1 and OPE-2. In the SSR markers, the maximum number of polymorphic loci were produced by primer *Xgwm-249*. The average number of polymorphic loci produced by RAPDs is 4.32 and in SSR is 4.46.

Our study has indicated that wild wheat relatives are genetically more diverse than modern cultivars. Their traits can be incorporated into bread wheat cultivars. Among the A-genome-based SHs studies with RAPD markers, five genotypes show maximum genetic diversity of 1 and least genetic diversity of 0.3 was shown by 45 genotypes. For the SSR markers, 20 genotypes had the maximum genetic diversity of 1 and the least genetic diversity of 0 was shown by 16 genotypes. The remaining genotypes fall in between. Comparing the RAPD and SSR results, the maximum number of diverse genotypes were shown using SSR markers and the results are more reliable.

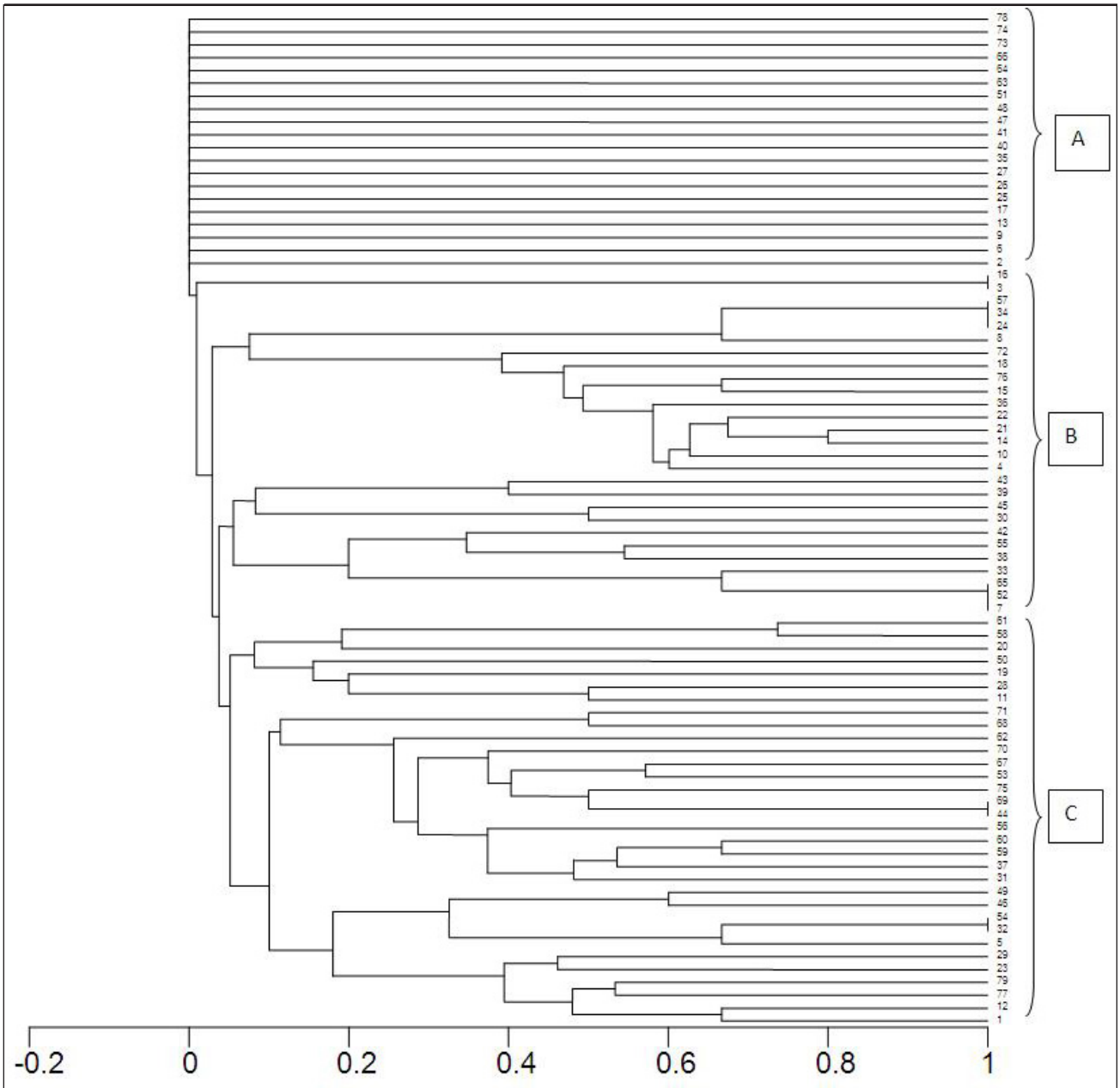

Fig. 9. Grouping of A-genome-based synthetic hexaploids (2n=6x=42; AAAABB) on the basis of genetic distance from SSR analysis.

for drought tolerance.

Muhammad Faheem, Talat Mahmood, Alvina Gul Kazi, Hafiz Asim Ayaz, and Abdul Mujeeb-Kazi.

Twenty-three drought tolerant, D-genome synthetic hexaploid wheats (Table 30, p. 181) were analyzed using 47 D-genome specific SSR primers to detect genetic diversity (Table 31, p. 181). A total of 136 alleles were detected with an average of 2.89 alleles/locus. The value of the polymorphic information content (PIC) ranged from 0 to 0.81. For phenological evaluation, the genotypes were grown under two environmental conditions; (a) in field conditions (control) with normal seasonal irrigation and (b) in rain shelters (drought stress) with only one presowing irrigation. Five plants/entry for each of the two growing conditions were used for phenolotypic evlaution. Morphological data was recorded for parameters days-to-heading, days-to-physiological maturity, plant height, awns, pubescence, spike length, number of grains/spike, and 1,000-kernel weight.

Table 30. Pedigrees of 23 genotypes of synthetic hexaploid wheats derived from durum wheat x *Ae. tauschii* cross combinations. * is the *Ae. tauschii* accession number in Wide Crosses Program working collection, CIMMYT, Mexico.

Name	Pedigree
S-1	Doy1/Ae. squarrosa (188)*
S-2	Altar 84/Ae. squarrosa (191)
S-3	D67.2/P66.270//Ae. squarrosa (213)
S-4	D67.2/P66.270//Ae. squarrosa (217)
S-5	Dverd-2/Ae. squarrosa (221)
S-6	D67.2/P66.270//Ae. squarrosa (223)
S-7	GAN/Ae. squarrosa (446)
S-8	Doy1/Ae. squarrosa (515)
S-9	68.111/RGB-U//Ward/3/FGO/4/Rabi/5/ Ae. squarrosa (629)
S-10	D67.2/P66.270//Ae. squarrosa (257)
S-11	Scot/Mexi_1//Ae. squarrosa (314)
S-12	Croc_1/Ae. squarrosa (507)
S-13	Croc_1/Ae. squarrosa (444)
S-14	Altar84/Ae. squarrosa (502)
S-15	Doy1/Ae. squarrosa (526)
S-16	Ceta/Ae. squarrosa (1024)
S-17	Dverd_2/Ae. squarrosa (1027)
S-18	Doy1/Ae. squarrosa (1018)
S-19	Ceta/Ae. squarrosa (1026)
S-20	Doy1/Ae. squarrosa (1026)
S-21	Doy1/Ae. squarrosa (1029)
S-22	Ceta/Ae. squarrosa (1031)
S-23	Dverd_2/Ae. squarrosa (1031)

Table 31. Microsatellite primers used for PCR amplification of alleles at 47 loci.

Locus	PIC	Locus	PIC
Xgwm2-3D	0.81	*Xgwm271-5D*	0.50
Xgwm3-3D	0.38	*Xgwm295-7D*	0.54
Xgwm16-5D	0.33	*Xgwm296-2D*	0.22
Xgwm30-2D	0.62	*Xgwm314-3D*	0.67
Xgwm33-1D	0.72	*Xgwm325-6D*	0.09
Xgwm37-7D	0.00	*Xgwm337-1D*	0.42
Xgwm52-3D	0.50	*Xgwm341-3D*	0.75
Xgwm55-6D	0.00	*Xgwm349-2D*	0.00
Xgwm102-2D	0.59	*Xgwm350-7D*	0.66
Xgwm106-1D	0.20	*Xgwm358-5D*	0.73
Xgwm111-7D	0.70	*Xgwm383-3D*	0.50
Xgwm157-2D	0.33	*Xgwm455-2D*	0.67
Xgwm161-3D	0.00	*Xgwm458-1D*	0.00
Xgwm165-4D	0.50	*Xgwm469-6D*	0.35
Xgwm182-5D	0.00	*Xgwm484-2D*	0.42
Xgwm183-3D	0.49	*Xgwm497-3D*	0.00
Xgwm192-5D	0.49	*Xgwm515-2D*	0.46
Xgwm194-4D	0.49	*Xgwm539-2D*	0.60
Xgwm205-5D	0.00	*Xgwm565-5D*	0.73
Xgwm210-2D	0.00	*Xgwm583-5D*	0.66
Xgwm212-5D	0.62	*Xgwm608-2D*	0.40
Xgwm232-1D	0.00	*Xgwm635-7D*	0.00
Xgwm249-2D	0.37	*Xgwm642-4D*	0.25
Xgwm261-2D	0.00		

We used 23 SH genotypes with drought tolerance to characterize and evaluate the genetic diversity by means of morphological and molecular parameters for drought tolerance. We assumed that the variation observed in the morphological parameters was due to water inavailability and not to any other factor, such as high temperature. Awns were present in all genotypes, which is considered a drought-tolerance trait because it increases the net rate of photosynthesis of the spike and causes a considerable increase in yield under conditions of limited water supply (Evans et al. 1972). Pubescence also is considered a trait that enables moisture retention due to its hairy nature. Pubescence on the spike glumes also is known to contribute towards water stress tolerance (Erdei et al. 1990). Breeders select drought-tolerant material based on pubescence. Most of the SH wheats used in this study were pubescent on the outer side of the glume.

Table 32. Basic statistic parameters for morphological traits in genotypes from control (C.) and drought stress (DS) conditions. ** indicated significance at p = 0.01.

Trait	Conditions	Mean	S.E.	CV (%)	t-Value
Days-to-heading	Control	140.87	1.51	5.15	36.46 **
	Drought	83.13	0.29	1.7	
Days-to-phyisological maturity	Control	175.61	1.1	3.01	45.12**
	Drought	112.65	0.6	2.56	
Plant height (cm)	Control	125.4	3.11	11.91	13.6**
	Drought	80.29	1.85	11.05	
Spike length (cm)	Control	12.5	0.35	13.45	14.89**
	Drought	6.46	0.21	15.61	
Grains/spike	Control	32.8	3.05	44.64	5.57**
	Drought	15.45	0.67	20.92	
1,000-kernel weight	Control	43.6	2.1	23.2	3.9**
	Drought	33.15	1.07	15.57	

In Table 32, the t-values indicate that highly significant differ-

ences were present between the means of all parameters of the two treatments. Average spike length under control conditions was significantly different from the mean value in drought-stress conditions. Similarly, the number of grains/spike in the control was double that in drought stress. Ehdaie and Waines (1996) reported that drought stress at grain-filling reduces yield dramatically. Significant differences in means also were observed for 1,000-kernel weight, suggesting that drought also affects this trait. The effect of drought on these characteristics also were reported by Dencic et al. (2000) and Blum (1993). Our results show that despite the low yield of SH wheats in extremely water limited conditions, they were able to survive in conditions that are lethal for most other wheat genotypes. On the other hand, the mean values for plant height, spike length, number of grains/spike, and 1,000-kernel weight were found to be higher than the mean values for these parameters in Nesser, the check cultivar in the experiment. Among the genotypes studied, S-5 and S-21 were found to be the best phenotypically. They performed well in water-stressed conditions, suggesting that these SH wheats have the diversity to perform well under drought conditions. These lines will provide an efficient source to enrich and improve the wheat germ plasm by exploiting the variation present in the D genome.

For molecular characterization, 47 D-genome-specific microsatellite markers for 47 loci were used. A total of 136 loci were detected. Some allelic variation also was observed for some loci . The number of alleles/locus ranged from one for *Xgwm*37-1D, *Xgwm55-6D, Xgwm161-3D, Xgwm182-5D, Xgwm205-5D, Xgwm210-2D, Xgwm232-1D, Xgwm261-2D, Xgwm349-2D, Xgwm458-1D, Xgwm497-3D*, and *Xgwm635-7D* to seven for *Xgwm2-3D*. The average number of alleles/locus was 2.89.

The average PIC value for these primers was 0.38, ranging from zero to 0.81 (Table 31, p. 181). No polymorphism was observed for the primers having a zero PIC value, whereas primer *Xgwm2-3D* showed the maximum polymorphism with a maximum PIC value.

To estimate the genetic diversity and relatedness among the 23 genotypes, SSR amplification data was used to generate a similarity matrix. The similarity coefficient value of these genotypes ranged from 0.114 to 0.795. A minimum similarity of 11.40% was for S-2 with S-18. The genotypes with maximum similarity were S-15 and S-16. Das et al. (2007) also reported that the similarity coefficient among drought-tolerant synthetic and conventional wheat ranged between 0.16 and 0.79.

The genetic distances among 23 SH genotypes were used to construct a dendrogram for determining grouping among these genotypes on the basis of similarities and differences. These genotypes were grouped in two main clusters (Fig. 10). Cluster A had nine genotypes. Genotypes S-21, S-11, S-20, S-19, S-12, and S-10 clustered together in group AI (Fig. 10, p. 184). Genoptyes S-2, S-3, and S-18 formed cluster AII. Except for S-1, which was found to be the most diverse genotype of cluster B, the other remaining 13 genotypes formed two groups. Genotypes S-4, S-5, S-6, S-13, and S-14 were clustered in group BI and S-7, S-8, S-9, S-15, S-16, S-17, S-22, and S-23 formed the BII cluster (Fig. 10). Morphological evaluation showed that S-1 had the highest mean values for the number of grains/spike (40.6) and 1,000-kernel weight (60.60 g) in the control environment compared to the other genotypes. Under drought

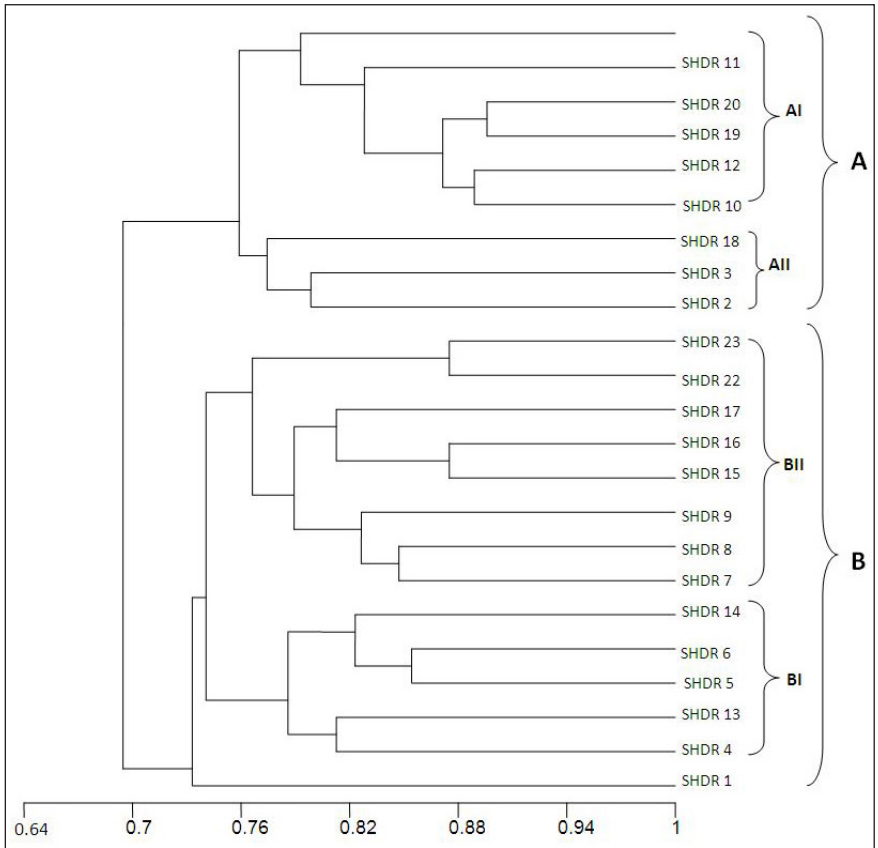

Fig. 10. SSR-based cluster formation of 23 genotypes of synthetic hexaploid wheats.

stress, however. the mean values for grains/spike was 16.7 and 1,000-kernel weight was 24.6 g, which clearly indicates the effect of drought on the yield components. A plant height 136.4 cm was observed in the control conditions, which was reduced to 76 cm under water stress. The same trend was observed for spike length.

These findings demonstrate the substantial amount of genetic diversity of D genome in SH wheats, which possess novel genes for tolerance against abiotic stresses such as drought (Damaina et al. 1992). The unique drought-tolerance genes present in these SH wheats have made them ideal germ plasm for incorporating useful genes into elite Pakistani cultivars.

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Molecular and morphological evaluation of diversity for drought tolerance in a D-genome-based, double-haploid mapping population, its parents, and local drought-tolerant cultivars of wheat using SSRs.

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A morphological and molecular diversity analysis using SSRs, for 20 D-genome-based, double-haploid (DH) plants from mapping population (158 DH plants); the parent lines, Opata M-85 (drought susceptible, 2n=6x=42) and a synthetic hexaploid (SH-257, 2n=6x=42, drought tolerant); and the local drought-tolerant cultivars Nesser, Zarghoon, and Margalla, was conducted in the Wheat Wide Crosses (WWC) Program at the National Agriculture Research Centre (NARC), Islamabad, Pakistan. For SSR statistical analysis, unweighted pair group of arithmetic mean (UPGMA) function (Nei and Li 1979) was used to estimate genetic distance among the genotypes. Fifty-nine SSR (Table 33) primers yielded a total of 177

Table 33. SSR primers used for genetic analysis of 20 D-genome-based, double-haploid (DH) plants from mapping population (158 DH plants); the parent lines, Opata M-85 (drought susceptible, 2n=6x=42) and a synthetic hexaploid (SH-257, 2n=6x=42, drought tolerant); and the local drought-tolerant cultivars Nesser, Zarghoon, and Margalla.

#	Locus/primer	#	Locus/primer	#	Locus/primer
1	*Xgwm 2-3D*	21	*Xgwm194-4D*	41	*Xgwm358-5D*
2	*Xgwm3-3D*	22	*Xgwm205-5D*	42	*Xgwm383-3D*
3	*Xgwm16-5D*	23	*Xgwm210-2D*	43	*Xgwm428-7D*
4	*Xgwm30-2D*	24	*Xgwm212-5D*	44	*Xgwm437-7D*
5	*Xgwm33-1D*	25	*Xgwm232-1D*	45	*Xgwm455-2D*
6	*Xgwm37-7D*	26	*Xgwm249-2D*	46	*Xgwm456-3D*
7	*Xgwm52-3D*	27	*Xgwm261-2D*	47	*Xgwm458-1D*
8	*Xgwm55-6D*	28	*Xgwm269-5D*	48	*Xgwm497-3D*
9	*Xgwm71-3D*	29	*Xgwm271-5D*	49	*Xgwm539-2D*
10	*Xgwm102-2D*	30	*Xgwm272-5D*	50	*Xgwm565-5D*
11	*Xgwm111-7D*	31	*Xgwm292-5D*	51	*Xgwm583-5D*
12	*Xgwm121-7D*	32	*Xgwm295-7D*	52	*Xgwm608-2D*
13	*Xgwm157-2D*	33	*Xgwm296-2D*	53	*Xgwm608-4D*
14	*Xgwm161-3D*	34	*Xgwm314-3D*	54	*Xgwm624-4D*
15	*Xgwm165-4D*	35	*Xgwm320-2D*	55	*Xgwm635-7D*
16	*Xgwm174-5D*	36	*Xgwm325-6D*	56	*Xgwm642-1D*
17	*Xgwm182-5D*	37	*Xgwm337-1D*	57	*Xgwm645-3D*
18	*Xgwm183-3D*	38	*Xgwm341-3D*	58	*Xgwm654-5D*
19	*Xgwm190-5D*	39	*Xgwm349-2D*	59	*Xgwm664-3D*
20	*Xgwm192-5D*	40	*Xgwm350-7D*		

polymorphic bands in sizes ranging from 50–900 bp. The dendrogram demonstrated that the genotypes from the mapping population were genetically distinct from the local drought-tolerant cultivars and the parent lines Opata M-85 and SH-257. The seven best DHs with ample genetic distance were 2 (85.80%), 9 and 15 (74.19%), 18 and 20 (66.67%), 1 (63.00%), and 14 (62.31%). The genetic distance of these DHs was nearly similar or better than that of SH-257 (65.20%). Genetic distance of the local drought-tolerant cultivars were Nesser (42.17%), Margalla-99 (42.17%), and Zarghoon (58.49%), all less than SH-257 (65.20%). Opata M-85, with genetic distance of 83.49%, was distinct from SH-256 and the mapping population.

Under stress, good variability for morphological characters was observed in DHs 2, 6, 9, 14, 18, and 19. Doubled haploids 1, 2, 9, 14, 18, and 20, with good morphological and molecular diversity, are recommended for wheat yield improvement programs in Pakistan (Table 34). Overall, the DH mapping population depicted a good deal of genetic diversity for drought tolerance over the local/elite drought-tolerant cultivars because of the D-genome in the synthetic parent SH-257. These results suggest that using SH wheat is an efficient way to enrich the genetic background of wheat, especially with the genetic variation of the D genome from *Ae. tauschii*. The results also demonstrate the utility of microsatellite markers in detecting DNA polymorphism and estimating genetic diversity.

Evaluating genetic diversity. The 59 SSR primers yielded a total of 177 polymorphic bands ranging from 50–900 bp. The highest number of scorable bands was obtained with primer *Xgwm174-5D* (40) and the lowest with primer *Xgwm2-3D* (2). Maximum genotypes (19) were amplified by both primers *Xgwm261-2D* and *Xgwm271-5D* and minimum (1) by *Xgwm2-3D*. Different primers varied in their ability to detect polymorphism. Primers *Xgwm232-1D* and *Xgwm349-2D* showed highest polymorphism with five polymorphic bands each.

Table 34. Comparative morphological data (mean values) of mapping population entries under control (irrigated) and stress (rain-sheltered) conditions. For growth habit, a + indicates a prostrate habit; for pubescence, a + indicates hariness; for awn color, AW = amber white and LY = light yellow.

DH no.	Plant height (cm)		Days-to-flowering		Days-to-maturity		Awn length (cm)		Spike length (cm)		Grains/spike		1,000-kernel weight (g)		Growth habit		Pubsence		Awn color	
	Control	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress
2	125	62.5	112	84	165	122	8.2	6.6	11.7	4.5	42	19	49.0	24.6	–	–	–	–	AW	AW
4	128	72.5	117	75	163	121	8.5	8.8	13.0	7.0	28	10	48.0	19.6	–	–	–	–	AW	AW
14	116	69.0	117	75	169	120	8.8	6.5	12.3	5.5	60	14	37.4	22.5	–	–	–	–	LY	LY
41	132	87.0	118	77	167	118	9.5	7.0	11.5	6.0	68	17	51.0	34.1	–	–	–	–	AW	AW
52	122	57.0	117	75	163	114	7.7	5.5	15.8	6.0	46	12	47.3	28.2	–	–	–	–	LY	LY
61	135	79.0	119	85	163	116	10.2	7.7	15.7	5.5	50	28	45.1	31.6	–	–	–	–	AW	AW
68	116	72.5	119	84	163	123	6.7	6.3	11.0	5.5	32	15	27.3	38.9	–	–	–	–	LY	LY
73	112	67.0	118	77	161	119	8.3	6.5	10.3	5.0	56	11	39.0	30.5	–	–	+	+	LB	LB
74	138	68.0	119	79	161	118	10.2	8.9	11.6	4.5	42	11	49.5	39.3	–	–	–	–	AW	AW
76	127	63.0	113	84	171	114	4.6	4.3	11.1	4.5	24	15	39.5	38.4	–	–	–	–	LY	LY
78	129	79.0	113	77	162	116	8.8	5.6	12.7	5.0	49	12	42.0	32.0	–	–	–	–	AW	AW
80	149	65.0	112	77	166	125	7.6	8.0	11.1	4.0	27	10	38.7	23.6	–	–	–	–	LY	LY
81	110	67.0	114	75	166	113	7.3	7.2	10.3	5.0	45	12	38.1	21.0	–	–	–	–	LY	LY
114	119	77.0	121	86	176	119	8.3	6.4	11.3	7.0	50	19	30.0	29.8	–	–	–	–	AW	AW
117	140	66.0	124	86	176	118	7.2	7.3	10.7	6.0	43	19	44.0	30.3	–	–	–	–	LY	LY
123	120	75.0	125	88	171	120	8.7	6.0	11.1	6.0	39	11	39.0	18.4	–	–	–	–	LY	LY
127	121	67.0	117	104	165	117	8.6	4.5	12.1	5.0	48	11	34.2	21.5	–	–	–	–	AW	AW
144	111	51.0	113	77	173	115	9.5	6.5	11.0	4.0	47	8	38.4	29.6	–	–	–	–	AW	AW
145	125	72.0	114	73	173	114	7.5	4.7	12.8	5.0	46	6	33.0	19.7	–	–	–	–	AW	AW
148	107	71.0	119	77	163	112	8.5	7.1	12.8	6.0	38	12	24.3	23.8	–	–	–	–	AW	AW

Interpreting the similarity matrix. The SSR amplification data was used to obtain a similarity matrix. The similarity coefficient value ranged from 0 to 70%. Genotypes with 0% similarity were 1 with 2, 7, 19, and Opata M-85; 2 with 5, 6, 8, 14, 16, Nesser, Zarghoon, Margalla, and Opata M-85; 3 with 7 and Opata M-85; 4 with 7; 5 with 7; 7 with 9, 11, 16, 17, 20, Opata M-85, and SH-257; 15 with 18 and 19; 19 with 20; and SH-257 and 20 with Zarghoon. Genotypes with 70% similarity were 5 with 6. The similarity of the remaining genotypes was found to be between 0 and 70%.

Dendrogram interpretation. A dendrogram was formulated based on genetic distance was divided into two main clusters A and B (Fig. 11). Cluster B was subdivided into four subclusters, B1, B2, B3, and B4. Cluster A included five genotypes, all of which belonged to the mapping population. DH 2 had the maximum genetic distance of 85.80% from all other four genotypes of this cluster and, hence, was the most diverse. Subcluster B1 had three genotypes, where DHs 9 and 15, with a genetic distance of 74.19%, were genetically similar. Opata M-85, with a maximum genetic distance of 83.49%, was the most diverse line in this subcluster. Subcluster B2 had four genotypes, the most diverse was SH-257 with a maximum genetic distance of 65.20% with rest of the genotypes. In subcluster B3 with nine genotypes, DHs 5 and 6 were genetically similar. The most diverse DH was line 14 with a maximum genetic distance of 62.31%. The conventional, drought-tolerant cultivars Nesser and Margalla were genetically similar, whereas Zarghoon was distinct from both. In subcluster B4 with four genotypes, DH 1, with a maximum genetic distance of 63.00%, was the most diverse of the genotypes. The DHs 10 and 3 were genetically similar.

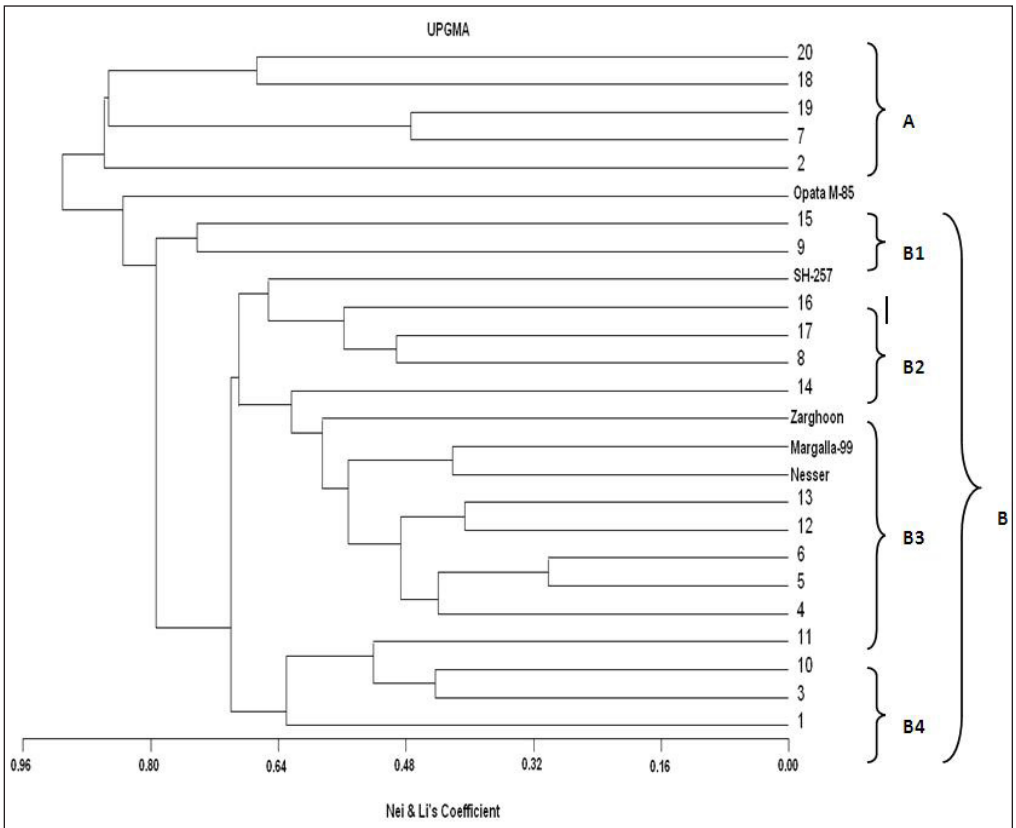

Fig. 11. Dendrogram based on genetic distance for SSR primers analysis of drought tolerance test germ plasm.

Dwarf height is a favorable character to counter lodging. For the mapping population under control conditions, the minimum plant height was 107 cm in DH 20. Under stress conditions, the minimum height was 51 cm in DH 18. The minimum height among the local, drought-tolerant cultivars was 58 cm (Nesser). The heights of Opata M-85 and SH-257 were 94 cm and 99 cm, respectively. The minimum number of days-to-flowering is a desirable character for earliness. Minimum days-to-flowering for the mapping population under control conditions was 112 days in DHs 1 and 12 and under stress condition was 73 days (DH 19). The local, drought-tolerant cultivars had minimum of 75 days (Margalla). Opata M-85 flowered in 110 days and SH-257 in 134 days. The minimum number of days-to-maturity for the mapping population under control conditions was 161 for DHs 8 and 9, whereas under stress conditions was 112 days (DH 20). The minimum number of days in the local, drought-tolerant cultivars was 109 days (Margalla) and for Opata M-85 and SH-257 were 159 and 170, respectively (see Table 35, p. 188).

For the mapping population under control conditions, maximum spike length was 15.8 cm in DH 5 and 7 cm in DHs 2 and 14 under stress conditions. The minimum spike length of the local, drought-tolerant cultivars was 5.5 cm (Nesser). The maximum number of grains/spike was 68 in DH 4 under control conditions and 28 for DH 6 under stress conditions. The maximum grains/spike of the local, drought-tolerant cultivars was 23 (Margalla). For Opata M-85 and

Table 35. Morphological data (mean values) of the parents of a double-haploid mapping population, Opata M-85 (drought susceptible, 2n=6x=42) and a synthetic hexaploid (SH-257, 2n=6x=42, drought tolerant); and the local drought-tolerant cultivars Nesser, Zarghoon, and Margalla. For growth habit, a + indicates a prostrate habit; for awn color, AW = amber white and LY = light yellow.

Trait	Nesser	Zarghoon	Margalla	Opata M-85	SH-257
Height (cm)	58.0	76.5	73.5	94.0	99.0
Days-to-flowering	82	91	75	110	134
Days-to-physiological maturity	112	113	109	159	170
Awn length (cm)	7.0	3.2	4.0	6.4	8.0
Spike length (cm)	5.5	6.0	6.0	19.5	10.0
Grains/spike	12	20	23	28	10
1,000-kernel weight (g)	34.8	37.8	29.3	23.5	49.0
Growth habit	–	–	–	–	–
Pubescence	–	–	–	+	–
Awn color	AW	AW	AW	LY	AW

SH-257, grains/spike were 28 and 10, respectively. The maximum 1,000-kernel weight in the mapping population under control conditions was 49.5 g for DH 9 and under stress conditions was 39.3 g for DH 9. Maximum 1,000-kernel weight for the local, drought-tolerant cultivars was 37.8 g (Zarghoon), 23.5 g for Opata M-85, and 49.0 g for SH-257.

Observing this phenotypic data, we established that the mapping populaiton had better morphological characters than modern wheat cultivars because of D genome of synthetic parent (SH-257). Morphological analysis of the mapping populaiton under control conditions showed that DHs 1, 4, 5, 8, 9, 12 and 20 were the most diverse for the different morphological traits. Under stress conditions, DHs with good variability were 2, 6, 9, 14, 18, and 19. The seven best DHs from the mapping population with high molecular diversity were 2 (85.80%), 9 and 15 (74.19%), 18 and 20 (66.67%), 1 (63.00%), and 14 (62.31%). The genetic distance of these DHs were nearly similar or better than the genetic distance of the SH-257 (65.20%) parent. The genetic distance of the local, drought-tolerant cultivars Nesser (42.17%), Margalla-99 (42.17%), and Zarghoon (58.49%) were less than that for SH-257. Finally, we recommend DHs 2, 9, 14, and 18, with good morphological and molecular diversity, for wheat yield improvement programs in Pakistan.

The dendrogram generated from SSR data revealed that seven DHs of the mapping population have significant molecular diversity; 2 (85.80%), 9 and 15 (74.19%), 18 and 20 (66.67%), 1 (63.00%), and 14 (62.31%). The genetic distance of these DH lines was similar or better than that of SH-257 (65.20%). The genetic distance of the local, drought-tolerant cultivars Nesser (42.17%), Margalla-99 (42.17%), and Zarghoon (58.49%) was less than that of SH-257. This data establishes that the mapping population was better morphological than modern wheat cultivars and the synthetic parent. Morphological analysis under control conditions showed that DHs 1, 4, 5, 8, 9, 12, and 20 were diverse for the different morphological traits. Under stress, DHs 2, 6, 9, 14, 18, and 19 were the best.

Finally, DHs 2, 9, 14, and 18, with good morphological and molecular diversity, are recommended for wheat yield improvement programs in Pakistan. Overall, the primary and derived synthetic wheats analyzed in this study showed mmore genetic diversity for drought tolerance than the local/elite, drought-tolerant cultivars because of D genome of synthetic parent (SH-257).

Evaluating wheat germ plasm for salt tolerance.

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Various approaches to improve the salt tolerance of wheat, such as the introduction of new salt-tolerant gene/s, screening of large germ plasm/cultivar collections, conventional breeding, and nonconventional crossing with wheat relatives, have been used. The ultimate aim is to exploit the salt-tolerance variation within wheat and its progenitors or close relatives to produce new wheat cultivars with greater tolerance. Success has been achieved in finding tolerant wheat germ plasm by screening the large number of international wheat collections.

Physiological approaches, based on the mechanisms of salt tolerance using physiological traits to select germ plasm with low sodium uptake or with high selectivity for K^+ over Na^+, have successfully contributed in selecting for diversity in salt tolerance. In this study, the genetic diversity of conventional and novel (synthetic hexaploids) wheat germ plasm was assessed on the basis of K^+:Na^+ ratio, chlorophyll content, soluble sugar levels, soluble protein content, and biomass. *In vitro* experiments were conducted in growth chambers in the Plant Physiology Program of the Crop Sciences Institute (CSI) at NARC, Islamabad.

Ten-day-old seedlings were exposed to 75 mM NaCl stress in a hydroponics culture solution. The testing protocols were essentially similar to those established by Gorham et al. (1987) and Shah et al. (1987). Based on physiological parameters, genotypes Calafia, S-24, Shorawaki, Chinese Spring, Galvez S87, Cochimi, SH-13, Oasis, SH-10 from the Elite 1 SH subset (Mujeeb-Kazi 2003), and SH-12 from the SH salinity subset (Mujeeb-Kazi 2002) were found to be salt tolerant. SH-6, SH-9 (from Elite 1), Ciano, and SH-11 were semitolerant. The remaining genotypes were sensitive at the 75 mM NaCl salinity testing level (Fig. 12). The K^+:Na^+ ratio in the tolerant genotypes ranged from 3 to 6.64 and from 1.0 to 2.40 in the semitolerant. Sensitive materials had a range level from 0.23 to 0.77. Susceptibility of the international standard PDW 34 and the tolerance of Chinese Spring prove to be the valid indices for our data. Shoot biomass of the tolerant genotypes was relatively higher than that of the semitolerant and sensitive genotypes. Tolerant genotypes showed higher chlorophyll content, soluble sugar and soluble protein contents compared with semi tolerant and sensitive genotypes (Table 36). The chlorophyll content of the tolerant genotypes ranged from 13–15 mg/g D wt, 10–12.4 mg g D wt in the semi-tolerant lines, and 8.3–9.0 mg/g D wt in the sensitive genotypes. The soluble sugar content in tolerant genotypes ranged from 24 to 30 mg/g F wt, 19–23 mg/g F wt for the semitolerant genotypes, and 13.3–19.0 mg/g F wt for the susceptible genotypes. Soluble protein content in the tolerant genotypes ranged from 1.5 to 1.96 mg g F wt, 1.27–1.4 F wt in the semitolerant, and 0.67–1.19 F wt in the sensitive lines.

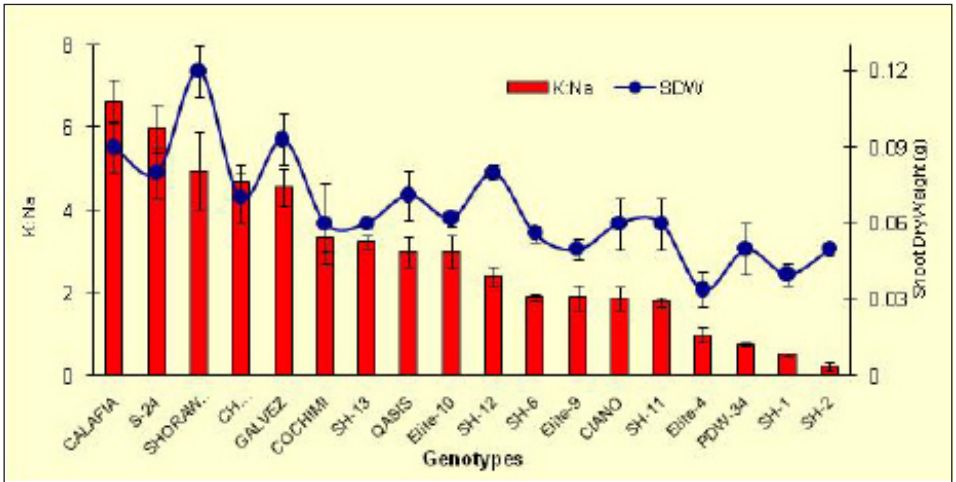

Fig. 12. K^+:Na^+ ratio and shoot dry weight (SDW) of wheat genotypes at 75 mM NaCl stress. Each bar represents the mean value of ten plants with standard error of mean.

Table 36. Chlorophyll, soluble sugar, and soluble protein content of wheat genotypes at 75 mM NaCl stress. The data represents the mean value of ten plants with standard error of mean. Values followed by the same letter (s) are not significantly different at $P < 0.05$ according to the DNMRT test.

Cultivar	Chlorophyll (mg/g D wt)	Soluble sugar (mg/g F wt)	Soluble protein (mg/g F wt)
Calafia	15±0.53 a	30±2.4 a	1.83±0.07 ab
S-24	14±0.7 a	28±3 ab	1.77±0.11 abc
Shorawaki	14±0.3 a	28±1.5 ab	1.96±0.21 a
Chinese Spring	14.5±2.4 a	24±3.4 abc	1.77±0.38 abc
Galvez	14±1.7 a	24±3.2 abc	1.75±0.15 abc
Cochimi	13±0.6 abc	25±1.1abc	1.59±0.17 abcd
SH-13	14±1.3 a	26±3.2 abc	1.7±0.17 abc
Oasis	13.8±0.5 a	23±2.6 abcd	1.60±0.48 abc
Elite-10	13.2±1 ab	24±2 abc	1.5±0.3 abcde
SH-12	13.3±1.7 ab	24±3 abc	1.54±0.10 abcd
SH-6	12±1.5 abc	20±2.9 bcde	1.4±0.18 bcdef
Elite-9	12.4±1.2 abc	22±1.6 abcd	1.27±0.08 cdef
Ciano	11.5±0.28 abc	23±3.2 abcd	1.38±0.10 bcdef
SH-11	10±2 bc	20±2.9 bcde	1.31±0.08 bcdef
Elite-4	9±2.2 c	19±2.5 cde	0.67±0.07 c
PDW-34	8.3±0.4 c	17.8±3.4 cde	1.19±0.06 def
SH-1	8.5±0.5 c	13.7±1.6 e	0.89±0.09 efg
SH-2	9±0.8 bc	13.3±1.2 e	1.04±0.15 e

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New sources of salt tolerance identified in wheat landraces evaluated at different growth stages and environments.

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Introduction. Salt stress is one of the major factors affecting wheat productivity in arid and semiarid regions of the world, including Pakistan. Breeding for salt-tolerant crops has been neglected over the years with few efforts to breed salt-tolerant wheat. The lack of interest by plant breeders mainly is due to complex nature of salt tolerance and its high level of dependence on environmental factors. This project was designed to identify new sources of salt tolerance in wheat by tapping in unexplored landrace collections maintained at Gene Bank of Plant Genetic Resources Program of the NARC. This collection consists of landraces collected from the salt- and drought-prone areas of Pakistan Pakistan and other parts of the world, including Syria, Iran, and Egypt. About 200 landraces were tested at germination, seedling, and maturity under different salt-stress regimes (from 200 to 300 mM salt stess). Some check cultivars with known salt tolerance also were used. The genotypes were tested for two years at germination stage under laboratory conditions at 200, 250, and 300 mM stress, and hydroponically at the vegetative stage in at 200 and 250 mM salt stress. The same set of genotypes also was tested at three locations for two years in salt-affected field conditions with variable stress levels (from moderate to high stress).

2007–08 season. About 200 wheat accessions, including some known salt-tolerant genotypes, were collected and analyzed in the laboratory for their germination at 200 mM salt stress during 2007–08. The same 200 lines also were tested in hydroponic cultures in the vegetative stage at 200 mM salt stress. A salt-tolerance trait index (STTI) for the germination and vegetative stages was calculated by the formula:

$$\text{STTI} = \frac{\text{Value of each trait under stress condition}}{\text{Value under controlled condition}} \times 100$$

Salt-tolerance index (STI) was calculated as the mean of salt-tolerance trait indices (STTIs).

The accessions were tested at reproductive stage at three locations in salt-affected areas at the Soil Salinity Research Institute, Pindi Bhattian District, Hafizabad; the Postgraduate Agriculture Research Station (PARS). and the Biosaline Agriculture Research Station, Pacca Anna, Faisalabad. The genotypes behaved differently at different growth stages. The wheat lines that performed better under different growth-stage testing were 10756 10783, 10790, 10793, 10800, 10806, 10807, 10810, 10812, 10821, 10824, 10828, 10831, 10833, 10841, 10850, 10851, 10859, 11186, 11214, 11287, 11299, 11383, 11385, 11401, 11409, 11417, 11453, 11454, 11460, 11466, 11478, 11526, 11545, 11898, 11907, 11909, 11915, 11917, 11922, 11925, 4098775, 4098805, SARC IV, and SARC VII.

2008–09 season. The selected wheat lines again were tested at germination (250 and 300 mM salt stress), hydroponically (250 mM salt stress), and in two salinity hot spots in the field at the Soil Salinity Research Institute Farm and the Biosaline Research Station during 2008–09. Overall, 21 lines gave good results, including 10756, 10783, 10807, 10833, 10851, 11186, 11299, 11383, 11454, 11460, 11466, 11545, 11898, 11907, 11915, 11917, 4098805, SARC IV, SARC VII, the local white cultivar, and Pasban 90. Pasban 90 is the national salt-tolerance standard and a derivative of *Th.*

distichum (Inia/*Th. distichum*//Inia/3/Genaro). A few accessions also survived the 300 mM stress at germination stage including 11299, 11466, 11907, 11460, 11915, 11454, and 11383. The selected germ plasm will enter our recombination breeding program after determining its diversity status.

Phenotypic characterization and SSR-based diversity estimates of conventional and novel wheat germ plasm with salinity tolerance.

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Genetic diversity of 32 genotypes, consisting of both conventional and novel (synthetic hexaploid) wheat germ plasm, was assessed using SSR primers. The material also was evaluated for its salt-tolerance potential and phenotype. The average K^+/Na^+ value for conventional germ plasm was 3.20 and 1.24 for synthetic hexaploids. Genotypes Calafia, Lu26 S, Chinese Spring, Shorawaki, Galvez S 87, Kharchia 65, and SH-13 were found to be the most tolerant to salinity. Based on phenotypic parameters and yield attributes, Kharchia 65, LU26 S, Mepuchi, Oasis F 86, PBW-343, Calafia, and Pericu showed good performance for days-to-heading, days-to-physiological maturity, plant height, grains/spike, and grain weight. On the other hand, genotypes SH-3, SH-5, SH-7, SH-8, and SH-12 had the highest 1,000-kernel weight and a higher number of grains/spike. Ninety SSR primers specific for the A, B, and D genomes were used to estimate genetic diversity of germ plasm. A total of 347 polymorphic loci was obtained with an average of 3.86 loci/primer. The average similarity coefficient for conventional germ plasm was 0.419 and 0.399 for the synthetics. Conventional genotypes showed a high level of tolerance and the synthetics showed higher genetic diversity. The results suggested that along with salt tolerance, ample genetic diversity is available in both types of germ plasm, especially in synthetic hexaploids, which can be exploited in wheat breeding programs for development of material tolerant to salinity.

Phenotypic characterization (Table 37, p. 190). All genotypes in the conventional germ plasm had an erect growth habit. Among the SHs, three genotypes had a prostrate growth habit, four were moderately prostrate, and the rest were erect. Pubescence was absent in most of the entries in both conventional genotypes and synthetics. Genotypes Sakha 8, Ciano T 79, Mepuchi, PBW 34, and Cochimi, and SH-1, SH-6, and SH-8, were pubescent. Plant height ranged from 86 to 111 cm in the conventional entries. The synthetics were taller, ranging from 83 to 156 cm. Awn color in both types of material was brown, yellow, or amber white. The majority of entries in conventional set had amber white awns; brown was most common in the synthetics. Only Chinese Spring was awnless.

The conventional entries were early heading, with days-to-heading ranging from 110 (PDW34) to 126 (LU26 S). In the synthetics, days-to-heading ranged from 119 (SH-2 and SH-6) to 144 (SH-4). Days-to-maturity ranged from 174–186 days in conventional entries with a majority of the genotypes maturing in 174–180 days. In the synthetics, maturity was from 173–189 days. Spike length ranged from 10–15 cm in conventional entries; the synthetics had longer spikes 10–17 cm. The number of spikelets/spike ranged from 19 (Kharchia 65) to 26 (Ciano T 79) in thef conventional entries and from 16 (SH-9) to 26 (SH-10 and 13) in the synthetics. The number of grains/spike ranged from 34–79 in conventional entries and 18–66 in synthetics, indicating lesser seed set. Thousand-kernel weight ranged from 21 g to 46 g for the conventional entries. The SHs showed a relatively higher grain weight ,ranging between 37.8–71.8 g. Grain color in both types of germ plasm was brown, dark brown, or light brown (Table 37, p. 190).

K^+:Na^+ Discrimination. The germ plasm was screened at 75 mM NaCl, and a high level of tolerance among the conventional germ plasm was noted (Table 37, p. 190). The average K^+/Na^+ values for the conventional material ranged from 0.96 to 6.5. All genotypes showed a K^+/Na^+ value greater than 1 except PDW 34, which was found to be salt susceptible at 75 mM with a K^+/Na^+ value of 0.96. The genotypes Calafia, LU26 S, Chinese Spring, Shorawaki, Galvez S 87, and Kharchia 65 were the most tolerant to salinity. Genotypes Cochimi, Mepuchi, Sakha 8, KRL 1-4, Oasis F 86, Pericu, and Ciano T 89 were semitolerant. All other genotypes in this group were less tolerant to NaCl salinity with K^+/Na^+ values less than 2.

Among the SHs, the K^+/Na^+ valued ranged from 0.35 to 3.08. Six genotypes had a value greater than 1 and the remaining lines were susceptible at a salinity level of 75 mM NaCl. Among the tolerant genotypes, SH-13 was the most tolerant with a K^+/Na^+ value of 3.08, followed by SH-11 (2.98). The least K^+/Na^+value in this group was 0.35, which was for SH-2.

Table 37. Pedigree, phenotypic data, and mean K^+/Na^+ values of conventional and novel wheat germ plasm. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prosrtate (–), moderately prostrate (M), or erect (+); PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; PMA = days–to–physiological maturity; HT = plant height at maturity; SL = spike length (cm); SL/S = number of spikelets/spike; G/S = number of grains/spike; TKW = 1,000–kernel weight; GC = grain color, DB = dark brown, LB = light brown, B = brown, and W = white; AWN = awn color, DB = dark brown, LB = light brown, B = brown, AW = amber white, and Y = yellow; and K/Na = average K^+/Na^+ value.

Line No.	Pedigree	GH	PUB		PMA	HT (cm)	SL (cm)	SL/S	G/S	TKW	GC	AWN	K/Na
1	Shorawaki	–	–	120	179	94.0	13.00	24	34	29.4	B	B	4.96
2	Sakha 8	–	+	112	177	103.0	14.00	20	65	39.0	DB	AW	2.95
3	WH 157	–	–	120	179	111.0	12.00	20	46	33.4	B	AW	1.93
4	Kharchia 65	–	–	114	174	93.0	13.50	19	52	40.0	LB	AW	3.75
5	LU26 S	–	–	126	186	86.0	9.60	18	46	46.0	B	Y	6.00
6	PDW 34 (susceptible durum)	–	–	110	179	102.6	15.50	22	53	34.4	LB	B	0.96
7	SNH.9	–	–	114	177	101.3	13.25	22	66	39.2	LB	AW	1.76
8	KRL 1-4	–	–	116	183	91.3	14.50	26	58	33.2	W	AW	2.79
9	Galvez S 87	–	–	116	173	95.6	13.25	25	70	29.4	LB	AW	4.50
10	Oasis F 86	–	–	125	178	89.3	15.00	24	79	32.0	DB	AW	2.76
11	Chinese Spring	–	–	123	174	120.0	10.25	23	67	24.4	B	Awn-less	5.00
12	Ciano T 79	–	+	122	183	96.0	12.75	26	72	25.2	DB	AW	2.09
13	Yecora F 70	–	–	116	182	100.6	10.50	22	45	38.6	DB	AW	1.20
14	Mepuchi	–	+	118	179	105.0	12.25	20	62	42.0	LB	AW	3.02
15	PBW 343	–	+	116	174	86.0	15.00	22	58	38.6	B	AW	1.70
16	Cochimi	–	+	118	177	90.0	11.25	20	58	21.0	B	AW	3.35
17	Calafia	–	–	123	176	99.0	13.50	23	75	41.8	LB	AW	6.50
18	KRL-19	–	–	122	174	99.6	13.25	21	47	31.6	DB	AW	1.38
19	Pericu	–	–	120	174	90.3	13.50	24	66	39.6	B	AW	2.35
SH-1	68.111/RGB-U//WARD Re-sel/3/STIL/4/Ae.tauschii (781)	–	+	122	181	156.0	12.16	22	37	38.4	LB	B	0.52
SH-2	68.111/RGB-U//WARD/3/ FGO/4/RABI/5/Ae. tauschii (882)	–	–	119	189	115.0	12.40	24	42	45.6	B	AW	0.35
SH-3	68112/WARD//Ae. tauschii (369)	M	–	142	189	132.3	14.00	22	38	67.0	DB	B	0.93
SH-4	Altar 84/Ae. tauschii (224)	M	–	144	189	116.6	10.66	21	23	40.4	LB	AW	0.87
SH-5	Altar 84/Ae. tauschii (502)	M	–	142	186	118.0	9.16	18	19	62.0	DB	B	0.85
SH-6	Altar 84/Ae. tauschii (220)	–	+	119	173	103.0	13.67	24	42	380	B	B	1.50
SH-7	Altar 84/Ae. tauschii (211)	+	–	142	186	121.0	15.67	24	30	57.6	DB	Y	1.30
SH-8	Altar 84/Ae. tauschii (JBAN-GOR)	+	+	142	186	109.6	11.67	20	39	71.8	DB	Y	0.86
SH-9	CETA/Ae. tauschii (1027)	+	–	141	186	83.0	10.67	16	18	37.8	DB	B	0.95
SH-10	CETA/Ae. tauschii (895)	–	–	138	184	137.6	17.16	26	60	52.6	DB	DB	1.17
SH-11	CROC 1/Ae. tauschii (224)	–	–	138	186	144.6	17.16	24	66	48.2	DB	B	2.09
SH-12	D67.2/P66.270//Ae. tauschii (220)	M	–	139	186	115.3	12.33	18	22	55.2	B	B	1.37
SH-13	D67.2/P66.270//Ae. tauschii (213)	–	–	126	173	117.6	11.33	26	46	43.0	LB	AW	3.08

Considering both types of material, genotypes of the conventional set were found to be more tolerant compared to synthetics. Calafia, Chinese Spring, Shorawaki, Kharchia 65, LU26 S, SH-11, and SH-13 were amongs the best of all genotypes.

Molecular evaluation using SSR primers. A total of 90 SSR primer pairs were used for molecular evaluation of both conventional set and synthetic hexaploids. Out of 90, 55 primer pairs were specific for the D genome and used for amplification of both synthetics and conventional set entries, 20 primer pairs were specific for the B genome, and 15 were specific for the A genome. The primers of A and B genome were used for the tester set only.

The SSR primers used for molecular evaluation included *Xgwm3-3D*, *Xgwm469-6D*, *Xgwm16-5D*, *Xgwm484-2D*, *Xgwm30-2D*, *Xgwm497-3D*, *Xgwm33-1D*, *Xgwm515-2D*, *Xgwm37-7D*, *Xgwm539-2D*, *Xgwm52-3D*, *Xgwm565-5D*, *Xgwm55-6D*, *Xgwm583-5D*, *Xgwm71-3D*, *Xgwm608-2D*, *Xgwm106-1D*, *Xgwm645-3D*, *Xgwm111-7D*, *Xgwm654-5D*, *Xgwm121-5D*, *Xgwm30-3A*, *Xgwm121-7D*, *Xgwm33-1A*, *Xgwm157-2D*, *Xgwm33-1B*, *Xgwm161-3D*, *Xgwm47.1-2A*, *Xgwm165-4D*, *Xgwm47.2-2A*, *Xgwm174-5D*, *Xgwm47-2B*, *Xgwm182-5D*, *Xgwm55.1-2B*, *Xgwm183-3D*, *Xgwm55.2-2B*, *Xgwm190-5D*, *Xgwm71.1-2A*, *Xgwm192-5D*, *Xgwm71.2-2A*, *Xgwm194-4D*, *Xgwm77-3B*, *Xgwm205-5D*, *Xgwm95-2A*, *Xgwm210-2D*, *Xgwm99-1A*, *Xgwm212-5D*, *Xgwm107-4B*, *Xgwm232-1D*, *Xgwm108-3B*, *Xgwm249-2D*, *Xgwm120-2B*, *Xgwm261-2D*, *Xgwm122-2A*, *Xgwm271-5D*, *Xgwm124-1B*, *Xgwm272-5D*, *Xgwm131-1B*, *Xgwm292-5D*, *Xgwm136-1A*, *Xgwm295-7D*, *Xgwm148-2B*, *Xgwm296-2D*, *Xgwm153-1B*, *Xgwm314-3D*, *Xgwm191-2B*, *Xgwm320-2D*, *Xgwm210-2B*, *Xgwm325-6D*, *Xgwm257-2B*, *Xgwm337-1D*, *Xgwm264-1B*, *Xgwm341-3D*, *Xgwm374-2B*, *Xgwm349-2D*, *Xgwm388-2B*, *Xgwm350-7D*, *Xgwm413-1B*, *Xgwm358-5D*, *Xgwm448-2A*, *Xgwm383-3D*, *Xgwm512-2A*, *Xgwm428-7D*, *Xgwm515-2A*, *Xgwm437-7D*, *Xgwm614-2A*, *Xgwm455-2D*, *Xgwm630-2B*, *Xgwm456-3D*, and *Xgwm*666-1A.

The 90 primers yielded a total of 347 polymorphic loci in the size range of 50 to 1,000 bp out of which 264 were found for the conventional genotypes and 135 for the SHs. The average number of polymorphic loci/primer was 3.86, with a range of minimum of 2 *(Xgwm210-2D)* and a maximum of 15 (*Xgwm33-1B*). The highest number of scorable bands was obtained with primer *Xgwm565-5D* (95) and the lowest with primer *Xgwm210-2D* (1). The maximum number of genotypes (25) were amplified by primer *Xgwm565-5D* and the minimum (1) by *Xgwm210-2D*. All genotypes showed amplification with different primers. Genotype Shorawaki was amplified by the maximum number of primers, 58, and genotype SH-9 was amplified by only one primer, *Xgwm261-2D*. Shorawaki produced the maximum number of bands (85) with all 90 primers, and genotype SH-9 produced the minimum number of bands (2) with 55 D-genome primers.

Similarity coefficient. The similarity coefficient values (Nei and Li's similarity coefficient) for the conventional set ranged from 0 to 0.58. The average similarity coefficient value was 0.419, showing that the genotypes in this group were 58.1% diverse. The values for the SHs ranged from 0 to 0.727. The average similarity coefficient value for the synthetics was 0.399, indicating that these genotypes were 60.1% diverse. The average similarity coefficient value obtained from similarity matrix of all 32 genotypes was 0.418, which showed that there was 41.8% similarity among the genotypes of both groups.

Dendrograms. Dendrograms representing the clustering pattern of the 19 conventional wheat genotypes (Fig. 13) and 13 synthetic hexaploids (Fig. 14, p. 192) were obtained by cluster analysis based on genetic distances. the most distinct genotype of the conventional group was Ciano T 79, which showed an average of 92.1% difference with all other genotypes. A cluster of genotypes, LU26 S, PDW 34, SNH 9, KRL

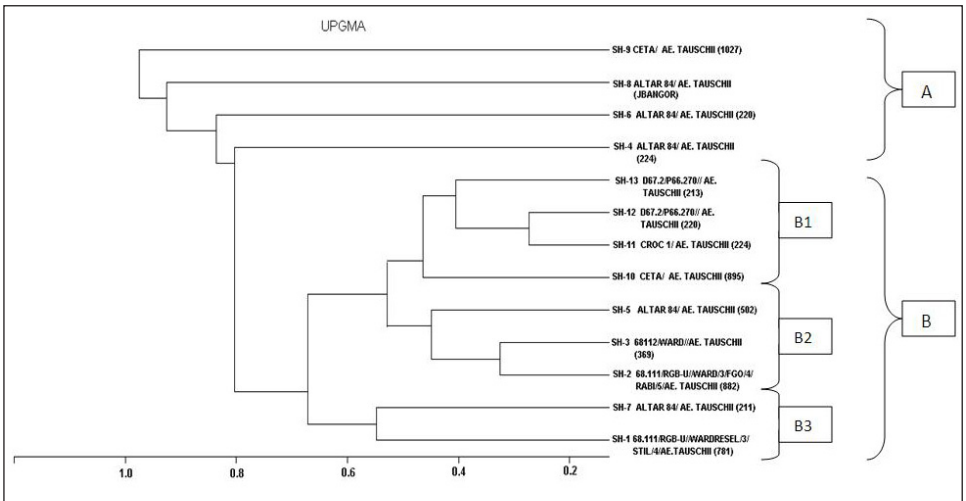

Fig. 13. Dendrogram showing clustering pattern of 19 conventional wheat genotypes based on genetic distance.

1-4, Cochimi, Yecora F 70, Mepuchi, and PBW 343, showed distinctness to another cluster consisting of KRL-19, Galvez S87, Shorawaki, Sakha 8, WH 157, Kharchia 65, Oasis F 86, Chine Spring, Calafia, and Pericu. The average distance between these two clusters was 86%.

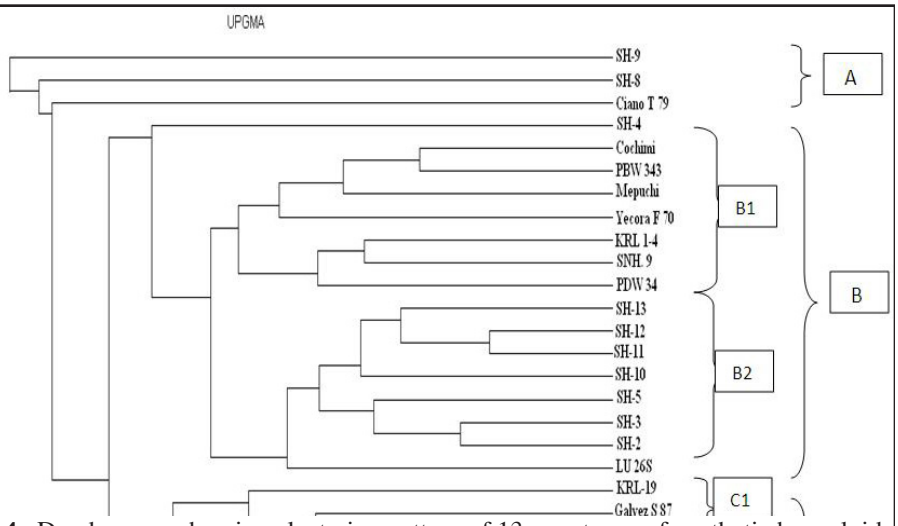

Fig. 14. Dendrogram showing clustering pattern of 13 genotypes of synthetic hexaploid wheats based on genetic distance.

Genotypes SH-9, SH-8, SH-6, and SH-4 were the most distinct among the SHs. In this group, the most diverse genotype was SH-9 with an average genetic distance of 97.5%. SH-8 showed 92.5% genetic distance with 11 other genotypes. SH-6 showed 83.6% genetic distance with ten other genotypes. SH-4 showed 80.4% genetic distance with nine other genotypes. Other genotypes of this group were comparatively less diverse, with a genetic distance ranging from 25% to 65%.

Genotypes of both the conventional and synthetic germ plasm were compared in the dendrogram involving all 32 entries (Fig. 15,). This grouping revealed that a high level of diversity exists between genotypes of conventional and synthetic material. Genotypes of both sets grouped distinctly, showing a relatively low level of diversity within the group anda high level of diversity between the groups. The most distinct genotype in this grouping was SH-9, which was 99% diverse from rest of the genotypes. Ciano T 79 also showed 92.7% diversity with a cluster of 29 other genotypes.

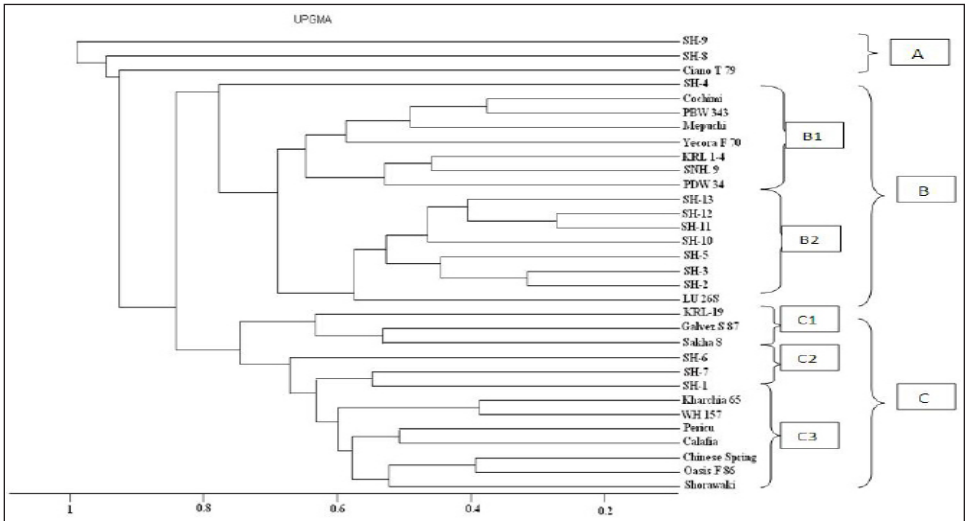

Fig. 15. Dendrogram showing clustering pattern of all 32 genotypes of conventional and synthetic germ plasm based on genetic distance.

Based on the phenotypic evaluation, Kharchia 65, LU26 S, Mepuchi, Oasis F 86, PBW 343, Calafia, and Pericu showed better performance for days-to-heading, days-to-maturity, plant height, grains/spike and grain weight. On the other hand, genotypes SH-3, SH-5, SH-7, SH-8, and SH-12 had the highest grain weight, more grains/spike, and were relatively tall.

Thousand-kernel weight is an important parameter determining yield. Based on grain weight, a genotype can be scored as high or low yielding. Synthetic hexaploid entries had a relatively high grain weight, ranging from 37.8 g to 71.8 g. The highest grain weight was in genotype SH-8. The average 1,000-kernel weight for the conventional material was 34.6 g and 50.5 g for the SH lines.

High K^+/Na^+ values indicate a high level of salt tolerance and a greater ability to exclude Na^+ and accumulate K^+ at high NaCl concentrations. Accumulating more K^+ compared to Na^+ under saline conditions is a character that deter-

mines salinity tolerance of wheat at seedling stage. K^+:Na^+ discrimination of several SHs was determined at different salinity levels. The average K^+/Na^+ value for the conventional set was 3.20 and 1.24 for the synthetics. The synthetic germ plasm deviated from previous results, where the average K^+/Na^+ value among the synthetics was 2.04, whereas that of the conventional germ plasm was 2.26. Data for PDW 34, a susceptible durum wheat, however, was within expected levels.

Analysis of the similarity matrices of both genotype groups revealed that the genetic diversity among the synthetics is greater than that of the conventional genotypes. Based on the dendrogram, Ciano T 79 and SH-9, SH-8, and SH-6 were highly diverse. The average genetic diversity was greater for the synthetics compared to the conventional genotypes. Thus, the SHs will provide a valuable genetic resource for future exploitation.

We concluded that the conventional material is a good source of tolerance to salinity compared to synthetics, however, synthetics are agronomically better with a high level of genetic diversity, which is a prerequisite for any crop-improvement program. Based on overall performance, genotypes LU 26S, Calafia, Galvez S 87, and SH-13 are recommended for their use in wheat breeding programs for the development of salinity-tolerant germ plasm.

Phenotypic evaluation and D-genome-based genetic diversity assessment of winter synthetic wheat germ plasm using SSR primers.

Uzma Hanif, Muhammad Munir, Alvina Gul Kazi, Iqbal Ayub Khan, Ghulam Shabbir, Tom Payne, and Abdul Mujeeb-Kazi.

Nonconventional plant resources for wheat improvement are present in primary, secondary and tertiary *Triticeae* gene pools and, of these, species within the primary gene pool are best for quick and practical output. One such resource is the diploid D-genome donor to bread wheat, *Ae. tauschii*. Of the three modes for utilizing this resource for wheat improvement, the one most utilized is bridge crossing. We focused on capturing the variation within the 58 new synthetic combinations that exploited high-yielding, winter durum wheats and *Ae. tauschii* accessions. The parameters analyzed were related to traits and molecular composition for diversity was differentiated by chromosome-specific SSR markers. According to the phenological data WS-11, WS-24, WS-46, WS-47, and WS-48 performed well in the field, especially for yield-enhancing characters. A cluster analysis using SSR primers revealed that WS-1, WS-24, WS-43, and WS-46 were the best lines.

Breeding and selection has resulted in the loss of a great number of alleles, causing difficulties in wheat improvement that have emerged for the modern agriculture system (Allard 1996; Hoisington et al. 1999). The narrow genetic base weakens the resistance of current wheat cultivars against biotic and abiotic stresses and threatens further advancement of wheat. Studies of synthetic hexaploid wheat developed from *T. turgidum* and *Ae. tauschii* has provided significant information on potentially useful characters in *Ae. tauschii* and/or *T. turgidum* for genetic improvement of hexaploid wheat (Mujeeb-Kazi et al. 2008).

Modern tetraploid durum wheat generally has been used to produce these new primary synthetic wheats. The primary synthetics are agronomically poor, difficult to thresh, generally tall, low yielding, and frequently have poor quality. However, they do carry useful and, often times, new variation for a range of economically important characteristics. Potentially new genetic variation among primary synthetics also has been found for tolerance to drought (Villareal et al. 1998), salinity (Gorham 1990), frost (Maes et al. 2001), heat (Yang et al. 2002), and nutrient stress (Cakmak et al. 1999).

This study is focused on capturing the variation within the 58 new synthetic combinations developed by crossing high-yielding, winter durum wheat with *Ae. tauschii* accessions. Winter SHs were developed for enhancing the diversity and to improve wheat quality and yield. These winter synthetics were grown in field after their production for their phenotypic evaluation and were then molecularly analyzed.

Phenotypic evaluation. Morphological characters of selected new winter SH wheats were assessed phenotypically (Table 38, pp. 194-196). Lines WS-11, WS-24, WS-46, WS-47, and WS-48 exhibited good morphological characters, early maturity, optimum plant height, large spike length, and higher 1,000-kernel weight.

Molecular evaluation. ***Evaluation of SSR primers for diversity estimates in winter SH lines.*** Microsatellite or inter simple sequence repeat (ISSR) markers and RAPD markers are the most polymorphic markers in wheat and are highly useful (Röder et al. 1998; Nagaoka and Ogihara 1997). In this study, SSRs were used to find genetic diversity among 58

winter synthetic wheat lines. These synthetics possess a high degree of polymorphism. The 65 D-genome-specific SSR primers were used to detect genetic diversity at DNA level in new D-genome-derived winter SHs included the following: *Xgwm2-3D, Xgwm295-7D, Xgwm3-3D, Xgwm296-2D, Xgwm16-5D, Xgwm314-3D, Xgwm30-2D, Xgwm320-2D, Xgwm33-1D, Xgwm325-6D, Xgwm37-7D, Xgwm337-1D, Xgwm52-3D, Xgwm341-3D, Xgwm55-6D, Xgwm349-2D, Xgwm71-3D, Xgwm350-7D, Xgwm102-2D, Xgwm358-5D, Xgwm106-1D, Xgwm383-3D, Xgwm111-7D, Xgwm428-7D, Xgwm121-5D, Xgwm437-7D, Xgwm121-7D, Xgwm455-2D, Xgwm157-2D, Xgwm456-3D, Xgwm161-3D, Xgwm458-1D, Xgwm165-4D, Xgwm469-6D, Xgwm174-5D, Xgwm484-2D, Xgwm182-5D, Xgwm497-3D, Xgwm183-3D, Xgwm515-2D, Xgwm190-5D, Xgwm539-2D, Xgwm192-5D, Xgwm565-5D, Xgwm194-4D, Xgwm583-5D, Xgwm205-5D, Xgwm608-2D, Xgwm210-2D, Xgwm608-4D, Xgwm212-5D, Xgwm609-4D, Xgwm232-1D, Xgwm624-4D, Xgwm249-2D, Xgwm635-7D, Xgwm261-2D, Xgwm642-4D, Xgwm269-5D, Xgwm645-3D, Xgwm271-5D, Xgwm654-5D, Xgwm272-5D, Xgwm664-3D,* and *Xgwm292-5D*.

The 65 primers yielded a total of 1,114 bands in the range of 50–1,000 bp out of which 250 were found to be polymorphic. The highest number of scorable bands (74) was obtained with primer *Xgwm*337-1D and the lowest number (1) with primer *Xgwm*437-7D. The maximum number of genotypes (36) were amplified by primer *Xgwm*608-2D and the minimum (1) by *Xgwm*437-7D, *Xgwm358-D*, and *Xgwm583-5D*. Different primers showed variation in their ability to detect polymorphism. Primer *Xgwm529-2D* and *Xgwm325-6D* showed the highest polymorphism and primers *Xgwm15-5D*, *Xgwm106-1D*, *Xgwm261-2D*, and *Xgwm320-2D* had the lowest.

WS-5 was amplified by maximum number of primers (30) whereas WS-56 was amplified by only one primer. Genotypes WS-1, WS-24, and WS-43 showed the maximum diversity. The efficiency of these primers to amplify the

Table 38. Pedigree and morphological data (mean values) of winter synthetic hexaploid wheats (2n=6x=42; AABBDD) derived from 'winter durum/*Aegilops tauschii*' cross combinations. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prosrtate (–), moderately prostrate (M), or erect (+); PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; PMA = days–to–physiological maturity; HT = plant height at maturity; #S = total number of spikes/plant; SL = spike length (cm); SL/S = number of spikelets/spike; G/S = number of grains/spike; TKW = 1,000–kernel weight; GC = grain color, DB = dark brown, LB = light brown, B = brown, and W = white; and AWN = awn color, DB = dark brown, LB = light brown, B = brown, AW = amber white, and Y = yellow.

Line No.	Pedigree	GH	PUB		PMA	HT (cm)	#S	SL (cm)	SL/S	G/S	TKW	GC	AWN
1	Aisberg/*Ae.tauschii* (221)*	+	–	159	185	77	15	12.3	19	17	28.4	LB	AW
2	Aisberg/*Ae.tauschii* (310)	+	–	149	185	87	18	13.3	19	14	39.6	B	LB
3	Aisberg/*Ae.tauschii* (369)	+	+	157	186	96	13	11.3	19	5	20.0	B	AW
4	Aisberg/*Ae.tauschii* (446)	+	–	153	186	94	20	11.6	21	3	34.0	LB	DB
5	Aisberg/*Ae.tauschii* (511)	+	–	153	185	98	20	12.0	20	14	42.2	B	AW
6	LEUC762.93/*Ae.tauschii* (409)	+	–	151	185	94	10	14.0	25	3	33.0	LB	DB
7	LEUC762.93/*Ae.tauschii* (424)	+	–	153	181	95	17	11.0	18	13	25.0	LD	AW
8	LEUC762.93/ *Ae.tauschii* (1027)	+	+	156	184	98	14	13.0	18	5	31.0	DB	LB
9	LEUC784693/*Ae.tauschii* (310)	+	–	152	178	93	7	11.0	18	2	20.0	B	LB
10	LEUC84693/*Ae.tauschii* (409)	+	+	150	189	81	10	11.6	16	13	32.0	B	B
11	LEUC84693/*Ae.tauschii* (1024)	+	–	151	183	93	11	13.6	17	3	48.0	D.B	B
12	LEUC84693/*Ae.tauschii* (1026)	+	–	156	189	83	11	14.0	19	5	33.0	LB	DB
13	UKR-OD 1169.91/*Ae.tauschii* (625)	+	–	164	191	54	1	12.0	17	4	27.0	B	LB
14	UKR-OD 1169.91/*Ae.tauschii* (1024)	+	–	154	190	67	3	11.3	15	8	29.0	B	B
15	UKR-OD 761.93/*Ae.tauschii* (191)	+	–	154	191	91	8	11.6	12	6	35.5	B	B
16	UKR-OD 761.93/*Ae.tauschii* (192)	+	+	155	188	98	15	11.6	15	3	35.0	LB	AW
17	UKR-OD 761.93/*Ae.tauschii* (219)	+	+	149	194	105	11	10.3	17	16	34.8	B	AW

Table 38 (continued). Pedigree and morphological data (mean values) of winter synthetic hexaploid wheats (2n=6x=42; AABBDD) derived from 'winter durum/*Aegilops tauschii*' cross combinations. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prosrtate (–), moderately prostrate (M), or erect (+); PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; PMA = days–to–physiological maturity; HT = plant height at maturity; #S = total number of spikes/plant; SL = spike length (cm); SL/S = number of spikelets/spike; G/S = number of grains/spike; TKW = 1,000–kernel weight; GC = grain color, DB = dark brown, LB = light brown, B = brown, and W = white; and AWN = awn color, DB = dark brown, LB = light brown, B = brown, AW = amber white, and Y = yellow.

Line No.	Pedigree	GH	PUB	FLOW	PMA	HT (cm)	#S	SL (cm)	SL/S	G/S	TKW	GC	AWN
18	UKR-OD 761.93/*Ae.tauschii* (392)	+	–	150	182	100	15	13.0	21	7	24.5	LB	AW
19	UK- OD 1704.94/*Ae.tauschii* (1031)	+	–	169	193	60	6	11.0	13	M	—	—	DB
20	UKR-OD 1704.94/*Ae.tauschii* (213)	+	+	154	185	100	18	11.0	17	9	33.6	B	AW
21	UKR-OD 1704.94/*Ae.tauschii* (217)	+	+	153	192	93	10	12.7	21	4	31.3	LB	AW
22	UKR-OD 1704.94/*Ae.tauschii* (369)	+	–	154	194	98	12	11.6	19	7	24.5	B	LB
23	UKR-OD 1704.94/*Ae.tauschii* (511)	+	–	161	189	94	11	11.0	15	1	27.7	B	AW
24	UKR-OD 1871.94/*Ae.tauschii* (213)	+	–	152	183	84	10	12.3	19	8	35.0	B	LB
25	UKR-OD 1871.94/*Ae.tauschii* (221)	+	–	153	183	92	17	14.0	19	8	41.0	LB	AW
26	UKR-OD 1871.94/*Ae.tauschii* (323)	+	–	154	183	84	12	12.6	21	3	28.0	B	LB
27	UKR-OD 1871.94/*Ae.tauschii* (1024)	+	–	165	192	52	6	10.3	17	2	29.0	LB	AW
28	UKR-OD 1871.94/*Ae.tauschii* (1027)	+	–	175	192	54	2	16	16	5	27.3	LB	LB
29	UKR-OD 952.92/*Ae.tauschii* (188)	+	–	186	194	45	3	10.0	17	7	29.5	B	AW
30	UKR-OD 952.92/*Ae.tauschii* (304)	+	+	172	190	50	4	11.6	15	8	30.0	LB	B
31	UKR-OD 952.92/*Ae.tauschii* (309)	+	–	172	192	56	9	8.6	16	5	28.0	LB	LB
32	UKR-OD 952.92/*Ae.tauschii* (311)	+	–	166	192	55	5	7.1	15	6	31.0	B	B
33	UKR-OD 952.92/*Ae.tauschii* (326)	+	–	156	186	89	14	12.3	19	5	36.0	LB	LB
34	UKR-OD 952.92/*Ae.tauschii* (358)	+	–	150	188	74	9	14.0	22	8	32.0	LB	LB
35	UKR-OD 952.92/*Ae.tauschii* (372)	+	–	170	187	52	5	10.6	16	7	27.0	B	AW
36	UKR-OD 952.92/*Ae.tauschii* (409)	+	–	166	192	60	3	10.0	13	8	36.0	LB	B
37	UKR-OD 952.92/*Ae.tauschii* (428)	+	+	166	186	49	1	10.0	16	5	29.0	LB	LB
38	UKR-OD 952.92/A*e.tauschii* (511)	+	–	158	185	71	3	11.3	21	7	26.6	B	LB
39	UKR-OD 952.92/*Ae.tauschii* (633)	+	–	153	185	81	9	13.3	20	4	37.3	LB	LB

Table 38 (continued). Pedigree and morphological data (mean values) of winter synthetic hexaploid wheats (2n=6x=42; AABBDD) derived from 'winter durum/*Aegilops tauschii*' cross combinations. * Number in parenthesis is the Wide Crosses working collection accession number maintained at CIMMYT, Mexico. GH = growth habit, prosrtate (–), moderately prostrate (M), or erect (+); PUB = pubescence, absence (–) or prescence (+); FLOW = days–to–flowering; PMA = days–to–physiological maturity; HT = plant height at maturity; #S = total number of spikes/plant; SL = spike length (cm); SL/S = number of spikelets/spike; G/S = number of grains/spike; TKW = 1,000–kernel weight; GC = grain color, DB = dark brown, LB = light brown, B = brown, and W = white; and AWN = awn color, DB = dark brown, LB = light brown, B = brown, AW = amber white, and Y = yellow.

Line No.	Pedigree	GH	PUB	FLOW	PMA	HT (cm)	#S	SL (cm)	SL/S	G/S	TKW	GC	AWN
40	UKR-OD 952.92/*Ae. tauschii* (1018)	+	–	156	180	64	4	8.0	23	12	25.0	AW	AW
41	UKR-OD 952.92/*Ae. tauschii* (1024)	+	–	156	180	77	7	8.7	23	28	23.2	AW	B
42	UKR-OD 952.92/*Ae. tauschii* (1028)	+	+	154	186	75	4	12.0	20	7	24.0	LB	B
43	UKR-OD 952.92/*Ae. tauschii* (1031)	+	–	152	180	76	16	10.0	19	5	23.0	AW	LB
44	UKR-OD 1530/*Ae. tauschii* (217)	+	–	149	180	92	12	11.6	17	12	37.5	LB	LB
45	UKR-OD 1530/*Ae. tauschii* (306)	+	–	152	185	80	9	12.3	19	5	39.5	AW	DB
46	UKR-OD 1530.94/*Ae. tauschii* (311))	+	–	153	187	95	11	11.0	17	7	48.0	AW	B
47	UKR-OD 1530.94/*Ae. tauschii* (310)	+	–	151	185	96	15	10.6	17	13	44.4	LB	B
48	UKR-OD 1530.94/*Ae. tauschii* (312)	+	–	152	185	91	12	13.0	17	7	43.3	LB	DB
49	UKR-OD 1530.94/*Ae. tauschii* (392)	+	+	152	184	85	8	11.3	17	12	35.3	LB	DB
50	UKR-OD 1530.94/*Ae. tauschii* (446)	+	–	157	186	92	9	12.3	18	9	32.5	Br	DB
51	UKR-OD 1530.94/*Ae. tauschii* (458)	+	+	155	181	89	17	14.0	20	10	27.0	AW	LB
52	UKR-OD 1530.94/*Ae. tauschii* (511)	+	–	158	184	94	7	10.2	19	5	32.0	AW	B
53	UKR-OD 1530.94/*Ae. tauschii* (629)	+	+	157	185	77	8	12.3	15	9	16.8	LB	LB
54	UKR-OD 1530.94/*Ae. tauschii* (1024)	+	+	152	182	89	18	13.3	10	2	15.0	AW	AW
55	UKR-OD 1530.94/*Ae. tauschii* (1027)	+	–	153	178	88	16	13.8	21	4	43.0	LB	B
56	PANDUR/*Ae. tauschii* (223)	+	–	150	182	67	4	11.0	18	4	30.0	LB	B
57	PANDUR/*Ae. tauschii* (409)	+	–	152	183	80	14	10.5	17	11	35.0	LB	DB
58	PANDUR/*Ae. tauschii* (515)	+	–	158	185	80	7	10.0	17	2	34.0	LB	B

genotypes ranged from 36 by primer *Xgwm608-2D*, 32 by primer *Xgwm337-1D*, 30 by primer *Xgwm456-2D*, and 28 by primer *Xgwm456-3D*.

SSR amplification data was used to generate a similarity matrix to estimate genetic diversity and relatedness among the 58 newly synthesized winter synthetics. The value of the similarity coefficient of winter synthetic wheat lines ranged from 0 to 75%. The average similarity coefficient value was 32% and, hence, 68% genetic distance.

This set of newly synthesized winter wheat SHs showed minimum similarity. Nearly all genotypes gave a 0% similarity coefficient value with one or more genotypes. Genotypes with 70% or more similarity were WS-49 with WS-

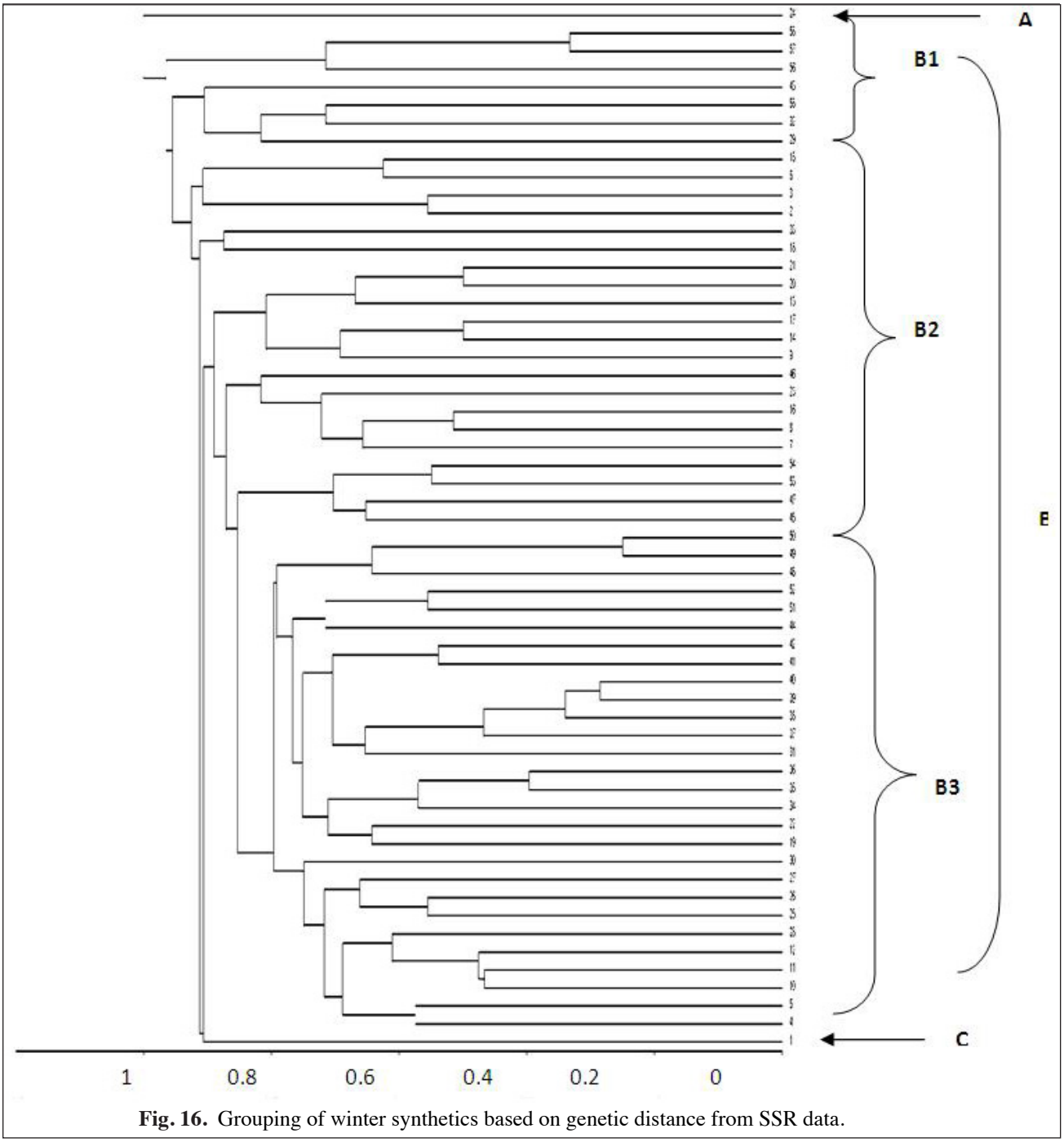

Fig. 16. Grouping of winter synthetics based on genetic distance from SSR data.

50 (75.0%), WS-39 withWS-40 (71.4%). The similarity of the remaining genotypes was between 0 to 70%.

The dendrogram of SSR based genetic diversity evaluation clearly indicates three main clusters, A, B, and C (Fig. 16). Genotypes in cluster A and C exhibited the maximum genetic diversity compared to all other clusters. Genotype WS-24 of cluster A is the most diverse line among the 58 winter synthetics with a maximum genetic distance of 100%. WS-1 also is considered to be a diverse line.

These winter synthetics are genetically diverse. They have traits that can be incorporated into modern cultivars by crosses with *T. aestivum*. Among these winter synthetics, genotypes WS-1, WS-24, WS-43, and WS-46 are recommended. Based on these data, winter wheat breeders can use these suggested winter synthetics expediently in their bread wheat improvement programs for the transfer of desirable genes.

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ITEMS FROM POLAND

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Instability of some endosperm traits in Trtiticum/Aegilops amphiploids.

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We studied endosperm instability in the following amphiploids: *T. turgidum* subsp. *dicoccum*/*Ae. tauschii*, *T. turdidum* subps. *carthlicum*/*Ae. tauschii*, *T. turgidum* subsp. *turgidum*/*Ae. tauschii*, *T. timopheevii* subsp. *timopheevii*/*Ae. longissima*, and *T. timopheevii* subsp. *timopheevii*/*Ae. umbellulata*. All hybrids were obtained from the Plant Germ-plasm Institute in Kyoto, Japan. Anatomy and cytology of this material were observed under light microscopes (polarized Amplival Carl Zeiss Jena and epifluorescence Olympus BX60) and documented with the use of Fuji 400 negatives.

The normal development of endosperm in grasses ends with the creation of interior starch tissue, the sub-aleurone, high-protein layer, and the outer-most aleurone. Normally, the aleurone is composed of one-cell layer with a special protein encapsulated in the aleurone grains. The aleurone layer can disappear or multiply under some genetic or environmental stimuli. An interesting example of multiplication of the aleurone layer in the vicinity of the caryopsis crease is presented in Fig. 1A (p. 199) for the *T. timopheevii* subsp. *timopheevii*/*Ae. umbellulata* amphiploid. A multi-celled layer is created as a result of several periclinal divisions. A two-celled aleurone is showed on the left (red arrow). This type of cell penetrates deeper into the starch tissue on the right (a green arrow). In these two adjacent, anticlinal rows of cells, the expression of aleurone phenotype differs distinctly. A starch phenotype can penetrate outside the starch tissue and appears, often in the form of a large, undivided anticlinally, cell between smaller aleurone cells (Fig. 1B for *T. turdigum* subsp. *carthlicum*/*Ae. tauschii*, p. 199). This tissue also is visible in the cross-section of caryopsis (Fig. 1C in *T. timopheevii* subsp. *timopheevii*/*Ae. umbellulata*, p. 199) where more cells of the starch phenotype develop. The most surprising development is in *T. timopheevii* subsp. *turdigum*/*Ae. tauschii* (Fig. 1D, p. 199), where a very long starch cell, isolated by a hemicellulosic wall expressing blue autofluorescence. grows for a long time and finally is located between

the aleurone cells. This kind of development suggests that the status of a cell wall and a lack of the last periclinal cytokinesis can be factors in determining expression of the cell phenotype and that the expression of the starch phenotype is earlier developmentally than that of the aleurone grains.

Another special feature of the aleurone layer is the development of cells with various phenotypes. These phenotypes are represented by light (a few small globoids) or dark (many small globoids) protein masses. In addition, this phenotype also could be represented by large dark granules (globoids) in aleurone grains. We observed sister associations of light and dark cells; evidence of somatic crossing-over occurring during last anticlinal divisions in aleurone layer (Fig. 2A (*T. timopheevii* subsp. *timopheevii*/*Ae. umbellulata*) and Fig. 2B (*T. turdigum* subsp. *carthlicum*/*Ae. tauschii*)). The same phenomenon is related to a pair of cells with large or small globoids (Fig. 2B). The mutant cell having large globoids can be multiplied to create a large spot (Fig. 2C (*T. timopheevii* subsp. *timopheevii*/*Ae. longissima*)).

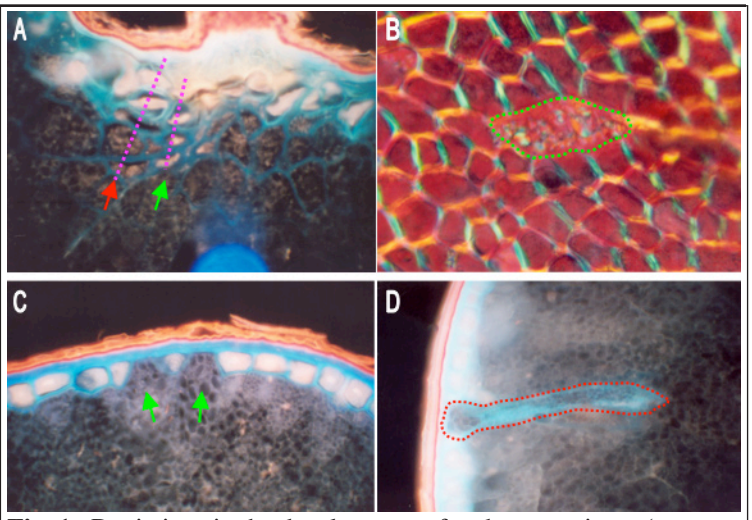

Fig. 1. Deviations in the development of endosperm tissue (cross-sections of caryopsis). A and C: *T. timopheevii* subsp. *timopheevii*/*Ae. umbellulata*, A–two series of aleurone cells filled with light protein or dark starch created by periclinal divisions along violet lines and C–two starch cells (green arrows) expressed within the aleurone layer; B–*T. turgidum* subsp. *carthlicum*/*Ae. tauschii*, a large cell of the starch phenotype (outlined green) within a proteinaceous aleurone layer; D: *T. turgidum* subsp. *turgidum*/*Ae. tauschii*, a large cell of the starch phenotype increased due to intrusive growth and penetrating the aleurone layer.

These examples were observed in the form of somatic mosaicism created by mitotic crossing-over.

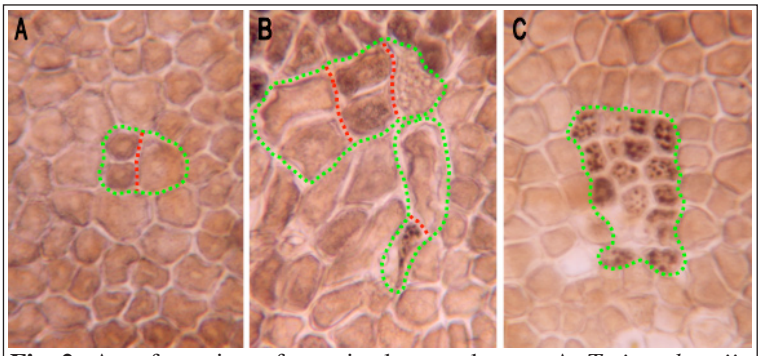

Fig. 2. A surface-view of mosaic aleurone layers. A: *T. timopheevii* subps. *timopheevii*/*Ae. umbellulata*, three sister cells filled by dark (left) and light (right) protein; B: *T. turgidum* subsp. *carthlicum*/*Ae. tauschii*, groups of cells of sister origin (green outlined) expressing different nature of protein; C: *T. timopheevii* subps. *timopheevii*/*Ae. longissima*, a clone of aleurone cells with large dark globoids.

Morphometry of lodicules on the diploid level in the Triticeae tribe.

R. Kosina.

A high correlation between mating system and size of lodicule was observed for a large set of Iranian grasses (Kosina 2005). In the tribe Triticeae, at least three components of the lodicule morphology are known: dimensions, hairiness, and shape (Kosina 2006).

Thirty-two diploid species of the tribe Triticeae were described by means of lodicule structure. Five characters, presenting dimensions, shape, and hairiness were used to arrange accessions within an ordination space by means of Kruskal's Nonmetric Multidimensional Scaling (nmMDS). Accessions of the following species were cultivated in the field: *Ae. speltoides* (Asp1, Asp2), *Ae. bicornis* (Ab), *Ae. comosa* (Aco1, Aco2), *Ae. caudata* (Ac), *Ae. searsii* (As), *Ae. sharonensis* (Ash), *Ae. tauschii* (Asq), *Ae. umbellulata* (Aum), *Ae. uniaristata* (Aun), *Ag. pectiniforme* (Ap1, Ap2), *Am. muticum* (Am1, Am2), *Critesion bogdanii* (Cb), *C. californicum* (Cc), *C. chilense* (Cch), *C. marinum* (Cm), *C. stenostachys* (Cs), *C. violaceum* (Cv), *Dasypyrum villosum* (Dv), *Hordelymus europaeus* (He), *Hordeum spontaneum* (Hs1, Hs2), *H. vulgare* (Hv), *Heteranthelium piliferum* (Het), *Pseudoroegneria libanotica* (Pl), *Ps. spicata* (Ps), *Psathyrostachys juncea* (Pj1, Pj2), *S. afganicum* (Sa), *S. digoricum* (Sd), *S. silvestre* (Ss), *S. vavilovii* (Sv), *Thinopyrum junceum* (Thj), *Taeniatherum crinitum* (Tae), *T. monococcum* subsp. *aegilopoides* (Tb), and *T. urartu* (Tu). The accessions were obtained from the collections of the Vavilov Institute in St. Petersburg (Russian Federation), IPK Gatersleben (Germany), and the USDA (USA).

A synthetic picture of the nmMDS arrangement of forms is presented in Fig. 3. Along the two ordinant axes (x and y) Cm, Aco1, Dv, and Hs1 are located as extremes. For the z axis (Fig. 3) Cm (min) and Hs1 (max) are the extremes. Within the ordinant space, several lodicule groups representing the main patterns of the reproduction system can be observed:

1. broad, long, and very hairy lodicules in Hs, Sa, Sd, Ss, and Dv; taxa probably having a highly allogamic system of breeding,
2. bare, narrow, and short lodicules with one lobe in Cm; cleistogamy is very probable, and
3. other intermediate forms of organs developed within a range; facultative autogamy–facultative allogamy.

In the same species, distances in the ordination space between two accessions (for example, Hs1–Hs2, Aco1–Aco2, and Pj1–Pj2) are of the similar rank like those interspecific. These results show that grasses have a flexible mating system permitting very successful intra- and interspecific microevolution.

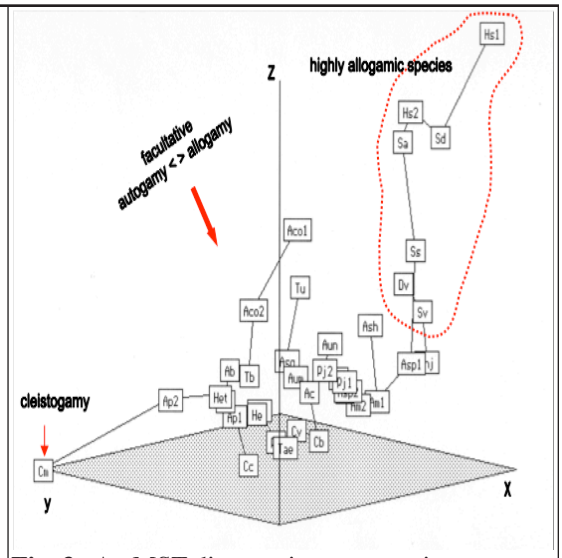

Fig. 3. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a scattering of diploid species of the Triticeae tribe described by lodiculae morphology.

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Kosina R. 2006. Zmienność strukturalna i funkcjonalna łuszczek traw. Fragmenta Floristica et Geobotanica Polonica 13:139-153 (In Polish).

Microstructure of endosperm in some intergeneric amphiploids and their parental species of the Triticeae tribe.

R. Kosina and P. Tomaszewska.

This study was made on microscopic slides of aleurone layer (surface view). Caryopsis cross sections of the following species and hybrids were obtained: *Leymus racemosus*, 2n = 28, *L. karataviensis*, 2n = 28, *L. arenarius*, 2n = 56; *L. multicaulis*, 2n = 28; *Elymus canadensis*, 2n = 28; *E. yezoënsis*, 2n = 28; *Pseudoroegnaria libanotica*, 2n = 14; *Critesion bogdanii*, 2n = 14 and their amphiploids '*Ps. libanotica*/*E. yezoënsis*', 2n = 42; '*L. multicaulis*/*L. karataviensis*', 2n = 56; '*E. canadensis*/*Ps. libanotica*', 2n = 42; '*L. arenarius*/*L. racemosus*', 2n = 84; and '*E. canadensis*/*C. bogdanii*', 2n = 42. The material was kindly provided by the late Dr. Douglas Dewey from the Utah State University.

We focused on several aspects of caryopsis development and structure; the duration of the cell cycle, clonal mosaics, expression of starch phenotype in the aleurone layer, and frequency of mitotic crossing-over. Cells in aleurone layer can be highly polyploidized, especially those of globular shape, and are very large (Fig. 4A and B). Sometimes they express a special type of intrusive growth, such as fibers, penetrating deeply into the starch endosperm. Such a growth can sometimes divide the endosperm into areas with different starch synthesis. Many patterns of

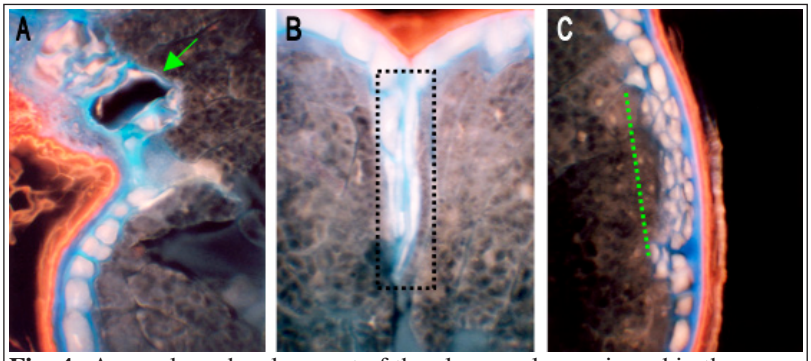

Fig. 4. Anomalous development of the aleurone layer viewed in the cross sections of caryopsis. A and B '*Pseudoroegneria libanotica*/*Elymus yezoënsis*' amphiploid, A, a highly polyploidized aleurone cell (green arrow) and B, a group of aleurone cells growing intrusively into the starchy endosperm; C '*Leymus arenarius*/*L. racemosus*', a clone of a small aleurone cell (along the green line) surrounded by cells of a normal cell cycle.

endosperm development composed of clones or cell mosaics are initiated by subsyncytial nature of this tissue (Kosina 1996). An example of a short cell cycle in the aleurone layer is presented in Fig. 4C (p. 200). A spot of small cells developing after anticlinal and periclinal divisions surrounded by larger ones is visible.

A mosaic pattern of development can be observed in various tissues of caryopsis. For example, large dark and light spots of aleurone cells were noted in the '*E. canadensis*/*Ps. libanotica*' amphiploid (Fig. 5A). These cells differ in the nature of the globoids in the aleurone grains and such mutations have been documented in barley (Ockenden et al. 2004). Another kind of mosaic was the expression of a starch phenotype in the aleurone layer (Fig. 5B and C). We documented numerous cases of mitotic crossingover, which caused 'double-spots' of sister origin. Exchanges in chromosomes created pairs of cells with different phenotypes, such as starch vs. protein, starch amylopectin rich vs. starch amylopectin poor, large starch grains vs. small starch grains, and light protein (not numerous small globoids) vs. dark protein (many large globoids). Numerous cross-overs within one cell clone and high instability of the tissue can be seen in Fig 5C.

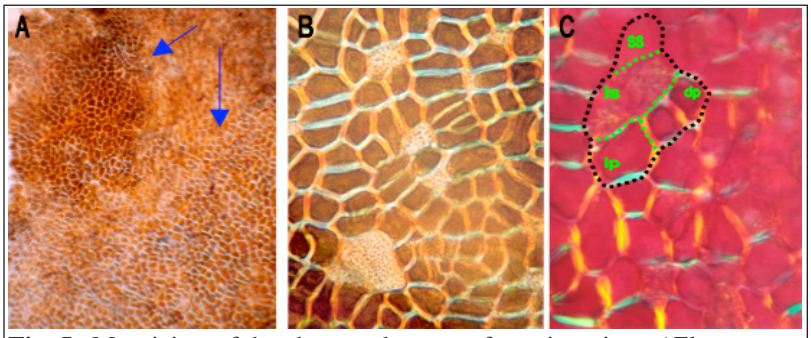

Fig. 5. Mosaicism of the aleurone layer; surface views in an '*Elymus canadensis*/*Pseudoroegneria libanotica*' amphiploid. A, two large spots of dark and light aleurone layer (blue arrows); B, cells of starch phenotype (light) scattered among proteinaceous aleurone cells; and C, a clone of aleurone cells (outlined in black) with phenotypes having large (ls) and small (ss) starch granules or light (lp) and dark (dp) aleurone grains.

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Ockenden I, Dorsch JA, Reid MM, Lin L, Grant LK, Raboy V, and Lott JNA. 2004. Characterization of the storage of phosphorus, inositol phosphate and cations in grain tissues of four barley (*Hordeum vulgare* L.) low phytic acid genotypes. Plant Sci 167:1131-1142.

Morphology of embryo in 32 species of the Triticeae tribe.

R. Kosina.

Thirty-two species of various ploidy levels of all taxa from the Triticeae tribewere evaluated for five morphological traits of the embryo describing the epiblast, coleorhizal papilla, and relative dimensions of coleoptile. These five characters were used to arrange OTUs within an ordinate space by means of Kruskal's Nonmetric Multidimensional Scaling (nmMDS). Accessions of the following species were cultivated: *Ae. cylindrica* (Aec), *Ae. triuncialis* (Aet), *Ag. cristatum* subsp. *cristatum* (Acc), *Ag. cristatum* subsp. *desertorum* (Acd), *Critesion californicum* (Cc), *C. chilense* (Cch), *C. hystrix* (Ch), *Elymus breviaristatus* subsp. *scabrifolius* (Ebs), *E. caninus* (Ec), *E. dahuricus* (Ed), *E. gmelinii* (Eg), *E. hystrix* (Eh), *E. mutabilis* (Em), *E. nutans* (En), *E. trachycaulus* (Etr), *E. tsukushiensis* (Et), *Elytrigia intermedia* subsp. *graeca* (Elig), *Eremopyrum bonaepartis* (Erb), *Hordelymus europaeus* (Hee), *Hordeum vulgare* subsp. *sponta-*

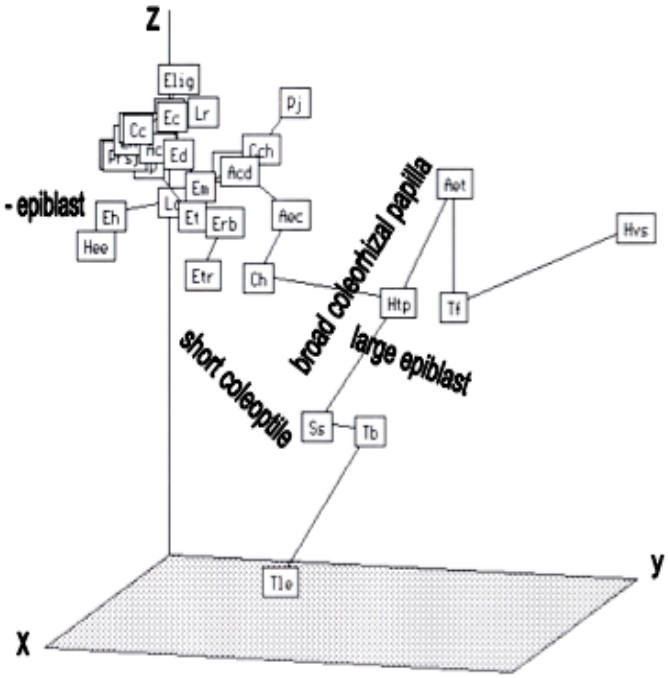

Fig. 6. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a scattering of Triticeae species characterized by means of embryo morphology.

neum (Hvs), *Heteranthelium piliferum* (Htp), *Leymus paboanus* (Lp), *L. racemosus* (Lr), *Lophopyrum nodosum* (Lon), *Pseudoroegneria strigosa* subsp. *jacutorum* (Prsj), *Psathyrostachys juncea* (Pj), *S. silvestre* (Ss), *Th. bessarabicum* (Thb), *Taeniatherum caput-medusae* (Tacm), triticale (Tle), *T. monococcum* subsp. *monococcum* (Tb), and *T. fungicidum* (Tf). The accessions were obtained from the collections of the Vavilov Institute in St. Petersburg (Russian Federation), IPK Gatersleben (Germany), and the USDA (USA).

In the MST diagram (Fig. 6, p. 201), some characteristic groups of species can be distinguished. In a large group described by high z axis values and low x and y values are species having embryos without an epiblast (Hee, Ebs, Lp, Eg, Prsj, Elig, Tacm, Eh, and En). Distant from this group are the species of *Triticum* and *Hordeum* with large epiblasts and distinct coleorhizal papilla. Other species, such as Tle, Ss, Tb, Tf, Etr, and Hee, are characterized by delayed longitudinal growth of coleoptile and are scattered between both of the above-mentioned groups. In annual and perennial species of *Brachypodium* (Kosina and Jaroszewicz 2007), the coleorhizal papilla play an important role during seed germination. Kosina (1995) described a short coleoptile as typical for AAGG wheats, whereas in AABB wheats, the growth of the coleoptile is more dynamic. A clear difference in embryo morphogenesis between annual or biennial (*Triticum*, *Aegilops*, and *Hordeum*) and perennial grasses can be seen (Fig. 6, p. 201), with the perennial grasses are separated on the left. Such a discrimination supports data on germination differences in the *Brachypodium* genus (Kosina and Jaroszewicz 2007).

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DNA RAPD profiles in Brachypodium distachyon, a model grass related to the Triticeae tribe.

R. Kosina and A. Jaroszewicz.

RAPD markers are commonly used to determine varietal or accession variation in gene banks. The level of variation expressed in electrophoretic DNA bands is different and depends on the PCR primer used in amplification. We estimated RAPD variation in a collection of 21 accessions of *B. distachyon* of various origin. This species, at present, is studied in detail, because its biology is well related to biology of members of the Triticeae tribe, including a broad spectrum of the genus *Triticum*. Twenty 10-nucleotide primers were used for PCR amplification. Some were poor (B-3), but others were rich and polymorphic (B-20). Determining the level of variation was done by two approaches; counting only strong bands or including all bands, even the very weak, for comparison.

Most of the bands were 500–1,000 bp. Two examples of primer amplification show that the pattern of DNA bands are accession-specific (Fig. 7). However, some similarity in banding patterns also was observed, e.g., B-3 for Pakistan–Morocco and Slovakia–Iran. No adequate accession was found for the item from Denmark Botanic Garden. Such an analysis can be helpful to identify material of unknown origin collected in the botanical gardens. Primer B-20 gave

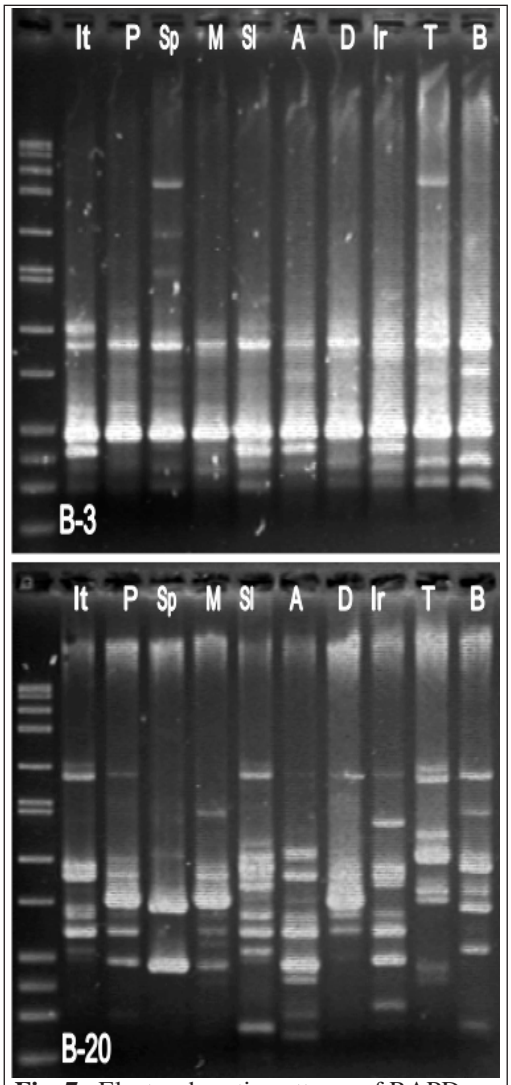

Fig. 7. Electrophoretic patterns of RAPD markers for two selected primers (B-3 and B-20). Lanes are for the DNA ladder and ten accessions of *Brachypodium distachyon* of the following origin: Italy (It), Pakistan (P), Spain (Sp), Morocco (M), Slovakia Botanic Garden (Sl), Australia (A), Denmark Botanic Garden (D), Iran (Ir), Turkey (T) and Bulgaria (B).

more accession-specific bands. Poor patterns were identified for accessions from Spain and Pakistan. Rich banding patterns were found for accessions from Slovakia, Australia, Iran, and Turkey. The data are being evaluated numerically at present.

RAPD variation in a 'Triticum timopheevii subsp. timopheevii / Aegilops umbellulata' amphiploid.

R. Kosina and K. Markowska.

Random amplified polymorphic DNA (RAPD) patterns are used not only to determine inter- and intra-population variation but also to study relationships between parental species and their hybrid progeny. We noted RAPD variation patterns for two parental species, *T. timopheevii* subsp. *timopheevii* (Tt) and *Ae. umbellulata* (Au) from IPK Gatersleben, Germany, and two amphiploid two accessions from the Plant Germ-plasm Institute, Kyoto, Japan. We used 40 10-nucleotide primers in the PCR amplification. Strong and very weak bands can be used to determine the level of variation.

Most of the bands were 500–750 bp. Some general observations were seen in DNA profiles (Fig. 8). If bands of both parents are present in the amphiploid, they often are of intermediate strength (Fig. 8, red arrow). For three profiles, some variation between the two amphiploid accessions were observed including the weak bands (Fig. 8, white arrow). Several primers had amphiploid-specific bands. The *T. timopheevii* subsp. *timopheevii* genome bands in the amphiploid are larger; DNA profiles for *Ae. umbellulata* are poor. We found species-specific bands for both parents. A RAPD analysis also will be made for the amphiploid after demethylation of the genomes. The data currently are being numerically evaluated.

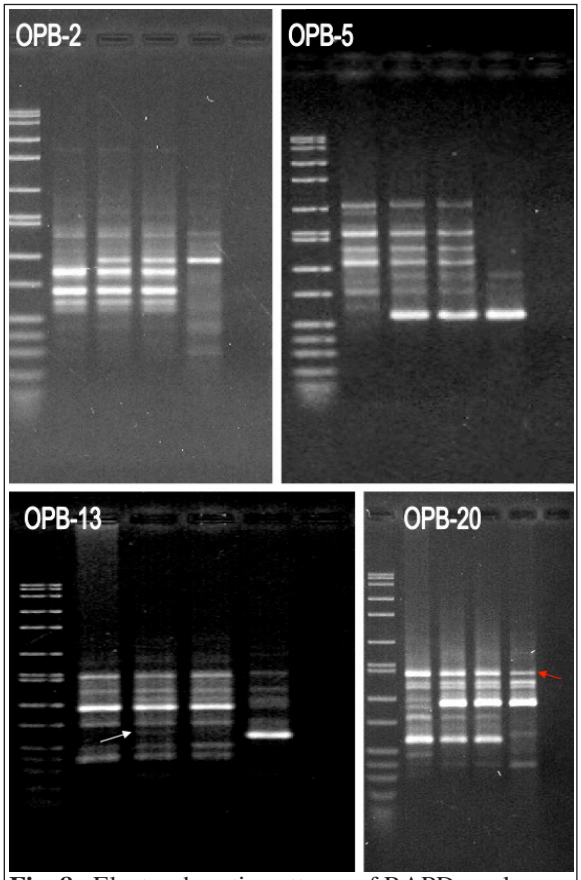

Fig. 8. Electrophoretic patterns of RAPD markers for four selected primers (OPB2, OPB5, OPB13, and OPB20). Lanes are 1, DNA ladder; 2, *Triticum timopheevii* subsp. *timopheevii*; 3, amphiploid 1; 4, amphiploid 2; and 5, *Aegilops umbellulata*.

Parental dominance of lemma and palea epidermal microstructure in some amphiploids of Triticeae.

R. Kosina.

Uniparental complex dominance is well known in hybrid plants (Grant 1981; Heslop-Harrison 1990). For Triticeae hybrids, such data were presented by Kosina (1996). We studied inflorescence bract morphology described by nine characters of the highly differentiated abaxial epidermis. The set of parental species and their amphidiploids were *Leymus racemosus* (Lr), *L. karataviensis* (Lk), *L. arenarius* (La), *L. multicaulis* (Lm), *Elymus canadensis* (Ec), *E. yezoënsis* (Ey), *Pseudoroegnaria libanotica* (Pl), *Critesion bogdanii* (Cb), '*Ps. libanotica*/*E. yezoënsis*' (PlxEy), '*L. multicaulis*/*L. karataviensis*' (LmxLk), '*E. canadensis*/*Ps. libanotica*' (EcxPl), '*L. arenarius*/*L. racemosus*' (LaxLr), and '*E. canadensis*/*C. bogdanii*' (EcxCb). Research material was provided by the late Dr Douglas Dewey from the Utah State University, chairman of the past International Triticeae Cooperative.

The investigated taxa (operational taxonomic units, OTUs) are scattered within a space created by means of Kruskal's Nonmetric Multidimensional Scaling (Fig. 9, p. 204). The genus *Leymus* is characterized by larger z axis values; other species have lower values, thus distinguishing both groups of species. A distinct, complex, maternal dominance is recognized only for two amphiploids, LaxLr and EcxCb. Parents of the latter are connected immediately with their hybrid. Weaker paternal dominance is noted for amphiploid EcxPl and weak expression of the maternal phenotype is noted for the PlxEy hybrid. OTUs are scattered along a positive regression line between the x and y axes. The OTUs form an ellipsoid sphere that rises from low to high values of the z axis. The shape of this sphere and its behavior is an

additional characteristic of the OTUs studied. The original variation patterns enabled us to extend the research of these forms and the results are presented here by Kosina and Tomaszewska.

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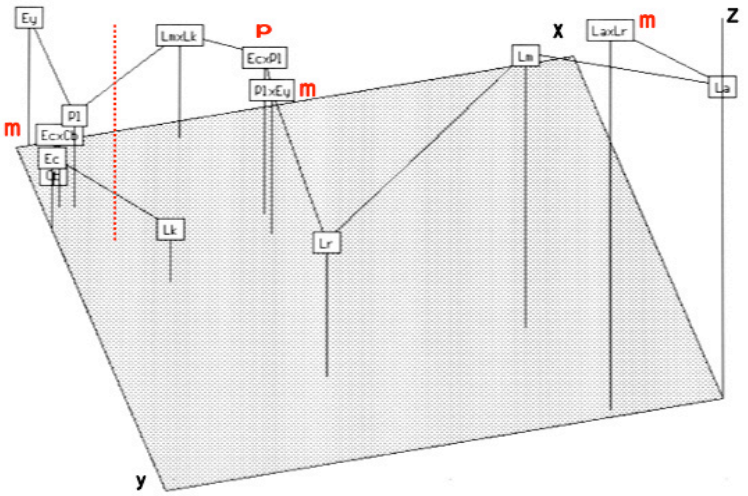

Fig. 9. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a uniparental dominance (m = maternal and p = paternal) of glumellae epidermal morphology in Triticeae amphiploids.

Expression of parental variation in caryopsis structure of some amphiploids in the Triticeae tribe

R. Kosina.

We analyzed a set of operational taxonomic units (OTUs) comprising parental species and some interspecific and intergeneric hybrids progeny, *Leymus racemosus* (Lr), *L. karataviensis* (Lk), *L. arenarius* (La), *L. multicaulis* (Lm), *Elymus canadensis* (Ec), *E. yezoënsis* (Ey), *Pseudoroegnaria libanotica* (Pl), *Critesion bogdanii* (Cb), '*Ps. libanotica*/*E. yezoënsis*' (PlxEy), '*L. multicaulis*/*L. karataviensis*' (LmxLk), '*E. canadensis*/*Ps. libanotica*' (EcxPl), '*L. arenarius*/*L. racemosus*' (LaxLr), and '*E. canadensis*/*C. bogdanii*' (EcxCb).

Nine caryopsis anatomy characters describing pericarp, testa, aleurone layer, pigment strand, nucellar projection, and starch grains were studied and calculated as a mean taxonomic distance between the OTUs. A matrix of taxonomic distances was recalculated by means of the non-metric multidimensional scaling to arrange OTUs into an ordination space (Fig. 10). Comparing parents and progeny showed a complex paternal dominace of caryopsis structure is characteristic for the LaxLr and EcxPl amphiploids. Maternal dominance is noted for the PlxEy amphiploid. The amphiploids are separated well from most of the parental species (a red line) and their interspecies variation is very large. However, two species, *L. racemosus* and *L. arenarius*, have a special position within a diagram. All OTUs are scattered along a negative regression line between the x and y axes, and this picture is completely

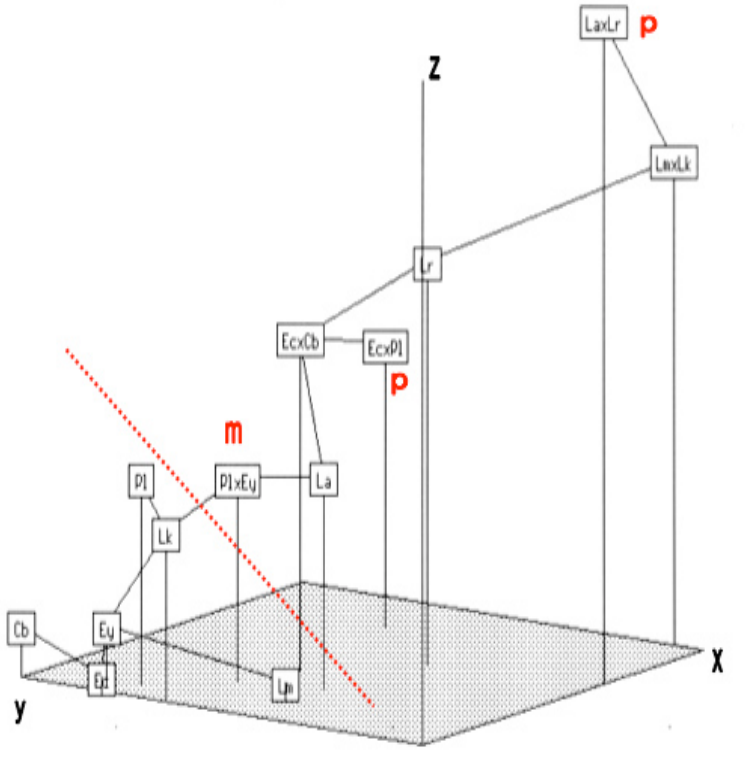

Fig. 10. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a uniparental dominance (m = maternal and p = paternal) of caryopsis structure in Triticeae amphiploids.

different when compared to that for lemma and palea epidermal traits (see contribution on p. 205). An ellipsoid sphere created by the OTUs starts from low values on the x and z axes and high values on y and rises to low values on the y axis and high values on x and z axes.

Variation of meristemoidal activity in abaxial epidermis of glumellae in 32 species of the Triticeae tribe.

R. Kosina.

Thirty-two species of the tribe Triticeae were described by means of morphology of well-differentiated epidermis of lemma and palea. Ten characteristics that describe morphogenesis of original epidermal short cells were used to arrange accessions within an ordination space by means of Kruskal's Nonmetric Multidimensional Scaling (nmMDS). Accessions of the following species were obtained from the Vavilov Institute, St. Petersburg, Russian Federation, IPK–Gatersleben, Germany, and the USDA, USA, and were cultivated in the field: *Ae. cylindrica* (Aec), *Ae. triuncialis* (Aet), *Ag. cristatum* subsp. *cristatum* (Acc), *Ag. cristatum* subsp. *desertorum* (Acd), *Critesion californicum* (Cc), *C. chilense* (Cch), *C. hystrix* (Ch), *Elymus breviaristatus* subsp. *scabrifolius* (Ebs), *E. caninus* (Ec), *E. dahuricus* (Ed), *E. gmelinii* (Eg), *E. hystrix* (Eh), *E. mutabilis* (Em), *E. nutans* (En), *E. trachycaulus* (Etr), *E. tsukushiensis* (Et), *Elytrigia intermedia* subsp. *graeca* (Elig), *Eremopyrum bonaepartis* (Erb), *Hordelymus europaeus* (Hee), *Hordeum vulgare* subsp. *spontaneum* (Hvs), *Heteranthelium piliferum* (Htp), *Leymus paboanus* (Lp), *L. racemosus* (Lr), *Lophopyrum nodosum* (Lon), *Pseudoroegneria strigosa* subsp. *jacutorum* (Prsj), *Psathyrostachys juncea* (Pj), *S. silvestre* (Ss), *Th. bessarabicum* (Thb), *Taeniatherum caput-medusae* (Tacm), triticale (Tle), *T. monococcum* subsp. *aegilopoides* (Tb), and *T. fungicidum* (Tf).

In the abaxial epidermis of glumellae, lemma, and palea, the frequency of short, specialized cells such as papillae, duplexes of silica and cork cells, triplexes (duplex + papilla), hairs, and other meristematic cytokineses were observed. Species in the MST diagram (Fig. 11), elaborated by means of nonmetric multidimensional scaling, are scattered according to activity of their epidermal meristemoids. *Critesion californicum* (Cc) express a very high activity of meristemoids and they are distinctly higher in lemma. A reverse relationship between activity in both glumellae is noted for *Ta. caput-medusae* (Tacm). A second pole of an ordinant space is occupied by species characterized by low activity of epidermal meristemoids, such as *Ae. cylindrica* (Aec) and *L. racemosus* (Lr). Interspecific patterns of epidermal morphogenesis are differentiated by various proportions of specialized cells within one organ and between both lemma and palea. These differences are demonstrated not only in a quantitative but also qualitative way. In addition, they appear as a presence or absence of a given kind of epidermal cell. This study of epidermal morphogenetic patterns is of high value for the taxonomic approach in the Triticeae tribe.

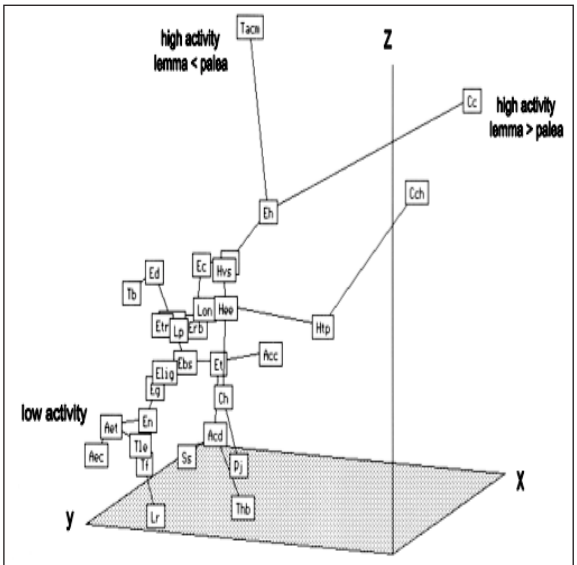

Fig. 11. An MST diagram of the Triticeae species described by means of meristemoidal activity of glumellae epidermis presented in a nonmetric multidimensional scaling ordination space.

Meristemoidal activity in abaxial epidermis of glumellae in Triticum–Aegilops amphiploids and some Triticeae species.

R. Kosina.

Species and amphiploid lines were obtained from the Kyoto Plant Germ-plasm Institute, Japan; R. de Pienaar, Republic of South Africa; Vavilov Institute, St. Petersburg, Russian Federation; IPK, Gatersleben, Germany; and the USDA, USA. Plants were cultivated in the field under uniform soil–climatic conditions. The abaxial epidermis of the lemma and palea was isolated and studied under light microscopy in *Ae. caudata* (Ac), *Ae. uniaristata* (Au), *Ae. sharonensis* (As), *Ae. tauschii* (At1, At2), *Ae. umbellulata* (Aum1, Aum2), *Lophopyrum elongatum* (Loe), *S. cereale* (Sc), *Th. bessarabicum*

(Thb), triticale (Tle), *T. monococcum* subsp. *aegilopoides* (Tb1, Tb2), *T. turgidum* subsp. *carthlicum* (Tc), *T. turgidum* subps. *durum* (Td), *T. fungicidum* (Tf), *T. kiharae* (Tk), *T. timonovum* (Ttm), *T. timopheevii* subsp. *timopheevii* (Tt), *T. turanicum* (Ttr), and the amphiploids Au/Tb, Tb/Au, Au/At (two forms), Aum/At, As/Aum, Aum/Au, Au/Aum, Ac/Aum, Tc/At, Ttr/At, and Td/Thb/Loe.

In this material, the frequency of short epidermal cells, such as papillae and duplexes, the latter composed of silica and cork cells, and the sum of all meristematic cytokineses, separately for lemma and palea, were calculated. A minimum spanning tree was obtained after using nonmetric multidimensional scaling (Fig 12). For many OTUs, morphogenesis of papillae dominates in the lemma and palea. However, *S. cereale* is completely different, where only duplexes in both glumellae were observed. For the species, a higher activity of epidermal meristemoids is characteristic but is low for both *Aegilops* species and the amphiploids. Paternal dominance of the studied traits was observed in the amphiploid Ttr/At. For the Td/Thb/Loe amphiploid, *Th. bessarabicum* (Thb) and *T. turgidum* subsp. *durum* (Td) are closer to their progeny, whereas the *Lo. elangatum* (Loe) parent is very distant. Distinct dominance is observed as a maternal or paternal component for many amphiploids created with *Ae uniaristata*.

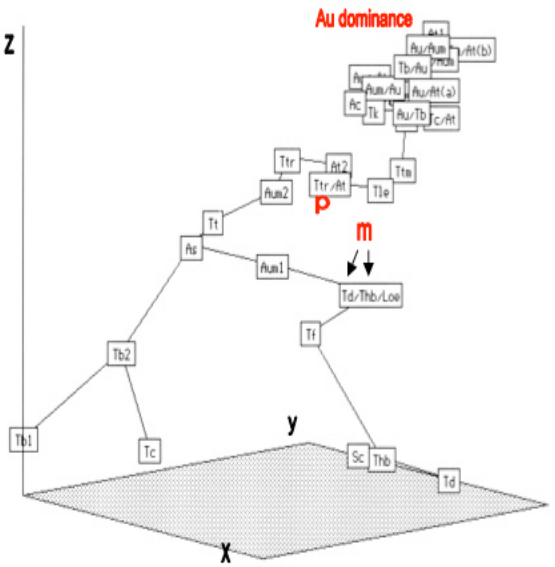

Fig. 12. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a uniparental dominance (m = maternal and p = paternal) of meristematic activity of glumellae epidermis for selected *Triticum–Aegilops* amphiploids.

Parental patterns of variation of embryo morphology in some amphiploids of the Triticeae tribe.

R. Kosina.

A set of operational taxonomic units (OTUs) comprised of parental species and their interspecific and intergeneric hybrids were used to study variation of embryo structure included *Leymus racemosus* (Lr), *L. karataviensis* (Lk), *L. arenarius* (La), *L. multicaulis* (Lm), *Elymus canadensis* (Ec), *E. yezoënsis* (Ey), *Pseudoroegnaria libanotica* (Pl), *Critesion bogdanii* (Cb), '*Ps. libanotica*/*E. yezoënsis*' (PlxEy), '*L. multicaulis*/*L. karataviensis*' (LmxLk), '*E. canadensis*/*Ps. libanotica*' (EcxPl), '*L. arenarius*/*L. racemosus*' (LaxLr), and '*E. canadensis*/*C. bogdanii*' (EcxCb). All lines were received from the Douglas Dewey collection maintained at the Utah State University, Logan. The embryo was described by four characteristics related to shape of the embryo, width of the scutellum, and length of the embryonic axis.

An MST diagram (minimum spanning tree, Fig. 13) presents the arrangement of OTUs within an ordination space constructed by means of nonmetric multidimensional scaling. Two extreme species, *L. multicaulis* and *C. bogdanii*, are 'epiblast' taxa. Distinct, complex parental dominance, maternal or paternal, is expressed by all amphiploids, a sign of differential expression of their genomes and, therefore, this material is very suitable for the study of nuclear architecture by means of GISH. The parental genomes very probablly occupy separate domains in the hybrid nuclei.

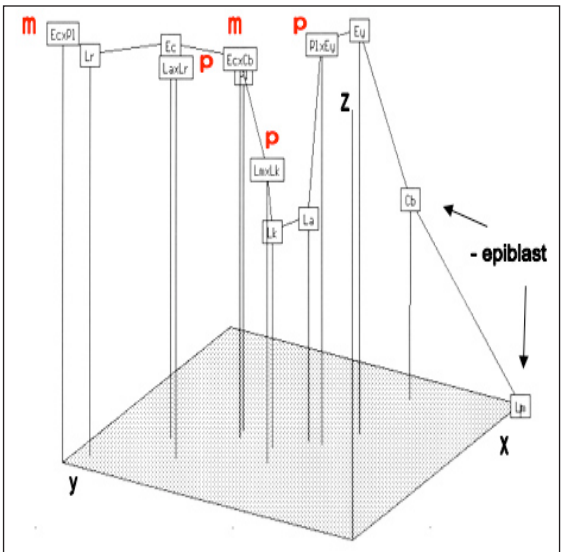

Fig. 13. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a uniparental dominance (m = maternal and p = paternal) of embryo morphology in Triticeae amphiploids.

Expression of parental dominance in the lodiculae morphology of some Triticeae amphiploids.

R. Kosina.

Operational taxonomic units (OTUs) represented by parental species and their interspecific and intergeneric hybrids were studied for variation in lodiculae structure. The OTUs were *Leymus racemosus* (Lr), *L. karataviensis* (Lk), *L. arenarius* (La), *L. multicaulis* (Lm), *Elymus canadensis* (Ec), *E. yezoënsis* (Ey), *Pseudoroegnaria libanotica* (Pl), *Critesion bogdanii* (Cb), '*Ps. libanotica*/*E. yezoënsis*' (PlxEy), '*L. multicaulis*/*L. karataviensis*' (LmxLk), '*E. canadensis*/*Ps. libanotica*' (EcxPl), '*L. arenarius*/*L. racemosus*' (LaxLr), and '*E. canadensis*/*C. bogdanii*' (EcxCb). All the materials were grown under the same climate and soil. Five characters were used to describe lodicule morphology. The uniparental dominance exhibited by the amphiploids is clear (Fig. 14). This uniparental dominance is of two types, maternal or paternal. In the '*E. canadensis*/*Ps. libanotica*' (EcxPl) and '*E. canadensis*/*C. bogdanii*' (EcxCb) amphiploids, the maternal dominance of *E. canadensis* is well expressed in the lodiculae and embryo morphology. A separation of some parental species (Lr, Lm, Pl, and Cb) and hybrids also is visible in the ordination space, which could indicate a change of mating system in the amphiploids.

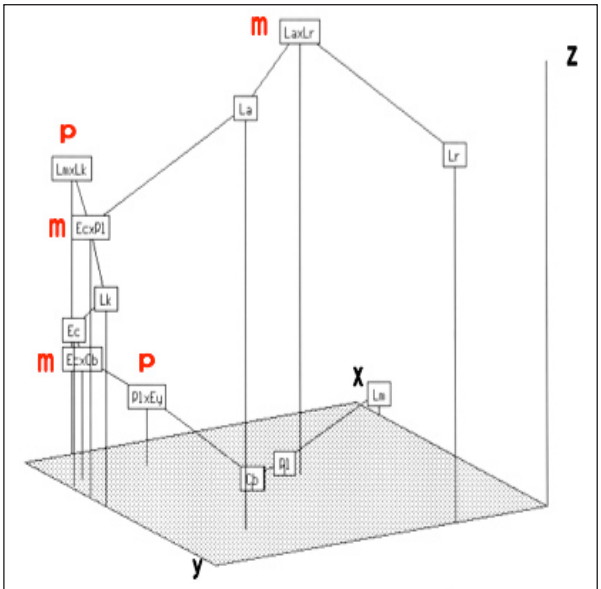

Fig. 14. An MST diagram in a nonmetric multidimensional scaling ordination space presenting a uniparental dominance (m = maternal and p = paternal) of lodiculae morphology in Triticeae amphiploids.

Patterns of variation in a Triticum timopheevii subsp. timopheevii–Aegilops umbellulata amphiploid after demethylation of genomes.

R. Kosina and K. Markowska.

Matroclinal or patroclinal parental dominance can be observed in natural hybrids and synthetic amphiploids. Kosina (1996) has reported such a phenomenon for distant hybrids in the Triticeae tribe. Additionally, a variation pattern expressed in hybrids also is ruled by an epigenetic arrangement of parental chromosomes in nuclei of an amphiploid (Kosina and Heslop-Harrison 1996). In this study, we investigated the patterns of variation of gross morphology of spike and spikelet, caryopsis anatomy, and changes in expression of RNA in wild and demethylated genomes of a *T. timopheevii* subsp. *timopheevii–Ae. umbellulata* amphiploid. Some comparisons were made with the parental species. Two amphiploid plant progeny (Fig. 15) produced polymorphic dark and light (d and l) grains. The gross morphology of the spike and spikelets were arranged inside of the ordination space by means of nonmetric multidimensional scaling. This picture very clearly shows that forms having wild genomes are intermediate between demethylated extremes. Demethylation does not offer a directional change in the variation pattern but causes some increase in the existing variability.

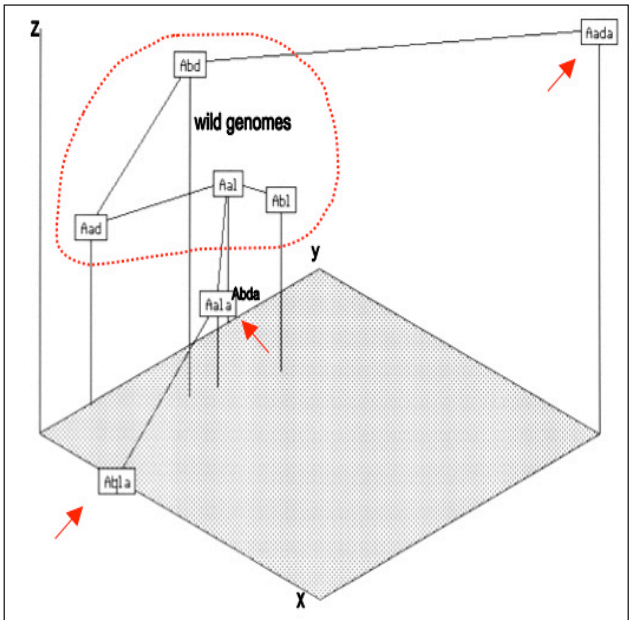

Fig. 15. A minimum spanning tree (MST) diagram representing the scattering of amphiploid progeny (A) with wild (red outline) and demethylated (red arrows) genomes described by means of gross morphology of the spike and spikelets. The progeny is located within a nonmetric multidimensional scaling ordination space. a or b = progeny of two plants, d or l = dark or light caryopses for demethylated progeny, a = aza-cytidine progeny.

Additional observations were made for cross sections of the caryopsis. Demethylation changed the cytological status of the pigment strand area where strong suberization was detected (Fig. 16B, dark brown layer). This development can influence the synthesis of starch and protein in the endosperm and modify the proportion. After demethylation, the synthesis of RNA increased (compare Fig. 16C and D).

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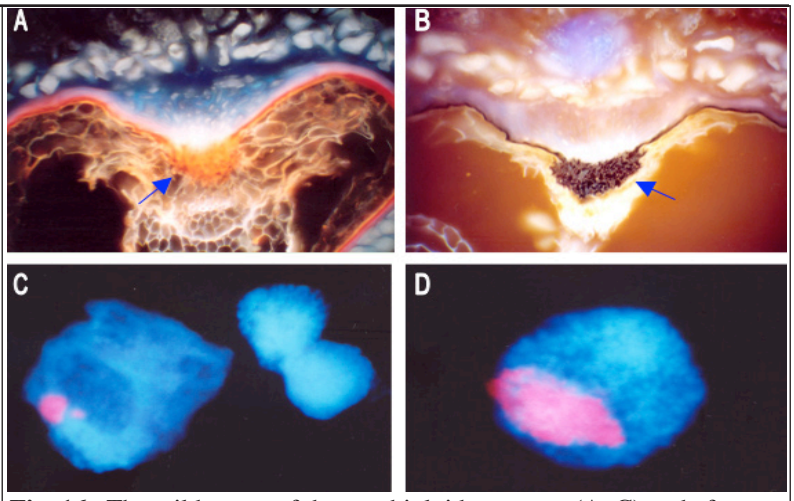

Fig. 16. The wild status of the amphiploid genomes (A, C) and after demethylation (B, D). A, B – autofluorescence of cross-sections of caryopsis transfer tissues; C, D – DAPI and PI fluorescence of root interphase nuclei. Strong changes in the pigment strand (blue arrows) are visible, which is a part of the tissue transfer system providing assimilates to endosperm as well as of RNA (red signals) synthesis in root interphase nuclei.

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ITEMS FROM THE RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE OF THE CENTRAL REGION OF NON-CHENOZEM ZONE
143026, Moscow region, Nemchinovka, Kalinina 1, Russian Federation.

A winter rye apomict.

V.G. Kyzlasov.

Zea mays L. ssp. *mays* and *Tripsacum dactyloides* L. hybrids are known among the cultivated cereals for regular apomixis (Sokolov et al. 2007). Hybrid lines of *Z. mays* with nine additional *Tr. dactyloides* chromosomes reproduce by apomixis. Nine is the minimum number of *Tr. dactyloides* chromosomes required for apomixis in the phenotype. The apomict was patented in the U.S. No other examples of apomictic reproduction among the cultivated cereals have been described in the literature. A high seed-set rate of plump seeds was discovered during experiments on the fertilization of an R-2 diploid spring rye with pollen of a A-1 soft spring wheat (Kyzlasov 2008). All offspring were found to be diploid (2n = 14) rye plants. The 2n = 42 pollen of soft wheat induced apomixis in rye. Becasuse of this fact, diploid rye can be reproduced by fertilization with soft wheat pollen. Polyhaploid offspring with partially fertile pollen arose in the reciprocal combination (wheat/rye, 2n = 28).

After long-term research, we have succeeded in creating an apomict of winter rye. The parent plant, R-1 rye, was found in a soft winter wheat crop as a species admixture (Kyzlasov 2005). Flowers were fertilized by the pollen of Nemchinovskaya 24 soft winter wheat. Seed set rate was ~20% of the number of fertilized flowers in the fertilization year. The formed caryopses were all plump and had a high germination rate. All offspring in the first generation contained fertile pollen, and they were completely identical with the diploid maternal plant. There were no hybrid plants. After refertilizing the maternal plants with soft wheat pollen, the offspring also was identical to the maternal plant. The results of the previous experiment have been repeated. The apomixis induced by soft wheat pollen in R-1 rye was manifested in both first and second generations. The maternal offspring varied in quantitative characteristics (stem length, spike productivity). The R-1 rye plant was heterozygous. This population was reproduced on an isolated plot under wind pollination. Apomictic embryo development in the flowers of soft wheat and triticale induced by R-1 winter rye pollen was known from previous experiments (Kyzlasov 2005, 2007). The technique for creating plants showing no segregation in the offspring has a practical application in breeding in the creation of lines of Nemchinovskaya 24 soft winter wheat with similar stem lengths. Initially, this cultivar was segregating for stem length for some obscure reasons. However, maternal families of Nemchinovskaya 24 obtained after fertilization with R-1 winter rye pollen were similar for stem length.

Plants with sterile pollen and abortive anthers were found in the next generation within the studied rye population offspring. Plants with sterile pollen showed involution in the development of quantitative characters; approximately 6% of the total number of plants in the population. Abortive anthers were removed to eliminate the possibility of self-pollination and emasculated spikes covered with paper cages. Isolated caryopses were formed in unpollinated flowers without the participation of a paternal parent. The caryopses from the paper cages without pollination were sown in a glass house and their offspring produced no seeds unless pollinated with a paternal plant. Their pollen was sterile. Plants with fertile pollen were allowed to wind pollinate on an insolated plot with the pollen of their own population. The derived seeds were sown in the field. Approximately 25% of offspring had sterile pollen at anthesis. Plants with fertile pollen and plants with sterile pollen were grown in wheat crops free from wind pollination. Seeds from the plants with sterile pollen were used for further research. Making genetic analysis of self-sterile plants with wind pollination presents great difficulties.

Seeds taken from plants without pollen were sown in the field. Among the derived offspring, approximately 67% formed normal pollen and 33% formed sterile pollen. At the beginning of anthesis, plants with fertile pollen were removed. The plants with sterile pollen were reproduced in a winter wheat crop. However, the fact that rye pollen brough in by wind from remote parts of the field on to pistils of the flowers with sterile pollen could not be absolutely excluded. Mean seed set of the plants without pollen under free wind pollination was 55.4%. The number of flowers in

a spike was 60.9, grains/spike was 33.8, 1,000-kernel weight was 28.9, and spike productivity was 0.98. The indices of the five best plants are presented in Table 1.

Table 1. Seed set and the development of spike productivity features of rye plants with sterile pollen under free wind pollination in a wheat crop.

Plant number	Seed set (%)	Flowers/spike	Grains/spike	1,000-kernel weight (g)	Spike productivity (g)
1	75.7	75.6	57.2	29.2	1.67
2	73.0	63.8	46.6	29.9	1.39
3	72.7	60.0	43.6	37.4	1.63
4	72.5	76.4	55.4	28.2	1.56
5	70.6	52.4	37.0	30.0	1.11

From the maternal plants of the previous generation with sterile pollen, 279 rye offspring were reproduced. The spikes of every plant were covered with paper cages before the beginning of flowering. One hundred eighty-eight plants produced normal pollen under the paper cages. Most likely, these plants were produced as a result of cross pollination of male-sterile flowers by rye pollen in the previous generation. Under self pollination, an average of 182 plants with fertile pollen produced one caryopsis/spike. The autosterility genes of these plants worked normally. Another six self-pollinated plants had from 32 to 65 caryopses/spike. These were self-fertile plants. Pollen fertility is a dominant feature. The distinctive feature of the 58 plants with sterile pollen was the ability to set seed without pollination under the paper cages. The other 33 plants with sterile pollen did not set seed under the paper cages. Small, nonviable germination of plants in the shape of a lamina rosette were produced instead of pistils within one such offspring. Apomictic reproduction and sterile pollen were inherited by the rye offspring as linked features. The distribution of rye plants with sterile pollen in the various series by seed-set rate under paper cages is given in Table 2. On average, 12.2 caryopses were produced per spike within the best group of plants. The ratio of produced seeds to flowers/spike was 18.4%.

Table 2. Distribution of rye plants in various series by the number of caryopses produced/spike.

Grain number class	No of families studied	Grains/spike	Flowers/spike	Seed set
0	33	0.0	60	0.0
< 1–3	36	0.7	58	1.2
> 3	22	11.2	61	18.4

Productivity rates of the eight best apomictic plants are presented in Table 3. High variation was discovered in the manifestation of all features excluding 1,000-grain weight.

Table 3. Rate of seed sete and development of spike productivity features of apomictic rye plants under paper cages without pollination.

Plant number	Seed set (%)	Flowers/spike	Grains/spike	1,000-kernel weight (g)	Spike productivity (g)
1	82	73	60.3	22.9	1.38
2	37	70	27.3	26.5	0.72
3	34	67	23.0	17.2	0.40
4	29	64	18.4	32.0	0.59
5	25	68	16.7	33.3	0.56
6	19	65	12.4	27.8	0.34
7	22	60	13.4	25.0	0.33
8	18	56	10.1	14.6	0.15

Pistils of the apomictic rye produced develop with normal germinating ability. Hybrid F_1 plants, produced after pollination of paternally sterile flowers by pollen from other plants, produce fertile pollen, indicating that the fetal sac cells in the rye are reduced. Diploid plants produced without a paternal parent inherit the sterile pollen feature, which is recessive. Apomictic plants with sterile pollen can be reproduced without pollination on isolated plots. They can be used for production of heterosis plants and genotypes, which are resistible to some pathogens. The production and identification of such offspring in allogamous species are complicated. Tetraploid apomicts can be produced by duplication of the chromosome set. High seed set is possible in the produced tetraploids. At the same time, they will be unable to cross with the source diploid rye. The ability of rye for apomictic reproduction may be transferred to other cultivated cereals species using genetic engineering techniques. Haploids are not seen among plants with both sterile and fertile pollen. The phenomenon of polyembryony was noticed in the apomictic offspring. Up to five viable germs are formed in a caryopsis without pollination.

The study of apomictic offspring was continued under glasshouse conditions. From an unknown cause, anthers with pollen formed in approximately a half of the studied offspring under insufficient light conditions, a surprising fact. However, almost all the pollen in these anthers was nonviable. Up to 12 caryopses were set in unpollinated flowers of each spike. Analysis of the genetic organization of the described rye apomixis is hampered by the fact that autosterility genes are manifested in the phenotype. The mechanism of embryogenesis also remains unknown. Perhaps, the endosperm of apomictic rye is diploid. Starch grains in apomictic rye endosperm are smaller to those in the endosperm of amphimixis plants. The aleurone layer is thinner than in amphimixis plants and is missing in some. The caryopsis coat is contiguous with the starchy endosperm in these irregular places. Apomict endosperm and embryo are not produced in every flower. Seed set under paper cages varies from 0 to 82% of the number of flowers in the spike. Sometimes endosperm or embryo remains abortive. When there is no budlet in the embryo, a scutellum will normally develop. If there is no embryo, but there is an endosperm in a caryopsis, the micropyle will be occluded thoroughly. As a result of the proliferation of external seed coat cells, a tightly closed protuberance in the shape of denticle or papilla, called a caruncle, is formed around the micropyle. The micropyle of apomict plants, as a rule is, occluded (Shishkinskaya 2005). In nearly all ripe, apomictic caryopses, the micropyle cavity and space between the embryo bottom and caryopsis coat is filled with a pink, vitreous substance. This pigment is not usually present in amphimict rye. Amphimict rye, unlike normal rye, has very thin floral glumes, especially the inner glumes.

Diploidy of apomictic rye offspring produced without a paternal parent indicates that they can develop from unreduced cells of the fetal sac or nucellus, such as in *Poa bulbosa* (Kordum 1970). There is no digenesis in these cases. Offspring completely identical to the maternal parent are produced. The nature of origin of adventive fetal sacs from the nucellus cells is similar to the origin of the budlet in the sporophyte phase. In apomictic plants, haploid cells of the fetal sac can give birth to a diploid embryo as a result of chromosome endoduplication (Maheshwari 1954). Apomictic rye plants have a prolonged period from the beginning of stem formation until anthesis. Perhaps that is why the pyles of the stigma and flower lodicules are overgrown. Kyzlasov (2006) discovered earlier that in rye with polygynous flowers, lodicules are converted into pistils. With no pollination, the life of the pistil in apomictic rye plants was 10–15 days longer; with no pollination, the stigmas die earlier than the ovaries.

In apomictic caryopses, the seed coat and endosperm are wrinkled. The seed coat hangs down from the endosperm. A translucent bubble of fetal integument forms at the bottom of embryo. In cross section, the caryopsis covering is porous and vesicular. Apomictic rye has a tendency to break between the cell proliferation layer of the seed coat and other parts of the caryopsis. The endosperm grows together poorly with a caryopsis cover and only partly occupies the pericarp. Sometimes a gap in the lower part of the suspensor of a ripe caryopsis consists of dark, mortified tissue that does not fasten at the micropyle and does not adjoin the caryopsis covering. A cavity often forms in the middle of the caryopsis. Caryopses are flat and compressed from two opposite sides and sometimes only a caryopsis cover without endosperm is formed in them. A large part of the caryopsis rises to the surface if submerged. The main root is often abortive.

The produced apomictic rye has the ability for sexual reproduction but differs from normal rye by pollen sterility. Seeds form after pollination with pollen from other plants. Normal rye plants are produced under such conditions. However, with no pollination, overriping and perishing pistils transform into caryopses without the participation of a paternal parent. The offspring are diploid plants. The study of winter rye apomict described in this article will be continued.

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One hundred years of breeding spring bread wheats in Saratov.

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Scientific selection at Saratov began on 1 March, 1910. During the long history of the spring bread wheat breeding laboratory, 52 cultivars were created and entered into the State Variety Testing Commission, 32 of which were released. Lutestsens 62, Sarrubra, Albidum 43, Saratovskaya 29 and others were created thanks to the joint efforts of a team-oriented staff consisting of laboratory specialists and talented scientists who headed the work, Drs. A.P. Shekhurdin (1911–51), V.N. Мамontova (1952–71), and L.G. Ilyina (1972–86). The first directors of the Saratov Agricultural Experimental Station, A.I. Stebut and academician G.K. Meyster, made great contributions in developing spring soft wheat selections.

Each new cultivar from the spring bread wheat breeding laboratory increases the yield capacity when compared with the standard cultivar, and the increase indicator does not decrease after one year of selection. For more than 50 years, the increasing yield rates in the red-grained wheat cultlivar group is about 12 kg/ha/year, compared with the white-grained cultivars where only recently has the level reached 10 kg/ha/year. Compared to Lutestsens 62, the yield capacity of Saratovskaya 74 and Saratovskaya 68 has increased up to 184% and 192%, respectively, almost double.

In 2010, the prospective new cultivar Saratovskaya 74 was given to the State Variety Testing Commission. Saratovskaya 74 is an albidum-type wheat, a typical Volga steppe ecological group representative. On average during the 4-year period (2006–09), considering fallow land production under grain yields of 2.43 t/ha, Saratovskaya 74 produced 0.95 t/ha more than Saratovskaya 55 (the standard cultivar). With a fore crop, winter wheat yielded 1.45 t/ha, producing 0.32 t/ha more. Saratovskaya 74 is medium ripening in the conditions of the Saratov region, ripening at the same time as Saratovskaya 55, 84–87 days. This new cultivar is practically resistant to red rust, loose smut, and has average resistance to mildew. Vunerability and damage by stem pests of Saratovskaya 74 is at the same as standard cultivar. Flour capacity corresponds to the standards required for the strong wheats, although for this trait Saratovskaya may have an advantage. Although both cultivars have equal of albumin and crude gluten content, Saratovskaya 74 greatly exceeds Saratovskaya 55 in volume bread output. Saratovskaya 74 is suggested for use in the Lower Volga area and the Ural region of the Russian Federation.

The evaluation of spring bread wheat cultivars, NILs, and promising introgression lines in the hard drought vegetation conditions of 2009.

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A hard drought was observed in 2009 during the spring bread wheat vegetative period. In the initial vegetation stage, the crop was highly infested with frit flies (*Oscinella fri*t (L.) and *O. pusilla* (Mg.)). Further degeneration of plants after defeat by insects was accompanied by an increasing drought. Lack of precipitation was observed during the entire vegetative period. Evaluation of a set NILs with alien leaf rust-resistance genes and thier combinations and promising introgression lines with gentic material from *T. turgidum* subsps. *durum*, *dicoccum*, and *dicoccoides*, *Ae. speltoides*, *Ae. umbellulata*, *Th. elongatum*, and *Th. intermedium* were evaluated for drought resistance.

Material from *T. turgidum* subsps. *durum* (cultivar Saratovskaya zolotistaya), *dicoccum*, and *dicoccoides*, *Ae. speltoides* (T2D·2S), *Ae. umbellulata* (*Lr9* translocation), and *Th. intermedium* (6Agi(6D) in bread wheat background does not confer resistance, but genetic material from *T. turdigum* subsp. *durum* (cultivar Melyanopus 26), *Th. elongatum* (*Lr19* translocation), and the combinations *T. turdigum* subsp. *dicoccoides* + *T. turdigum* subsp. *durum* (cultivar Ludmila + Saratovskaya zolotistaya) and *Th. elongatum* + *S. cereale* (*Lr19+Lr26* translocations) increase resistance to drought. The combinations with translocations *Lr19+Lr24* (*Th. elongatum*) and *Lr19+Lr25* (*Th. elongatum* + *S. cereale*) significantly decreased resistance to drought. In these lines, except for the direct influence on drought resistance, the other

significant influence were from the genes determining tolerance to frit flies and ensuring a fast regeneration of injured plants.

Agronomic performance of multilinear mixes on the basis of spring bread wheat cultivar Dobrynya in 2009.

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Previously, we reported on studying multilinear mixes of the spring bread wheat cultivar Dobrynya in the vegetative conditions of 2008, chacterized by moderate precipitations and a moderate leaf rust epidemic (Ann Wheat Newslet 55:174-175). The vegetative period in 2009 was characterized by a hard drought. We were interested in determining the reaction of the multilinear mixes to this very important abiotic stress.

The investigated mixes included four components: Dobrynya, Dobrynya *Lr19+Lr9*, Dobrynya *Lr19+Lr24*, Dobrynyfa *Lr19+Lr25*. All components were tested in equal parts. We also used mixes from the first (prepared in 2009), second (after cultivation in 2008), and third (after cultivation in 2007 and 2008) years. The control mix used all lines and the cultivar Dobrynya. We estimated heading date, plant height, 1,000-kernel weight, grain productivity, grain protein content, gluten content, gluten strength, and SDS evaluation.

For heading date, the multilinear mixes did not differ from components or the cultivar Dobrynya. For plant height, the components did not significantly differ among themselves, except for Dobrynya *Lr19+*, which had a smaller plant height. Multilinear mixes did not significantly differ for plant height from the components average. For 1,000-kernel weight, significant differences were not observed, but among the component lines, Dobrynya *Lr19+Lr24* had the highest. For grain productivity, the mixes did not differ significantly from the component average although the increase in grain productivity of mixes in the third year was 18%. In the second year, mixes had lower grain productivity. For grain protein content, gluten content, gluten strength, and SDS evaluation, the mixes did not significantly differ from the component average. However, among the component lines and mixes, the cultivar Dobrynya had the highest values for all estimated agronomical traits.

Resistance of wheat–Thinopyrum elongatum substitution line L3065 (3Age/3D) to a complex of fungal diseases.

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Thinopyrum elongatum is the donor of many genes for resistance to pathogens and pests, including leaf rust-resistance genes *Lr19*, *Lr24*, and *Lr29*; stem rust-resistance genes *Sr24*, *Sr25*, *Sr26*, and *Sr43*; and *Cmc2*, resistance to the mite *Aceria tosic hilla* (Acari: Eriophyidae). We studied the spring bread wheat line L3065 (Saratovskaya 55/*Th. elongatum* *3/Saratovskaya 29) for resistance to leaf rust, powdery mildew, stem rust, loose smut, and common bunt. Studies have shown that this line is susceptible to leaf rust, powdery mildew, and stem rust similar to the recipient cultivars Saratovskaya 55 and Saratovskaya 29, but is affected significantly less by loose smut and common bunt (Table 1). The line also has race-specific resistance to races of loose smut. The C-banding pattern of this lines showed *Th. elongatum* substitutions with chromosomes 3Age (3D), indicating that chromosome 3Age carries the gene(s) for resistance to loose smut and common bunt.

Table 1. The infection type of spring bread wheat lines and cultivars to leaf rust, powdery mildew, loose smut, and common bunt averaged over 6 years on cultivars and lines to race T18, F*=12.6

Cultivar, line	Leaf rust	Powdery mildew	Stem rust	Race pathotypes					
				Loose smut				Common bunt	
				T18*	I-505	I-164	I-C36	894	Tul5
L3065	3	2	3	21.38 a	8.8	26.3	24.0	0.0	0.0
Saratovskaya 55	3	3	3	66.85 c	63.2	62.5	65.5	25.0	8.6
Saratovskaya 29	3	3	3	52.22 b	36.8	22.7	52.9	38.6	24.5

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Haploid plants production in triticale-wheat hybrids.

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Triticale–wheat hybrids developed using modern local wheat and rye cultivar are a valuable, initial breeding stock with introgressions of D-genome genetic material. Plants in the F_3–F_4 of two selfed hybrids were used for haploid plant production using anther culture. An induction medium with sucrose, maltose, and 2 mg/L 2,4-D was used to obtain haploid embryo-like structures. Responding anthers were transferred for callus development on a regeneration medium with 2% sucrose and 1 mg/L IAA. The number of green and albino plants was counted after about 30 days depending on plant development. Well-rooted regenerants were subjected to colchicine treatment.

Our results did not confirm the role of a cold pretreatment of the donor spikes prior to culturing as a trigger for sporophytic microspore development. Altogether, 128 viable green plants and 104 androgenetic albino plants were obtained from 527 embryo-like structures. The frequency of embryogenic anthers (the number of embryogenic anthers/100 anthers) was 8.9–10.5%. The rate of embryo-like structures (the number of embryo-like structures/100 anthers) was 15.5–15.7%. Molecular techniques for DNA, storage protein analysis, and FISH will be used to identify alien chromosome insertions or substitutions in the callus. The DH lines will be multiplied and investigated for resistance to biotic and abiotic stresses.

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Physiological–morphological changes in wheat seedlings inoculated with Azospirillum bacteria.

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The physiological–biochemical bases for the functioning of plant–microbial symbioses is a topical problem in current agrobiology. With the known positive effects of interaction between the macro- and micropartners in symbioses, little attention has been paid to the functioning of root apical meristems, which serve as the formative and regulatory centers in the plant host (Ivanov 2004) and are a major site for the localization of associated bacteria (Bashan and Levanony 1989). We have investigated the mitotic activity of root meristem cells and the morphological parameters of wheat (cv. Saratovskaya 29) seedlings after root inoculation with the associative bacteria *Azospirillum brasilense* Sp7 and Sp245.

Etiolated, 3-day-old wheat seedlings were inoculated for 24 h in suspensions of *A. brasilense* Sp7 and Sp245 and the enterobacterium *Escherichia coli* K12 (cell density, 108 cells/ml). Other seedlings were treated with *A. brasilense* Sp245 prefixed with 2% glutaraldehyde. After inoculation, the seedlings were placed in water. The control was uninoculated plants grown in hydroponic culture. Samples were taken 2 days after inoculation. The functional activity of the root meristem cells was assessed by using two parameters: (1) determining the cell mitotic index and (2) comparative estimates of the content of the proliferative antigen of initials (PAI), a molecular marker for wheat meristem cells (Evseeva et al. 2002). To determine the mitotic index, root apex meristems were fixed in acetic acid–ethanol (1:3), stained with acetohematoxylin, macerated with cytase enzyme, and visualized at 400× magnification. PAI was revealed by enzyme immunoassay by using rabbit monospecific anti-PAI antibodies.

Inoculating wheat seedlings with live *Azospirillum* cells led to an approximately 2-fold increase in the mitotic activity of the root meristem cells and to an almost 1.5-fold increase in the PAI content in these cells. The effect of strain Sp245 did not differ essentially from that of strain Sp7. Shoot length increased by 30–40% and root length increased by 20–30%. The treatment of the seedlings with glutaraldehyde-fixed *A. brasilense* Sp245 did not substantially change the values for mitotic index of the root meristem cells, PAI content, or the morphological parameters. Our data agree with

those of Bashan et al. (1986), who showed that heat-killed azospirilla lose their adsorption ability, which indicates that active bacterial metabolism is needed for bacterial attachment to roots. *E. coli* K12 did not have a significant growth-promoting effect on wheat seedlings. The inoculation-induced enhancement of mitotic activity in root meristem cells is probably the main cause for the increase in the morphological parameters, although our results may indicate that the change in PAI content in root meristems is a parameter that characterizes the effectiveness of plant interactions with the soil microflora.

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Growth activation testing of wheat cultivars for aluminum toxiticy.

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Table 1. Increase of the vegetative part (cm) of the spring wheat cultivar Lada with the addition of Al (3 mg/L) into soil and solution.

Variant	Days-after-germination			
	6	8	10	12
Control	1.09± 0.35	1.76 ± 0.84	2.43 ± 0.81	3.16 ± 0.79
$AlCl_3$	1.63 ± 0.50	3.49 ± 1.45	4.67 ± 1.25	5.52 ± 1.29

Table 2. Increase in the leaf area (cm^2) of spring wheat cultivars with the addition of Al (0.72 mg/10 g soil) into soil and solution.

Variant	Cultivar		
	Voronezhskaya 14	Omskaya 24	Kerba
Control	51.98 ± 6.81	38.71 ± 7.65	38.18± 3.87
$AlCl_3$	68.16 ±14.84	45.07 ± 6 06	42.62 ± 3.78

The toxic influence of Al ions on plants is real and urgent in breeding Al-resistant cutlivars. Al-tolerance investigations have been conducted in solutions with 10, 30, 50, and 200 μM Al all over the world. Growth and changes in plants processes were researched in the investigations. At the genomic level, some cultivars have tolerance genes to Al ions, but the toxic effects of such ions appears in root shortening and chromosome aberrations.

At the same time, we discovered that Al ions cause root shortening as often as not and sometimes cause forcing of the vegetative part of wheat germ. Leaf length and area in several cultivars increase considerably Al (Tables 1 and 2). The length of the Lada seedlings in the Al variant increased by 74.74% over the control by the 12th growth day. Leaf area also increased in cultivars Voronezhskaya by 31.1 %, Omskaya 24 by 16.4%, and Kerba by 11.6% over the control. Stimulation of leaf growth could be caused by early sensitivity to Al toxicity.

The Al solution stimulated leaf growth but to different degrees among the three cultivars tested (Fig.1). The greatest

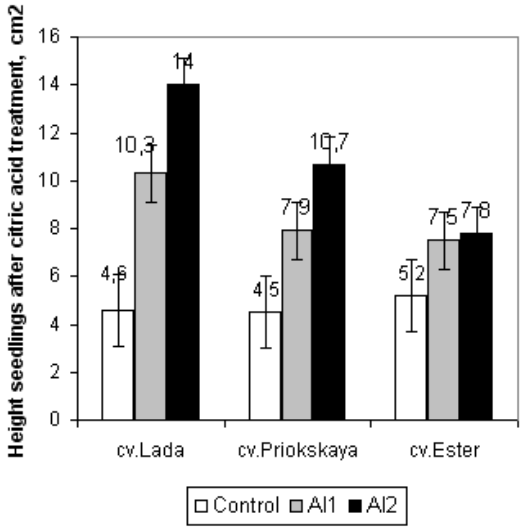

Fig. 1. Area of assimilating leaf surface (cm^2) of the spring wheat cultivars Lada, Priokskaya, and Ester atfter a preplanting seed treatment with citric area.

increase was in the leaf area of the cultivar Lada, which was 2.0% times the control. The leaf area of the cultivar Priokskaya increased 1.06% over the control and the cultivar Ester increased by 47.0%. The relationship between stimulation of leaf growth and plant productivity in Al-weak soils is the capability of greater productivity. We suggest that there is a possible adaptation mechanism of wheat cultivars that are able to initiate early growth because of Al in soils.

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Effect of bacterial lipopolysaccharide on the morphogenetic potential of wheat callus cells in vitro.

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The major problem when cultivating plants *in vitro* is ensuring that the cells preserve their morphogenetic potential. Plant-associated methylobacteria stimulate plant growth and morphogenesis *in vitro* (Kalyaeva et al. 2001). Volkogon et al. (2006) also found that the nitrogen-fixing bacteria *Azospirillum* promote potato growth in an *in vitro* culture. However, inoculation of plants with whole bacterial cells in a *in vitro* culture is fraught with methodology-related difficulties. In view of this, a problem is using bacterial cell components that are responsible for plant–bacterial interaction, and not a bacterial suspension, to treat explants. The outer-membrane lipopolysaccharide (LPS) of the nitrogen-fixing bacteria *Azospirillum* is an active cell component that not only determines bacterial contact interactions with the roots of plants but also is involved in processes inducing plant responses to these interactions (Matora et al. 1995; Evseeva et al. 2009). Our work examined the influence of LPS on the morphogenetic parameters of cultivation of somatic wheat calli differing in the *Rht-B1c* gene.

Immature embryos of two near-isogenic wheat lines (genetic background of cultivar Saratovskaya 29) differing in the *Rht-B1c* gene were placed on Linsmaier–Skoog medium, an experimental nutrient medium for callus initiation, that contained LPS at 1, 2.5, 10, and 100 μg/mL. The resulting morphogenic calli were transferred to a regeneration medium with the same LPS content. The standard medium did not contain LPS. The morphological characteristics of the calli were assessed on day 30 of culturing by using two parameters: yield of morphogenic calli and their content of proliferative antigen of initials (PAI), a molecular marker for wheat meristematic cells (Evseeva et al. 2002).

Callus formation in the wheat lines was high (close to 100%) in all treatments. The addition of 10 μg/ml of LPS to the nutrient medium had a positive effect on morphogenic callus formation in the line with the *Rht-B1c* gene. The yield of morphogenic calli in this line increased almost twofold. LPS at 10 μg/ml also increased the content of PAI in the callus cells of all genotypes studied. Compared with the tall sister line and the original cultivar, the line with *Rht-B1c* showed a significant difference. In other treatments, we did not record any significant effect of LPS on the morphogenetic activity of the calli. Similarly, no substantial differences in the 'mass of morphogenic calli' parameter were found between the standard and experimental nutrient–medium versions. Overall, this study confirmed the previously found positive effect of the *Rht-B1c* gene on all stages of *in vitro* tissue culture compared with the *Rht-B1a* allele (Tkachenko and Lobachev 2008). In most cases, the influence of genotype was greater than the effect of introducing LPS into the nutrient medium.

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Drought resistance in winter wheat.

Drought resistance is the ability of a plant to change metabolic processes as little as possible during conditions of insufficient water supply. The adaptiveness of a plant determines the structural degree of the fibers. The physiological functions of a plant are connected closely with its morphology and anatomy. The xerophytic structure of winter wheat promotes its resistance to drought during all vegetative periods. The harder and longer the drought, the greater the influence of xerophytic characters on yield elements.

The xerophytic nature of a plant can be assessed using stomata number per leaf area. To determine this value in wheat, we measured stomata/leaf are in flag leaves, in the middle of the leaf, and along the both sides of a central vein. The greater the number of stomata, the more xerophytic the cultivar. Other criteria for drought resistance are a water deficit determination, such as the lack of water present in a plant during a drought and residual water deficit, which is the amount of water present in the early morning. Our work revealed a correlation between residual water deficit signs with a level of variety drought resistance ($r = 0.91$). Field observations were made during the drought conditions in 2003, 2005, 2007, and 2009.

Xerophytic cultivars posses high levels of complex plant stability index (distinguished at the primary developmental stages). The greatest number of stomata/leaf area, i.e., more xerophytic, and water and temperature stress resistance were the cultivars Don 93, Ermak, and Zarnitsa. Winter wheat cultivars have a high ($r = 0.99$) correlation dependence of xerophytes value and complex resistance index. Xerophytic structure promotes the economic and efficient consumption of water by the leaves and is expressed more in genotypes resistant to drought. These conclusions were confirmed in the laboratory and by evaluating the drought resistance of winter wheat in a field experiment.

In the field, increased water content in the leaves increases drought resistance if not accompanied by a decrease in ventilation. We took into consideration the degree of leaf ventilation, i.e., we determined a number of open stomata per leaf square. Cultivars with an increase in xerophytic characteristics possess a high water holding ability. For example, Don 105 has the lowest residual water deficit at flowering (10%) and has the greatest number of stomata/leaf are ($27/mm^2$). The cultivars Deviz, Don 95, and Don Kolos, which had the greatest moisture deficits of 27, 30, and 36%, respectively, possessed the smallest number of stomata/leaf area, 13, 12, and $8/mm^2$, respectively. The correlation between xerophytic value and the residual deficit is $r = 0.42$ (medium).

Drought-resistant cultivars can lose water without harm and need not close stomata significantly longer, even in periods of a harvest drought, positively influencing assimilation speed, increasing CO_2, and strengthening the photosyn-

thesis process; these processes increase stomata conductivity. Drought-resistant cultivars have a better developed system for conserving water in the plant fibers, the greatest number of stomata/leaf area, and a more developed water conducting system in the stem and leaves.

Lodging in winter durum wheat.

E.V. Ionova, N.N. Anisimova, V.L. Gaze, and N.E. Samofalova.

Lodging significantly decreases the productivity of grain crops. Early and intense lodging can cause a productivity loss of 60%. All grain crops are subject to lodging, including such stable plants as sorghum and maize. In the field, lodging is preceded by a gradually increase of unfavorable changes in anatomic-morphologic and physiologic processes. Comparing the morphologic and anatomic characteristics during lodging reveals plant reaction during sprouting.

The level of lodging was determined after assessing the density of supporting fibers in durum winter wheat cultivars resistant and susceptible to lodging. Cross sections of the lower part of the first two main stem internodes at milkly ripe phase of grain were stained with a 1% safranin solution. Using an ocular-micrometer, the hypoderm thickness was measured the number of cells calculated. The hypoderm consists of a number of vascular-fibro bundles in hypodermis and parenchyma.

The thickness of the mechanical fibers in cultivars resistant to lodging are larger than those of susceptible cultivars. The thickness in resistant cultivars at the first internode is 8.7 mkm and 8.6 mkm at the second, compared to 7.4 mkm and 7.5 mkm, respectively, for susceptible cultivars. Cultivars resistant to lodging have 4.1 and 4.2 rows of mechanical internode fibers and susceptible cultivars have only 3.5 and 3.6 rows. The vascular bundles are situated in the stem walls. Bundles coming through the hypoderm are very tiny, located at great distances from each other. In the parenchyma next to the large vascular bundles form an inner ring in the stem. The bundle walls consist of mechanical fibers, comprised of thin, stretched fibers that strengthen the stalk. In resistant cultivars, 18.8 conducting bundles are in the mechanical fibers at the first internode and 20.0 at the second internode. In lodging-susceptible cultivars, there are 13.0 mechanical fiber conducting bundles at the first internode and 13.8 at the second internode. Stable cultivars have 29.1 conducting bundles in the parenchyma at the first internode and 30.6 at the second internode, whereas susceptible cultivars have 26.1 and 26.7 at the first and second internodes, respectively.

The diameter of the internode of resistant cultivars is 34 mkm or 18% more than that in susceptible lines. Significant differences were noted in the diameter of the first and the second internodes among the cultivars. Resistant samples have a first internode diameter of 39.8 mkm greater (390.4 mkm) compared with susceptible cultivars (350.6 mkm). The difference of the size of the second internode is a little greater among samples of the different stability groups, 418.9 mkm (resistant samples) and 377.0 mkm (susceptible samples).

Our experiments established that the growing conditions greatly influence the dimensions of the stalk fibers and their correlation. In dry conditions, the epidermal cells are larger, the walls thicker, parenchyma greatly diminishes although the dimensions of individual cells do not change much, the number of chlorophyll-carrying cells decreases, and the dimensions and number of vascular bundles change. The basic features that determine stability are those of the inner stem structure, number of vascular fiber bundles, thickness of the mechanical fabric ring, and the degree of sclerefication of all cell walls.

Lodging occurs more frequently when soil is extra moist. Stems in the lower part of the plant stretch, cell walls become thinner, mechanical fabrics develop weaker, and stem firmness decreases. The principal way to fight lodging is selection and introduction of nonlodging cultivars in agricultural production.

Root system development of winter wheat in drought conditions.

E.V. Ionova, N.N. Anisimova, V.L. Gaze, and T.A. Gritchanikova.

All structures and plant organs, including the root system, help form drought and heat resistance properties. The development of the primary root system of different winter wheat cultivars was evaluated in a growth chamber after 14

days with a 16-hour daylength (18,000 Lux), a day temperature of 19–20°C, and a night temperature of 11–12°C. The experiments was replicated three times. Experimental variants were optimal soil moisture, 70% PV (control), and 30% PV (soil drought). To determine the increase in roots, we germinated seed in filter paper rolls on a full nutrient mixture of Knopp's Solution under different soil temperature regimes (8-12°C, 14-16°C, and 28-32°C). The length of the main germ root was measured after 7 and 14 days; the difference is the increase of root dimension.

At 30% PV (experimental drought), the length of the longest root varied from 17.4 to 26.5 cm and from 22.3 to 30.5 cm at optimal moisture (control). The maximum root length under insufficient water conditions was in the cultivars Ermak (26.5 cm), Donskoy Surpriz (25.3 cm), and Don 93 (24.9 cm).

The germ root varied between 0.56 and 0.86 in drought and between 0.66 and 1.12 at optimal water provision. The largest values ere noted in cultivars Ermak (0.86), Deviz (0.81), and Don 93 (0.78). In the control treatment, Donskoy Surpriz (1.12), Don 93 (1.10), Ermak (1.0), and Donskoy Prostor (1.0) had the largest values. At 30% PV, the maximum dry root mass was in Ermak (10.0 mg), Donskoy Surpriz (9.2 mg), and Don 93 (8.6 mg). The largest ratio of absolute dry root mass to the greatest root length was in Donskoy Majak (0.39 mg/sm) and Ermak (0.38 mg/sm). These results indicated the best cultivars for all parameters of primary root system development were Ermak, Donskoy Surpriz, and Don 93.

Besides moisture, air and soil temperature greatly influence root system formation in wheat (Table 1). A maximum root increase (105.5–148.3%) was noted at 14-16°C. The greatest increase at this temperature was in Ermak, Dar Zernograda, Don 93, and Deviz. At 8–12°C, root increase was not more than 94.4–133.4% with the greatest increases in Ermak, Dar Zernograda, and Don 93. The increase in roots at 28-32°C was 87.3–120.1%. The minimum reduction in the roots under the influence of high temperature was noted in Ermak (13.3 and 28.2%) and Dar Zernograda (3.1 and 12.9%). The lowest increase at all experimental temperature regimes were in Donskaya Bezostaya.

Table 1. Increase in roots of winter wheat under different temperature regimes.

Cultivar	Root increase (%) at temperature		
	8–12°C	14–16°C	28–32°C
Dar Zernograda	130.8	140.6	127.7
Donskoy Majak	120.9	130.0	114.3
Ermak	133.4	148.3	120.1
Stanitchnaya	114.7	128.9	108.8
Donskoy Surpriz	115.6	123.0	105.2
Garant	109.9	129.2	109.9
Don 93	129.0	133.4	119.2
Donskaya Bezostaya	94.4	105.5	87.3
Donskoy Prostor	107.8	114.0	99.7
Deviz	121.0	131.1	111.4
Don 95	98.1	107.0	89.9

The evaluation of winter wheat root system development under different soil warming temperature in the laboratory were practically identical to those from field experiments in 2000–09. In the field experiments, root systems growing at 8–12°C soil temperature consisted of big, strong roots. Roots growing at 14-16°C soil temperature are greatly ramified and their dimensions are greater than those of the first regime. At 28–32°C, branching of roots increases, they become thin, and their color changes from white to brown. Roots growing at 40°C become thick, nutrient absorbtion slows, and, as a result, a decrease of root dry mass takes place (30–40%). Thus, winter wheat roots develop better at low soil temperatures. Substantial root systems depend on temperature and moisture. Changes in root activity in the right direction and selecting the best cultivars accordingly help the selection process.

Winter wheat selection in the Don area.

A.V. Alabushev, O.V. Skripka, T.A. Gritchanikova, N.E. Samofalova, and A.V. Gureeva.

Winter wheat is one of the most significant food grain crops in Russia. Winter wheat in the Don area in some years supplies up to 70% of the gross yield of grain in the Russian Federation. The area under winter wheat in 2009 in the Rostov region was 2,071.5 ha; 53,02% were winter wheat cultivars selected by the SPI ARRIGC. In the Rostov region, which is traditionally a strong and valuable wheat production zone according to its climatic conditions, the grain quality has become noticeably worse and dependent upon the natural climatic conditions, which have become more arable during the past years. The yearly amount of high-quality grain of strong and valuable wheat were 2,640 x 10^3 ton in 1990, 2.9 x 10^3 ton in 2000, 30.3 x 10^3 ton in 2001, and 3,526.2 x 10^3 ton in 2009. To decrease dependence, it is necessary to select

agricultural crops according to the zone more favorable for their cultivation and choose cultivars that have a stable, high-quality grain production.

The State Register recommended 47 winter wheat cultivars, including 24 (51%) selected by the SPI ARRIGC for the Rostov region for 2010. Thirty-nine of the cultivars (83%) are strong and valuable wheats according to their quality, including 23 cultivars (48.9%) selected by the SPI ARRIGC. The most important priorities for wheat selection in the Don area, together with an increase in potential productivity and ecologic stability are greater protein, gluten, baking, and macaroni properties. As a result of purposeful selection, the high-quality, drought resistant, highly productive winter wheats with a potential productivity of 8–10 tons/ha were Zernogradka-10, Zernogradka-11, Rostovtchanka-3, Konkurent, Tanais, and Rostovtchanka-5 for predecessors of black pairs and Don 93, Ermak, Stanitchnaya, Don 105, and Don Surpriz for nonpair predecessors.

Lately, an interes durum winter wheat has grown. The greatest achievement of domestic selection for macaroni/cereal usage were the cultivars Don Jantar, Aksinit, Gelios, and Kurant, being highly productive with a potential productivity of 7.0–9.0 t/ha, drought resistant, and winterhardy. These cultivars may help solve the deficit of durum grain in the North-Caucasus region.

Cultivars selected by the SPI ARRIGC are able to realize a high level of productivity and quality only when recommended cultivation technology is followed, such as use of fertilizer; feeding during the vegetative period; protection from diseases and pests including insects and the harmful tortoise; and timely harvest. Using quality winter wheat cultivars and the best cultivation technologies will allow agricultural producers to increase the production of high-quality grain.

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Necrotic genotypes in winter bread wheat in the Russian Federation.

V.A. Pukhalskij, S.P. Martynov, and E.N. Bilinskaya.

The hybrid necrosis genes (*Ne1* and *Ne2*) are valuable tools for comparing wheat species and their groups within the genus and evaluating anthropogenic influence on genetic erosion. Hybrid necrosis genes interact by a complementary mechanism (Kostyuchenko 1936). Both genes are located in the B genome. The *Ne1* gene is located on chromosome 5BL and the *Ne2* gene on chromosome 2BS. Allele series for each gene have been demonstrated. The alleles of the *Ne1* gene are *w*, *m*, and *s*, and the alleles of the *Ne2* gene are *w*, *wm*, *m*, *ms*, and *s* (Hermsen 1960, 1963; Chu et al. 2006). Knowledge of the necrotic genotype is also important for selection and evaluation of the original material during breeding of wheat and triticale. About ten new cultivars of common wheat recommended for commercial use are registered in the Russian Federation. Although the data on yield, vegetation period, and resistance to main phytopathogens are available, information concerning genes, and hybrid necrosis genes in particular, is missing. Our work analyzes the distribution of hybrid necrosis genes among wheats of Russia and other countries (Pukhalskiy 1996; Pukhalskiy et al. 2000, 2003).

Here we present our data on necrotic genotypes in 53 cultivars of winter bread wheat (Table 1, pp. 221-222). Most were produced after 2000. The following cultivars were used as testers: Felix (*ne1ne1Ne2Ne2*), Co725082 (*Ne1sNe1sne2ne2*), Mironovskaya 808 (*ne1ne1Ne2msNe2ms*), Nemchinovskaya 52 (*ne1ne1Ne2msNe2ms*), and Berthold (*ne1ne1Ne2mNe2m*). Crossings were conducted in the field by a twel-procedure. Hybrids were grown in the field. Necrotic symptoms were evaluated at different ontogeny stages. Pedigree analysis was conducted with an analytical GRIS system.

Table 1. Necrotic genotypes in 53 cultivars of winter bread wheat from the Russian Federation.

Cultivar	Pedigree	Year of release	Genotype
Zamena	Rubin/Krasnodarskaya 46	1987	*ne1ne2*
Bezostaya 2	Lutescens 314h147/Krasnodarskaya 46	1973	*ne1ne2*
Istok	Pavlovka/Donskaya ostistaya	1988	*ne1ne2*
Novoukrainka 83	Ukrainka/Marquis	1945	*ne1ne2*
Pavlovka	(S)Krasnodarskaya 39	1982	*ne1Ne2m*
Polukarlikovaya 49	Mironovskaya Yubileynaya Yubileynaya 50/Krasnodarskii karlik 1	1979	*ne1ne2*
Severokubanka	Krasnodarskaya 39/Krasnodarskaya 6	1980	*ne1Ne2m*
Sharada	KH-4333-9-1001/Obrii	2006	*ne1ne2*
Bat'ko	Lutescens 4217-G-25908-4228/Lutescens 5126-p-58-51//Lutescens 51	2003	*ne1ne2*
Krasota	AD206 (Tritikale)/Rubin//KH-17-t-3 (Tritikale)	2002	*ne1ne2*
Prikumskaya 140	Spartanka 10/Colt//Spartanka 10	2003	*ne1Ne2ms*
Stanichnaya	BP-566-86/BP-1302-82	2002	*ne1Ne2m*
Fortuna	Lutescens –1985-t-124/Soratnitsa	2006	*ne1ne2*
Fisht	Skifyanka *2/3/Tr.MI//Kavkaz	2004	*ne1Ne2ms*
Bezenchukskaya 616	Bezenchukskaya 380/Volgodar//Bezenchukskaya 380	2005	*ne1Ne2s*
Volzhskaya 100	Khar'kovskaya92/Unknown	2004	*ne1Ne2s*
Volzhskaya K	Kinel'skaya 4/Unknown	2004	*ne1Ne2s*
Omskaya 4	Mironovskaya 25(M)/Saratovskaya 8	2001	*ne1Ne2s*
Kazanskaya 560	(S) Meshinskaya 2	2002	*ne1ne2*
Levoberezhnaya 1	Krasnodarskaya 39/Donskaya ostistaya//Donskaya bezostaya/3/Ershovskaya	2003	*ne1ne2*
Mafe	86-KPM-684/KH-4636-h-202-56//KH-4336-h-202-56	2006	*ne1ne2*
Pionerskaya 32	Albidum 114/Bogarnaya 56//Dneprovskaya 521	2006	*ne1ne2*
Omskaya 5	(S) Sibirskaya niva	2004	*ne1Ne2s*
Svetoch	Chaika/Kavkaz//Don 85	2004	*ne1Ne2s*
Tau	NS-175-2// Lutescens 2002/Mironovskaya 808/3/Velutinum 4880	2001	*ne1ne2*
Veda	Leda//Polovchanka/Rufa	2005	*ne1Ne2ms*
Vostorg	Tr.MI/Kavkaz//4473- h-144-10	2005	*ne1Ne2s*
Basalt	Donetskaya 79/Albidum 114	1993	*ne1Ne2ms*
Odesskaya 200	Yubileynaya 75/Al'batros Odesskii	2006	*ne1ne2*
Petrovchanka	Erytrospermum G-124080/Yubileynaya 75	2007	*ne1ne2*
Prikumskaya 141	Donskaya bezoskaya/Lutescens G-102649	2004	*ne1Ne2m*
Stepchanka	Lutescens- G-95506/ Eritrospermum G-72134// BP-1648-KB	2006	*ne1Ne2m*
Chernozemka 88	Chernozevka 96/Ershovka 6//Odesskaya 75	2003	*ne1ne2*
Ariadna	Odesskaya 138/Ol'viya//Odesskaya 51/4/Odesskaya 51//Mironovskaya 808	2008	*ne1ne2*
Biruza	Lutescens 1985-h-331/Lutescens 4523-h-42//Zimorodok/6687-12	2008	*ne1Ne2m*
Bogdanka	M 508-97/Volzhskaya 16	2009	*ne1Ne2m*
Volzhskaya C 3	Khar'kovskaya 92/Unknown	2006	*ne1Ne2m*
Galina	Obrii/Pamyati Fedina//Inna	2005	*ne1ne2*
Gratsia	Kupava/ BP=90-178-a-20-5	2008	*ne1ne2*
Gubernator Dona	Erytrospermum 1122-93/Ukrainka Odesskaya	2008	*ne1ne2*
Deviz	Rostovchanka/Avrora	2008	*ne1Ne2m*
Dzhangal	Donskaya bezostaya /Khar'kovskaya 63/Bezostaya 1/Ershovskaya 3	2008	*ne1Ne2m*
Don 105	Don93/Dimetra	2008	*ne1Ne2m*
Kamyshanka 3	Lutescens 332/Khar'kovskaya 92	2009	*ne1Ne2m*
Korund	Apollo/Zentos//Zentos	2008	*ne1Ne2m*

Table 1 (continued). Necrotic genotypes in 53 cultivars of winter bread wheat from the Russian Federation.

Cultivar	Pedigree	Year of release	Genotype
L'govskaya 4	L'govskaya 77//Yubileynaya 58/3/L'govskaya 167/Polukarlikovaya	2008	*ne1ne2*
Moscovskaya 56	Mironovskaya poluintensivnaya/Inna//Moskovskaya 39	2008	*ne1Ne2m*
Nemchinovskaya 24	Donshchina/Inna	2006	*ne1Ne2m*
Odesskaya 267	Odesskaya 51/Inia 66//Bezostaya 1/Mironovskaya 808/3/World Seeds	2001	*ne1Ne2m*
Odesskaya 267	Odesskaya 51/Inia 66//Bezostaya 1/Mironovskaya 808/3/World Seeds	2001	*ne1Ne2m*
Rodnik Tarasovskii	Partisanka/Zirka//Belotserkovskaya 18/Zirka/3/Donskaya Yubilewy-naya	2003	*ne1ne2*
Resurs	Lutescens 1956-225/Al'batros Odesskii	2008	*ne1ne2*
Rostovchanka 5	Skorospelka 35/Mironovskaya 264	2008	*ne1ne2*
Yunona	Eika/ Lutescens 5573-h-16	2008	*ne1Ne2m*

Thirty cultivars (56.6%) had the *ne1ne1Ne2Ne2* genotype and 23 (43.4%) possessed the *ne1ne1ne2ne2* genotype. The data obtained clearly demonstrate the elimination of *Ne1*-carriers, but there is no definite explanation for this phenomenon (Pukhalskiy et al. 2008), especially taking into account that practical breeders have no information on hybrid necrosis genes during selection. For still unknown reasons, the *ne1ne1Ne2Ne2* genotype has selective advantage over the *Ne1Ne1ne2ne2* genotype. The *ne1ne1ne2ne2* genotype has a certain selective advantage.

In 27 cultivars, the strength of hybrid necrosis alleles was determined. Among them the moderate *m* alleles prevailed (63%), four cultivars possessed the allele *ms* (14.8%), and six carried the allele *s* (22.2%).

A pedigree analysis of the distribution of hybrid necrosis genes (Table 2, pp. 222-223) showed that, in most cases, the donors of the dominant allele of the *Ne2* gene in *ne1Ne2*-carriers are the cultivars Mironovskaya 808 and Kras-

Table 2. A pedigree analysis of the distribution of hybrid necrosis genes in cultivars of winter bread wheat from the Russian Federation.

Cultivar	Genotype	Presumed donor	Presumed source
Zamena	*ne1ne2*	Bezostaya 1	Bezostaya 1
Bezostaya 2	*ne1ne2*	Bezostaya 1	Bezostaya 1
Istok	*ne1ne2*	Donskaya ostistaya	Bezostaya 1
Novoukrainka 83	*ne1ne2*	Marquis or Ukrainka	Ukrainka or Hard Red Calcutta
Pavlovka	*ne1Ne2m*	Krasnodarskaya-39	Gostianum 237
Polukarlikovaya 49	*ne1ne2*	Krasnodar. karlik 1	Bezostaya 1
Severokubanka	*ne1Ne2m*	Krasnodarskii-39	Gostianum 237
Sharada	*ne1ne2*	Obrii	Odesskaya-51
Bat'ko	*ne1ne2*	Donskaya ostistaya	Bezostaya
Krasota	*ne1ne2*	Bezostaya 1	Bezostaya 1
Prikumskaya 140	*ne1Ne2ms*	Spartanka	Krasnodarskaya 39
Stanichnaya	*ne1Ne2m*	Donskaya polukarlikovaya	Mironovskaya-808
Fortuna	*ne1ne2*	Soratnitsa	Odesskaya 66 or Partizanka
Fisht	*ne1Ne2ms*	Skifyanka	Krasnodarskaya-39
Bezenchukskaya 616	*ne1Ne2s*	Bezenchukskaya 380	Mironovskaya-808
Volzhskaya 100	*ne1Ne2s*	Khar'kovskaya92	Mironovskaya-808
Volzhskaya K	*ne1Ne2s*	Kinel'skaya 4	Mironovskaya-808
Omskaya 4	*ne1Ne2s*	Saratovskaya 1	Lutestsens 230
Kazanskaya 560	*ne1ne2*	Chernomorskaya	Bezostaya 4
Levoberezhnaya 1	*ne1ne2*	Donskaya ostistaya	Bezostaya 1
Mafe	*ne1ne2*	Donskaya ostistaya	Bezostaya 1
Pionerskaya 32	*ne1ne2*	Al'bidum 114	Al'bidum 11
Omskaya 5	*ne1Ne2s*	?	
Svetoch	*ne1Ne2s*	Don 85	Mironovskaya 808

Table 2 (continued). A pedigree analysis of the distribution of hybrid necrosis genes in cultivars of winter bread wheat from the Russian Federation.

Cultivar	Genotype	Presumed donor	Presumed source
Tau	*ne1ne2*	Mironovskaya 808	Mironovskaya 808
Veda	*ne1Ne2ms*	Zernogradka 6	Mironovskaya 808
Vostorg	*ne1Ne2s*	Pavlovka	Krasnodarskaya 39
Basalt	*ne1Ne2ms*	Mironovskaya 808	Mironovskaya 808
Odesskaya 200	*ne1ne2*	Yubileynaya 75 or Al'batros Odesskii	Odesskaya 51
Petrovchanka	*ne1ne2*	Yubileynay 75	Odesskaya 51
Prikumskaya 141	*ne1Ne2m*	Donskaya bezostaya	Mironovskaya 808
Stepchanka	*ne1Ne2m*	Pavlovka	Krasnodarskaya 39
Chernozemka 88	*ne1ne2*	Odesskaya 51	Ukraika and/or Zemka
Ariadna	*ne1ne2*	Odesskaya 51	Ukrainka and/or Zemka
Biruza	*ne1Ne2m*	Krasnodarskaya 39, Zimorodok	Krymka and/or Gostianum 237
Bogdanka	*ne1Ne2m*	Volzhskaya 16	Mironovskaya 808
Volzhskaya C 3	*ne1Ne2m*	Khar'kovskaya 92	Mironovskaya 808
Galina	*ne1ne2*	Odesskaya 51	Ukrainka and/or Zemka
Gratsia	*ne1ne2*	Leda (Odesskaya 51)	Ukrainka and/or Zemka
Gubernator Dona	*ne1ne2*	Odesskaya 51	Ukrainka and/or Zemka
Deviz	*ne1Ne2m*	Don 85, Kolos Dona	Mironovskaya 808
Dzhangal	*ne1Ne2m*	Donskaya bezostaya, Ershovskaya 3	Mironovskaya 808 and/or Lutestsens 230
Don 105	*ne1Ne2m*	Demetra, Don 93	Mironovskaya 808
Kamyshanka 3	*ne1Ne2m*	Khar'kovskaya 92	Mironovskaya 808
Korund	*ne1Ne2m*	Carstens VIII, Trumpf, Apollo	Krymka and/or Noe and/or Red Fife and/or Prince Albert
L'govskaya 4	*ne1ne2*	Yantarnaya 50, Zarya Bezostaya 1	?
Moscovskaya 56	*ne1Ne2m*	Mironovskaya poluintensivnaya	Mironovskaya 808 and/or Noe
Nemchinovskaya 24	*ne1Ne2m*	Donshchina	Mironovskaya 808
Odesskaya 267	*ne1Ne2m*	Mironovskaya 808, Inia 66	Mironovskaya 808, Frontana
Rodnik Tarasovskii	*ne1ne2*	Belotserkovskaya 198, Partizanka	Ukrainka and/or Autonomia
Resurs	*ne1ne2*	Al'batros Odesskii, Odesskaya 51	Ukrainka and/or Zemka
Rostovchanka 5	*ne1ne2*	Tarasovskaya 29, Peresvet, Odesskaya 51	Mironovskaya 264 and/or Ukrainka
Yunona	*ne1Ne2m*	Yugtina	Mironovskays 808 and/or Siete Cerros

nodarskaya 39. In the latter cases, the source of the dominant *Ne2* allele is Gostianum 237, an old cultivar of the Saratovskaya region. The donors of the recessive genotype *ne1ne1ne2ne2* in most instances are Bezostaya 1 and Odesskaya 51, which originate from Bezostaya 1. The donor of recessive alleles is the old cultivar Ukrainka.

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J.A. Martín-Sánchez and E. Sin.

Ascorbate peroxidase induction in wheat lines infected by Heterodera avenae.

The cereal cyst nematode (CCN) (*Heterodera avenae* Woll.) is the most widely distributed and damaging species on cereals cultivated in less temperate regions. This nematode species has been detected in many countries and it is responsible for yield losses in wheat of up to 30%. The CCN induces syncytial feeding sites in the roots of its hosts. Infective, second-stage juveniles (J2) enter the plant roots at the level of the differentiation zone and penetrate intracellularly towards the vascular cylinder. Here, they select and pierce with their stylet a single cell where they release oesophageal secretions. In the following hours, the affected plant cells start to develop the feeding structures (Das et al. 2008). Plants defend themselves from nematodes using a variety of mechanisms, including rapid induction of localized necrosis at the site of infection (the hypersensitive response: HR), increased expression of defense-related proteins, production of antimicrobial compounds, lignin formation, and oxidative burst. Among the altered biochemical pathways are those involving peroxidases, which comprise a large group of enzymes that use different peroxides (ROOH) as electron acceptors. According to Welinder (1992) these enzymes in plants are classified into three classes (I, II, and III). Class-I enzymes are intracellular and are known as ascorbate peroxidase (APX, EC 1.11.1.11). Reactions catalyzed by APX and the cycle-coupled of AsA–GSH prevent the accumulation of toxic levels of H_2O_2 in photosynthetic organisms. APX activities are located in chloroplasts (chAPX), cytosol (cAPX), peroxisomes, or microbodies (pAPX) and mitochondria, each cellular compartment possessing one or several APX isoforms. In *Arabidopsis*, the same protein is dually targeted to mitochondria and chloroplast stroma (Chew et al. 2003).

Changes in APX enzyme activity in response to nematode *H. avenae* attack were studied in roots of three hexaploid wheat lines carrying *Cre2*, *Cre5*, and *Cre7* resistance genes and the susceptible *T. aestivum* cultivar Anza. Spectrophotometric analysis to study these changes was carried out with root extracts of infected and uninfected plants 4, 7, 11, and 14 days after nematode infection. APX induction in all infected resistant genotypes was higher than in the susceptible control. We analyzed whether this increase of activity was related to an increase of APX gene expression. This study was performed with the introgression wheat–*Ae. ventricosa* H-93-8 line, carrying *Cre2* gene, using its parental H-10-15 as susceptible control. APX genes of cytosolic location were induced in roots of plants attacked by the nematode. This induction took place earlier and with more intensity in the resistant line than in the susceptible one, and it was bigger in the root area where the nematode was settled down. Our results suggest that APX present in wheat roots could play a role in *Cre*-mediated resistance to *H. avenae*, either directly or indirectly. They also demonstrated that the biochemi-

cal basis of defence in hexaploid wheat against the Ha71 pathotype of *H. avenae* could be the same in all the genotypes tested.

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J. Del Moral and F. Pérez Rojas.

New Hessian fly resistant lines releases.

Hessian fly (Hf) is a significant insect pest of wheat in many of the wheat-producing areas around the world. Since its detection in Spain in 1896, it has become a major economic pest of common wheat. At this moment, deployment of resistant cultivars is providing the most efficient and economical means of crop protection against this damaging insect (Berzonsky et al. 2003). The continuous evolution of virulent biotypes makes necessary the identification of new resistance genes from wheat or relative species. The will grass genus *Aegilops* has been recognized as an important potential donor of genes that govern characteristics of agronomic interest, such as resistance genes (Schneider et al. 2008, review). Previous work from our group has demonstrated the transference of *H30* gene, conferring resistance to *Mayetiola destructor*, from *Ae. triuncialis* to hexaploid wheat *T. aestivum* (Martín-Sánchez et al. 2003). Breeding lines (2n=42) were obtained by backcrossing introgression line TR-3531 (with 42 chromosomes) as donor parent of Hf resistance, and hexaploid wheat cultivars carrying good agronomic characteristic as alternative recurrent parent. The *Acph-U1* marker linked to gene *H30* on this line was used for MAS. Advanced wheat lines were evaluated for Hessian fly resistance (described in Delibes et al 1997) in field and growth chamber tests, and for other agronomic traits during several crop seasons at different localities of Spain. Hessian fly resistance level of lines was high but, in all cases, it was lower than its progenitor *Ae. triuncialis*. In collaboration with Agrosa Semillas Selectas SA, we have obtained several wheat lines with good performance for resistance and/or agronomic characteristics. Two of them were recently submitted to the Spanish Plant Variety Office for their evaluation. T-2004 (TR-3531/Betrés//Alcotán/3/Recital/4/3*Betrés) and ID-2105 (TR-3531/Be-

trés//Alcotán/3/Recital/4/5*Betrés) are two-awned and facultative wheat lines, which present tolerance to the population of Hessian fly present in southwestern Spain. These lines are medium-maturing, medium tall, with thin stems, and have dark green foliage at anthesis, with medium-strong glaucosity of sheath and spike.

Cooperation with other institutions. We are cooperating with 'Agrosa Semillas Selectas SA'.

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ITEMS FROM UNITED KINGDOM

JOHN INNES CENTRE
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Genetic biodiversity for stripe and stem rust resistance in African wheat genotypes.

Zakkie Pretorius, Davinder Singh, Ruth Wanyera, Susanna Dreisigacker, Cornel Bender, Denise Liebenberg, Ruth MacCormack, Lesley A. Boyd, and Renée Prins.

Over 500 African wheat genotypes have now been screened for resistance to the new virulent stem rust, *Puccinia graminis* Ug99-derived strains, and to stripe rust, *P. striiformis*, at Njoro, Kenya. Some 300 genotypes have been selected for genetic diversity and association analyses using SSR and DArT markers. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK; Prof. Zakkie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA; Dr. Ruth Wanyera and Davinder Singh, KARI, Njoro, Kenya; and Dr. Susanna Dreisigacker, CIMMYT, Mexico. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative.

Fine mapping of durable resistance to stripe rust in the South African wheat cultivar Kariega.

Gloudi Agenbag, Ruth MacCormack, Zakkie Pretorius, Debbie Snyman, Lizaan Rademeyer, Lesley A. Boyd, and Renée Prins.

Adult-plant resistance to stripe rust has previously been identified in the South African cultivar Kariega, with major QTL being identified on chromosomes 7D and 2B, and minor QTL on chromosome 4A. EST have been mapped to both 2BS intervals and to 4AL in the target QTL interval. These EST provide anchors for further EST-derived marker development within the QTL intervals. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK and Prof. Zakkie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA. The student working on this project is Miss Gloudi Agenbag. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative.

Genetic mapping of adult-plant, stripe rust resistance within the European wheat cultivar Cappelle Desprez.

Gloudi Agenbag, Zakkie Pretorius, Cornel Bender, Debbie Snyman, Lizaan Rademeyer, Lesley A. Boyd, and Renée Prins.

Cultivar Cappelle Desprez was grown in Western Europe throughout the 1960s and 1970s, being a known source of durable adult-plant resistance (APR) to stripe rust. The stripe rust resistance in Cappelle Desprez has remained effective under South African conditions since 2001, and programs are underway to select for this APR in a cross to the South African cultivar Palmiet. A genetic map has been constructed for a RIL population derived from the cross 'Cappelle Desprez/Palmiet', which currently is being used to genetically map the QTL for stripe rust resistance derived from Cappelle Desprez. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK and Prof. Zakkie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA. The student working on this project is Miss Gloudi Agenbag. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative and the Winter Cereal Trust (SA).

Biological and transcriptional defence responses of wheat to non-adapted and adapted species of the blast fungus, Magnaporthe.

Hale A. Tufan, Graham R.D. McGrann, Patrick Schweizer, Ulrich Schaffrath, Rients Niks, and Lesley A. Boyd.

The *Magnaporthe* species complex infects over 50 graminaeceous plant species, *M. oryzae* pathotypes colonising cultivated cereals, whereas *M. grisea* attacks wild grass species. In Brazil, *M. oryzae* has become a field pathogen of wheat, causing wheat blast. We have investigated resistance in the wheat cultivar Renan against species of *Magnaporthe* that are either adapted or not adapted to wheat. Early defence responses against both adapted and unadapted species involved the production of a diffuse autofluorescent HALO structure around the site of attempted fungal penetration. In the case of the unadapted *M. grisea* pathotype, very few infection attempts were able to progress beyond the HALO stage. In contrast, the adapted *M. oryzae* pathotypes were able to develop past the HALO stage, and colonize the leaf. In these cases, whole-cell autofluorescence was often observed, indicative of a hypersensitive response.

Transcriptome analysis of both the adapted and non-adapted *Magnaporthe*–wheat interactions has identified a number of candidate genes integral to the resistance reaction. Functional genomic analysis of these candidate defence genes is currently underway. This program is now funded by a ERA-PG grant, TriNonHost, and forms a new collaboration with Patrick Schweizer, IPK, Gatersleben, Germany; Ulrich Schaffrath, RWTH, Aachen, Germany; and Reints Niks, WU, Wageningen, The Netherlands.

Publications.

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ITEMS FROM THE UNITED STATES OF AMERICA

INDIANA

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Wheat production.

According to the USDA National Agricultural Statistics Service, harvested wheat acreage in Indiana in 2009 totaled 450,000 acres. Wheat production was down from 560,000 acres in 2008. Total production was estimated at 30.1 million bushels, with an average yield of 67 bu/ac. Winter survival of wheat during the winter of 2008–09 was excellent. However, average temperatures from February to mid-June were below normal and soil moisture was higher than normal due to frequent rainfall, resulting in delayed growth and development of wheat and limited uptake of nitrogen, resulting in poor wheat growth in low and wet areas of fields. By mid-June, temperatures were higher and near normal, and there was mild soil moisture due to dry soil conditions, resulting in slightly reduced grain test weight.

Wheat disease summary.

Wheat diseases were generally at low levels throughout central and northern Indiana in 2009. Stagonospora leaf blotch and Septoria leaf blight were problematic in southern Indiana early, and a prolonged period of rainy and humid weather in early May contributed to significant Fusarium head blight (FHB) throughout southern Indiana. The resulting disease caused significant yield loss and reduction in grain quality due to the mycotoxin DON, especially on susceptible cultivars. Due to cool weather conditions, FHB developed late in the season in mid to northern Indiana, and was less severe than in the southern third of the state, although there was some grain yield loss. Leaf rust moved into Indiana late in the growing season, and stem rust was observed in southern Indiana, however, both diseases arrived too late in the growing

season to cause significant yield loss. Several viral diseases of wheat, including wheat streak mosaic virus, wheat spindle streak mosaic virus, soil-borne wheat mosaic virus, and barley yellow dwarf virus were confirmed in Indiana.

Performance of new cultivars.

Herb Ohm.

Cultivar INW0731 yielded well in Indiana and nearby regions. INW0731 has moderate resistance to yellow dwarf, moderate resistance to fusarium head blight from Freedom and Fundulea 201R, moderate resistance to yellow dwarf, leaf rust, resistance to powdery mildew, Stagonospora nodorum blotch, Septoria leaf blotch, soilborne wheat mosaic and wheat spindle streak mosaic viruses, and is susceptible to Hessian fly, stripe rust, and stem rust in Indiana. This cultivar, adapted to southern Indiana and surrounding regions, has survived winters very well in central and northern Indiana, but winters have been mild since 1996.

Cultivar INW0801, which has gene *Bdv3*, also performed well. INW0801 is well-suited to southern Indiana and adjacent areas because yellow dwarf is present many years, and its early maturity is suited to doublecropping, seeding soybeans no-till after wheat harvest.

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, Benjamin Campbell, Judy Lindell, Andy Linvill, Yanyan Liu, Dan McFatridge, Mahboobullah Nang, Brett Ochs, Kristen Rinehart, Wali Salari, Samantha Shoaf, Jin Sun, and Xiangye Xiao.

Fusarium head blight. *Bdv3* and *Qfhs.pur-7EL* were combined in coupling on 7DL; *Qfhs.pur-7EL* is more distal than *Bdv3*. *Bdv2* also was moved from 7DL to 7BL (both objectives were part of Ph.D. thesis research by K. Rinehart). We also combined *Qfhs.pur-7EL* and *Fhb1*, which is located on 3BS. The disease rarely spreads beyond the inoculated floret or spikelet in lines with these two strong FHB-resistance factors in our tests using point inoculation (inoculation of a single floret at flowering with 500 *F. graminearum* macrospores in 10 μl dH_2O and placing a plastic bag over inoculated spikes for 3 d). The disease severity averaged 0.75 diseased spikelets at 21 dai in greenhouse and field tests.

We completed the fourth and last phenotyping experiment to characterize a recombinant inbred population for type-II FHB resistance of a selection of the line Xing 117. Phenotyping in the four tests was carried out by undergraduate students Charlie Zila, Jill Recker, and Emily North; and visiting graduate student from Denmark, Stine Petersen; and Judy Lindell and Yanyan Liu, who also are screening the parent lines, bulks, and population with markers to map the resistance.

Stem and yellow rust. We have identified and obtained germ plasm lines that have resistance to stem rust race TTKS (Ug99) and yellow rust. We have developed recombinant inbred populations from crosses of the new resistant lines x susceptible lines. In collaboration with the USDA–ARS laboratory (Dr. Yue Jin) at St. Paul, MN (Ug99), and at Purdue University for resistance to our local isolates of the causal fungal pathogens, the populations are being phenotyped for resistance. We are mapping the resistance using the bulked-segregant analysis approach.

Marker-assisted seletion. 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.

We released three soft winter wheat cultivars: **INW0801** (very early, moderate resistance to FHB and *Bdv3*), **INW0803** (early, short and stiff straw, excellent for high management), and **INW1021** (moderate resistance to FHB, yellow dwarf disease, WSSMV, SBMV, leaf, stripe and stem rusts (has *Lr37*, *Yr17*, and *Sr38*), powdery mildew, SNB, STB, susceptible to Hessian fly biotype L; is widely adapted, good soft wheat milling and baking qualities, has the *Bx70e* strong gluten allele, and the *Ppd* daylength insensitive allele).

Released germ plasm. Seed of the **91193/92201** RIL population (194 lines plus the two parent lines) was submitted to the UDSA–ARS GRIN, Aberdeen, ID.

Wheat management.

Kiersten Wise and George Buechley.

Fungicides for Fusarium head blight control. Research activities in 2009 focused on evaluating integrated management strategies for control of FHB. A trial conducted in west central Indiana tested the combined effects of a foliar fungicide application at Feekes 10.5.1, and cultivar susceptibility for improved FHB management. The fungicide Prosaro® was applied to experimental plots of six cultivars of varying susceptibility to FHB. Two susceptible cultivars, two moderately susceptible, and two resistant cultivars were included in the experiment. Unsprayed plots also were included.

Fungicide-treated plots had significantly (P = 0.05) lower FHB incidence, severity, FHB index, foliar disease severity, % FDK, and DON levels. Fungicide-treated plots also had significantly greater yields compared to untreated plots, however test weights were not significantly different. In comparisons between fungicide-treated and untreated plots of the same cultivar, fungicide-treated plots had lower disease levels and higher yields in all cultivars except one. Levels of FHB were generally low in 2009 at the research location, which may have contributed to why significantly reduced levels of FHB or DON were not observed in moderately resistant compared to susceptible cultivars. Additionally, yield and test weight results may have been confounded by BYDV infection in moderately resistant cultivars.

The results of this research project indicate that a well-timed fungicide application can significantly reduce the impact of FHB and DON in wheat cultivars and increase yields in most culariv ars. This information is of primary importance to growers and will be presented in extension programs and summarized in extension articles to aid growers in managing FHB and DON in wheat. Additional research is needed to more thoroughly investigate the interaction between fungicide and cultivar susceptibility under Indiana conditions.

Hessian fly: Interactions of wheat with virulent and avirulent Hf larvae.

Christie Williams, Jill Nemacheck, Kurt Saltzmann, Marcelo Giovanini, and Subhashree Subramanyam.

Wheat response to Hessian fly attack. A sequence encoding a new candidate type-1 lipid transfer protein from wheat, Hfr-LTP, was identified and its expression compared to a previously identified Hessian fly-responsive wheat LTP gene, *TaLTP3*. LTPs may be involved in maintaining the integrity of healthy cells. Although attack by a single virulent Hessian fly larva was sufficient to cause a detectable decrease in Hfr-LTP mRNA abundance, higher infestation levels led to near silencing of the gene with a 196-fold decrease in transcript abundance. Hfr-LTP transcript levels were not affected by other biotic factors or abiotic factors tested, so the response appears to be fairly specific to Hessian fly attack. Although TaLTP3 transcript abundance was confirmed to increase in resistant plants, a much larger effect was seen when quantified through eight days after egg hatch in susceptible plants. TaLTP3 mRNA abundance decreased markedly in susceptible plants, as was seen for Hfr-LTP. These decreases in wheat LTP transcript abundance in susceptible plants may contribute to degradation of epidermal cells at the larval feeding sites, resulting in nutrient delivery.

The potential role of reactive oxygen species (ROS) in defense of wheat and rice against Hessian fly larvae was examined. This study compared the rice non-host response to the wheat gene-for-gene response. A similar rapid and prolonged accumulation of H_2O_2 was detected in resistant wheat and rice plants at the attack site. Changes were detected in the abundance of 250 wheat transcripts and 320 rice transcripts from genes believed to be involved in generating ROS. Class-III peroxidase transcripts increased in abundance in both wheat gene-for-gene resistance and rice non-host interactions, whereas the levels of these transcripts decreased in susceptible wheat. In addition, elevated enzymatic activity of peroxidases was detected at the attack site in resistant wheat plants and non-host rice interactions. Thus, rice non-host resistance and wheat gene-for-gene resistance shared common elements in their defense against Hessian fly attack.

Williams Lab members. Subhashree Subramanyam is a Purdue University postdoctoral researcher, Kurt Saltzmann was a USDA–ARS postdoctoral researcher but now is an Assistant Professor at Purdue University, Jill Nemacheck is a

USDA–ARS research technician, Marcelo Giovanini was a joint student with Dr. Herbert Ohm who currently is a corn breeder for Monsanto in his home country of Brazil.

Ultrastructural changes in the midguts of Hessian fly larvae feeding on resistant wheat.

Richard H. Shukle, Christie E. Williams, and Subhashree Subramanyam.

The focus of this study was to compare ultrastructure in the midguts of Hessian fly larvae under different feeding regimens. Larvae were either fed on Hessian fly resistant or susceptible wheat, and each group was compared to starved larvae. Within three hours of larvae initiating feeding on resistant wheat midgut microvilli were disrupted, and after six hours midgut microvilli were absent. The disruption of midgut microvilli in larvae feeding on resistant wheat were similar to those reported for midgut microvilli of European corn borer larvae fed a diet containing the lectin wheat germ agglutinin. Results from the present ultrastructural study, coupled with previous studies documenting expression of genes encoding lectin and lectin-like proteins is rapidly up-regulated in resistant wheat to larval Hessian fly attack, are indications the midgut is a major target for toxic compounds elicited during the defense response of resistant wheat.

Development of a bioassay to evaluate the effects of toxic proteins on Hessian fly larvae. We have developed a bioassay to evaluate the effects of toxic proteins on Hessian fly larvae. Three lectins have been assayed to date and their effects on development and midgut ultrastructure of larvae documented. Additionally, we have obtained an expression clone for the 72-kDa toxic protein produced by the bacteria *Bacillus thuringiensis* subsp. *israelensis*, which is effective against mosquitoes and the close relatives of the Hessian fly the fungus gnats, and are currently expressing it for bioassay with Hessian fly larvae. Results impact development of transgenic resistance to compliment native resistance in wheat to Hessian fly.

Differential expression of genes encoding novel secreted salivary gland protein in the larval Hessian fly.

Richard H. Shukle and Alisha J. Johnson.

In collaboration with Dr. Ming-Shun Chen (USDA–ARS, Manhattan, KS) we are analyzing the salivary gland transcriptome of Hessian fly larvae using a custom Hessian fly Affymetrix array developed by Dr. Chen. These analyses are being conducted with three lab lines (vH9, vH13, and white), a field collection from Israel, and field collections from four states within the United State (Alabama, Georgia, Colorado, and Texas). Biotype GP is the reference 'wild-type' line. Initial results indicate significant differential expression in genes encoding novel secreted salivary gland proteins (SSGPs), which are hypothesized to be effectors in this insect/plant interaction. These results suggest each lab line and field collection evaluated has its own transcriptional signature with respect to genes encoding the SSGPs. Results impact knowledge of the interaction of Hessian fly larvae at the molecular level with wheat.

Multiplexed virus assays.

Mahua Deb and Joseph M. Anderson.

The addition of the high plains virus (HPV) and *Triticum* mosaic virus (TriMV) to a multiplex RT–PCR diagnostic assay previously developed for barley and cereal yellow dwarf viruses (CYDV), wheat spindle streak mosaic virus (WSSMV), wheat streak mosaic virus (WSMV), and soil-borne wheat mosaic virus (SBWMV).

A recent publication by Burrows et al. (2009, Plant Health Prog doi:10.1094/PHP-2009-0706-01-RS) demonstrated that TriMV and HPV as well as WSMV were the primary wheat viral pathogens in the Great Plains area. In response to this information, we have refined our wheat virus detection multi-plex PCR assay (Deb and Anderson 2008, J Virol Meth 148:17-24) to include TriMV and HPV. Like WSMV, these two viruses are vectored by the wheat curl mite and cause symptoms such as yellowing and stunting of plants that are similar to many other viruses attacking wheat. Because the disease phenotypes are similar, it makes a visual diagnosis quite difficult. ELISA is the standard diagnosis

method. Although a very effective detection method, it requires separate assays to identify which of these viruses are present. The multiplex PCR method we have developed uses a specific set of primers that detects the target viruses, TriMV and HPV, at 560 bp and 490 bp, respectively, in the presence of the other wheat and small grain viruses: B/CYDVs -PAV, -MAV, -SGV, -RPV, -RMV, WSSMV, SBWMV and WSMV at 295, 175, 237, 400, 365, 154, 219, and 193 bp, respectively. The different size virus-specific amplicons produced are readily visualized by agarose gel electrophoresis or capillary electrophoresis using a fluorescently tagged forward primer. All ten viruses can be amplified in a single reaction. Having the ability to detect all ten wheat viruses in a single test reduces the cost of the diagnostic assay and can readily identify mixed infections and also the presence of viruses. Therefore, this method reduces cost and leads to an improved diagnostic capacity.

Septoria tritici blotch.

Stephen Goodwin, Braham Dhillon, Yoon-E Choi, Jessica Cavaletto, and Ian Thompson.

Disease resistance. The Septoria tritici blotch resistance gene *Stb3* was mapped previously to chromosome 6DS by linkage to a single microsatellite locus. Additional markers on 6DS were tested to refine the map location and provide additional tools for marker-assisted selection. However, none of these markers was linked, indicating that the original location was incorrect. To find the correct location, more than 250 microsatellite primer pairs were tested by bulked-segregant analysis, but the level of polymorphism was quite low. Target region amplification polymorphism (TRAP) analysis identified a single linked marker that was located on chromosome 7A by analysis of nullisomic-tetrasomic stocks. Subsequent analyses of more than 50 SSR loci on chromosome 7A revealed that the correct location for *Stb3* is on the short arm. Locations of the SSR loci were confirmed by analysis of 7A deletion stocks. The linkage on 7AS was verified by analysis of two independent progeny sets. One SSR marker co-segregated with *Stb3* on all 97 doubled-haploid progeny so appears to be very tightly linked.

Work to backcross the resistance genes *Stb1–Stb8* into the highly susceptible, spring wheat background Taichung 29 are continuing. A progeny set of more than 700 lines is being developed for fine-scale mapping of the *Stb2* gene on chromosome 3BS. This work is aided by a stem inoculation technique that seems to give more reliable results compared to spray inoculation.

Work to develop isogenic lines of many of the *Stb* genes in the highly susceptible wheat background Taichung 29 is progressing. Many of the crosses are at the BC_3 or BC_4 stage. Ultimately, these lines can be used to analyze the effects of each *Stb* gene in a common susceptible background, and the progenies being developed can be used to validate previously published map locations.

Fungal genomics. Analysis of the repetitive content of the *M. graminicola* genome sequence identified a gene for methylation that is in multiple telomeric copies but occurs as a single copy in all other species analyzed. Further analysis revealed that the original copy in *M. graminicola* probably was duplicated and moved to a telomeric location, and then was amplified and spread to other chromosomes as part of the telomeric repeats. After becoming repetitive the gene seems to have become visible to the machinery for repeat-induced point mutation (RIP), a mechanism in fungi for inactivating transposable elements by introducing mutations that cause stop codons. The result of the RIP process was that all copies of the methylation gene appeared to be inactivated. To test this directly, DNA from several isolates of *M. graminicola* plus representatives of two close relatives, the barley pathogen *Septoria passerinii* and the banana pathogen *M. fijiensis*, was assayed for cytosine methylation. No methylation was detected in *M. graminicola*, but it appeared to be normal in the other two species, one of which (*M. fijiensis*) is known to have an unRIPed copy of the gene based on its genomic sequence. Therefore, *M. graminicola* is deficient in methylation, but with no obvious effect on phenotype.

Initial analysis of the genome sequence of *M. graminicola* is nearing completion. The genome sequence is finished, with 20 chromosomes from telomere to telomere and one telomere missing from the final chromosome. There are only two internal gaps. Eight of the chromosomes appear to be dispensable and could help give rise to the ability of the pathogen to adapt to new environments. Comparative genomics analyses with other sequenced relatives should soon provide an unprecedented understanding of the genetic content of these organisms.

Analysis of the function of genes in the *M. graminicola* genome is being pursued by developing knock-out mutants for particular genes of interest. So far, a number of new genes have been implicated in pathogenicity and that work will continue during the coming year.

Goodwin 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 and genomics and Yoon-E Choi is a USDA postdoc who started during July of 2009.

Personnel.

Kristen Rinehart completed the PhD degree, August 2009, advisor Herb Ohm, and is in a corn breeding position with Pioneer stationed at Des Moines, IA. Yanyan Liu is a postdoctoral researcher since August 2009 with Herb Ohm.

Publications.

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Elevated Carbon Dioxide: Soil and Plant Water Relations.

M.B. Kirkham.

I have finished writing a book entitled ***Elevated Carbon Dioxide: Soil and Plant Water Relations***, now being considered for publication by Wiley-Blackwell. The book is developed from research that we in the Evapotranspiration Laboratory at Kansas State University did between 1984 and 1990 with field-grown sorghum, winter wheat, and rangeland plants under elevated carbon dioxide. Such experiments had not been done before in the semiarid Great Plains of the U.S. The rising levels of carbon dioxide in the atmosphere were of interest to the Department of Energy, which funded our work.

As the years have passed, the carbon dioxide levels in the atmosphere have increased, along with increasing interest concerning their effects. The carbon dioxide concentration in the atmosphere was first recorded by Charles D. Keeling (1928–2005) of the Scripps Institution of Oceanography, University of California, San Diego. He monitored it beginning in 1957 at Mauna Loa, Hawaii, and in Antarctica at the South Pole. In the 50-year period between 1958 and 2008, the carbon dioxide concentration in the atmosphere increased from 316 ppm to 385 ppm. Because no book documents soil- and plant-water relations under elevated carbon dioxide, I wrote this book to put the information in one source. It has been 26 years since we started our first experiments (1984–2010), so we can make some predictions, based on our early results, about how plants in the semiarid Great Plains of the U.S. are responding to elevated carbon dioxide, which has increased 55 ppm (from 330 ppm to 385 ppm) during this time.

Water and carbon dioxide are the two most important compounds affecting plant growth. In introductory botany textbooks, we have seen the familiar equation for photosynthesis, which shows carbon dioxide (CO_2) joining with water (H_2O), in the presence of light and chlorophyll, to form sugar ($C_6H_{12}O_6$) and oxygen (O_2), as follows:

$$6CO_2 + 6H_2O \xrightarrow[\text{chlorophyll}]{\text{light}} C_6H_{12}O_6 + 6O_2$$

Life on earth would not be possible without photosynthesis. We survive because of the oxygen produced by photosynthesis, as well as the food (sugars) produced by photosynthesis. Therefore, it is of critical importance to look at the water relations of plants under elevated carbon dioxide.

The book is technical and is based on information from peer-reviewed journal articles. I have written the book as if I were speaking to my graduate students and is organized as follows. I start with an introductory chapter

dealing with drought, because it is predicted that the central Great Plains, where Kansas is located, will become drier as the carbon dioxide concentration in the atmosphere increases. In this chapter, I give a preliminary overview of the three types of photosynthesis: C3, C4, and Crassulacean acid metabolism.

The book then takes the water from the soil through the plant and out into the atmosphere. This is the way that water moves through the soil–plant–atmosphere continuum. Four chapters deal with soil. After I discuss soil and elevated carbon dioxide, I move the water into the root. One chapter deals with elevated carbon dioxide and root growth. And the following chapter deals with the effects of elevated carbon dioxide on plant water potential, osmotic potential, and turgor potential. Then the next two chapters deal with stomata under elevated carbon dioxide. Next, I take the water out of the plant into the atmosphere and discuss the effects of elevated carbon dioxide on transpiration, evapotranspiration, and water use efficiency. One chapter compares C3 and C4 plants under elevated carbon dioxide and goes into detail about C4 photosynthesis, its advantage, and how it has evolved. One chapter deals with plant anatomy under elevated carbon dioxide focusing on xylem (including wood), because this is the tissue that carries water in plants. One chapter deals with phenology and how elevated carbon dioxide affects it. The final chapter deals with growth of many different kinds of plants under elevated carbon dioxide and well-watered conditions.

Here follows a brief summary of the effects of elevated carbon dioxide on soil and plant water relations. The key factor is stomatal closure under elevated carbon dioxide. Stomata are extremely sensitive to the concentration of carbon dioxide in the atmosphere and close when the concentration increases. For example, in our first study, with grain sorghum in 1984, we elevated the atmospheric carbon dioxide 155 ppm above ambient. During that season, the average stomatal resistance of the plants under the ambient concentration (330 ppm) was 0.86 s/cm, wereas under elevated concentration (485 ppm), the stomatal resistance was 0.97 s/cm, an increase of 13%. When the stomata close, transpiration and evapotranspiration are reduced, resulting in more water in the soil. Less water is needed to produce a certain amount of grain, so water use efficiency is increased under elevated carbon dioxide. With an increased soil water content under elevated carbon dioxide, the plants have more water for uptake, and this results in an increased (less negative) plant water potential. Even though stomata close, the elevated carbon dioxide still stimulates growth, and consequently yield is usually increased under elevated carbon dioxide. When drought occurs, the elevated carbon dioxide often compensates for reduction of growth due to the drought stress. In our three-year (1984–1987) experiment with winter wheat, the grain yield of wheat under drought (half field capacity) and elevated carbon dioxide (825 ppm) was the same as the grain yield of wheat under well-watered conditions (field capacity) and ambient carbon dioxide (340 ppm). The year-to-year increase in wheat yields that have been observed over the last 50 years may be related in part to the increased carbon dioxide concentration in the atmosphere.

News.

Master's degree graduate student, Nicole A. Rud, graduated in December, 2009, and is now pursuing a Ph.D. at the University of Toledo in Ohio. Her results showed that one cause of the physiological disorder, edema, which occurs under greenhouse conditions, is a lack of ultra-violet light. When she added UV-B light back to tomato plants grown in a greenhouse (UV-B light is filtered out by the glass of the greenhouse), the plants developed no edema.

Ms. Kalaiyarasi Pidaran (kalai@ksu.edu), started work toward the master's degree in the autumn of 2009. She is working jointly under the direction of M.B. Kirkham and R.M. Aiken. She is studying growth of sorghum under different planting patterns (clumped versus a standard row spacing).

Ms. Rattiypaorn Jaidee, a Ph.D. student at the University of Khon Kaen in Khon Kaen, Thailand, spent six months (July–December, 2009) in the laboratory of M.B. Kirkham. She studied the effect of drought on the uptake of phosphorus by two cultivars of soybean, a traditional Thai cultivar and a commercially developed cultivar.

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Notice of release of KS11WGGRC53-J AND KS11WGGRC53-O leaf rust and stripe rust resistant hard red winter wheat germ plasms.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS11WGGRC53-J AND KS11WGGRC53-O hard red winter wheat (*T. aestivum* L.) germ plasm with resistance to leaf rust and stripe rust for breeding and experimental purposes. Scientists participating in this development were Vasu Kuraparthy, Crop Science Department, North Carolina State University, Raleigh, NC 27695; Parveen Chunneja, Department of Genetics & Biotechnology, Punjab Agricultural University, Ludhiana, Punjab, India; Shilpa Sood, Crop Science Department, North Carolina State University, Raleigh, NC 27695; H.S. Dhaliwal, Biotechnology department, Indian Institute of Technology, Roorkee, Uttaranchal, India; Deven See, USDA–ARS Western Regional Small Grains Genotyping Laboratory, Washington State University, Pullman, WA 99164-6420; and Duane Wilson and B.S. Gill, Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506.

KS11WGGRC53-J and KS11WGGRC53-O are derivatives of WL711 (TA5602) with the rust resistance genes *Lr57* and *Yr40* in the form of a wheat-goat grass (*Ae. geniculata*) recombinant chromosome T5DL·5DS-5M^{g}S(0.95). The recombinant chromosome consists of the long arm of wheat chromosome 5D, most of the short arm of 5D, and a small distal segment derived from the short arm of the *Ae. geniculata* chromosome 5M^{g} harboring *Lr57* and *Yr40*. KS11WGGRC53-J is derived from the cross 'WL711 (T5DL·5DS-5M^{g}S(0.95)/3*Jagger'. KS11WGGRC53-O is derived from the cross 'WL711 (T5DL·5DS-5M^{g}S(0.95)/3*Overley'. The F_4-derived families are homozygous for *Lr57* and *Yr40* but segregating for other traits.

Small quantities (3 grams) of seed of KS11WGGRC53-J and KS11WGGRC53-O 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.

Notice of release of KS11WGGRC54-J and KS11WGGRC54-O leaf rust resistant hard red winter wheat germ plams.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS11WGGRC54-J and KS11WGGRC54-O hard red winter wheat (*T. aestivum* L.) germ plasm with resistance to leaf rust for breeding and experimental purposes. Scientists participating in this development were Vasu Kuraparthy, Crop Science Department, North Carolina State University, Raleigh, NC 27695; Parveen Chunneja, Department of Genetics & Biotechnology, Punjab Agricultural University, Ludhiana, Punjab, India; Shilpa Sood, Crop Science Department, North Carolina State University, Raleigh, NC 27695; H.S. Dhaliwal, Biotechnology department, Indian Institute of Technology, Roorkee, Uttaranchal, India; Gina Brown-Guedira, USDA–ARS, Small Grains Genotyp-

ing Laboratory, North Carolina State University, Raleigh, NC 27695; and Duane Wilson and B.S. Gill, Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506.

KS11WGGRC54-J and KS11WGGRC54-O are improved derivatives of WL711 (TA5605) with the rust resistance gene *Lr58* in the form of a wheat–*Ae. triuncialis* recombinant chromosome T2BS·2BL-2^{t}L(0.95). The recombinant chromosome consists of the short arm of wheat chromosome 2B, most of the long arm of 2B, and a small distal segment derived from the long arm of the *Ae. triuncialis* chromosome 2^{t}L harboring *Lr58*. KS11WGGRC54-J is derived from the cross 'WL711 (T2BS·2BL-2^{t}L(0.95))/3*Jagger'. KS11WGGRC54-O is derived from the cross 'WL711 (T2BS·2BL-2^{t}L(0.95))/3*Overley'. The F_4-derived families are homozygous for *Lr58* but segregating for other traits.

Small quantities (3 grams) of seed of KS11WGGRC54-J and KS11WGGRC54-O 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.

Evaluation of wild wheat lines in the field for various foliar diseases.

Duane L. Wilson, Bikram S. Gill, and W. John Raupp.

We evaluated a collection of *Triticum monococcum* subsp. *monococcum* in the field at Manhattan, Kansas, during the spring of 2010 for leaf rust, stripe rust, and barley yellow dwarf virus; heading dates also were recorded (Table 1, pp. 238-242). We also evaluated a representative sample of accessions from the primary and secondary gene pools (Table 2, pp. 242-245). Field plots at the Rocky Ford Research Area north of Manhattan were inoculated on 7 May with a mixture of leaf rust and stripe rust spores. Spores were in a suspension of oil and mist applied in late evening. The leaf rust culture used is referred to as 'Lr Composite'. This culture is a composite of the following cultures: 2003 wild culture, 2007 wild culture, and PRTUS3, 6, 42, 50, and 52. The stripe rust culture is referred to as 'PST-100'. These cultures were kindly supplied by Dr. Bob Bowden, UDSA–ARS, Manhattan, Kansas. Infection type was described using the Cobb scale and visual assessment. The Cobb scale is a combination of the percent of leaf area covered by rust and the pustule size. The number in the score is the percentage of leaf area covered by pustules, which could be from 1 to 100. The second part of the scoring are letter designations for size of pustules present as follows: 0 = no infection visible, R = resistant or very small pustules, MR = moderately resistant or small pustules, M = moderate or intermediate reaction, pustules larger, MS = moderately susceptible or large pustules, and S = susceptible with very large pustules in both diameter and height of the pustule. For example, an IT of 10R indicates 10 percent of the leaf area infected with very small pustules, 40M indicates 40 percent of the leaf area infected with moderate to larger pustules, and 60MS indicates 60 percent of the leaf area infected with large pustules. Plants were artificially inoculated with cultures mentioned but most likely, natural infection also occurred. Commonly, leaf rust and occasionally stripe rust are present in the wheat plots at the experiment station.

Table 1. Field observations on a *Triticum monococcum* subsp. *monococcum* collection for leaf rust, stem rust, barley yellow dwarf virus, and heading date in 2010. For most accessions, at least two replications were evaluated. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	Leaf rust		Stripe rust		Barley yellow dwarf		Heading date	Country of origin
	26/5/10	2/6/10	26/5/10	2/6/10	13/5/10	26/5/10		
136	30R	30MR	0	5R	M	H	31/5	Sweden
	10R	10R	1R	5R	H	H	31/5	
137	5R	20MR	0	5R	M	M	2/6	Turkey
	30R	30MR	5R	10MR	H	H	1/6	
138	5R	15MR	0	1R	L	M	16/5	USA
	30R	30MR	5R	10MR	L	L	23/5	
	15MR	15MR	5MR	10MR	L	M	16/5	
139	1R	20MR	0	5MR	L	M	2/6	USA
	10R	10R	0	1R	H	H	5/6	
141	1R	15MR	0	1R	L	M	3/6	Unknown
	15R	15MR	0	5R	L	M	3/6	
	10R	25R	0	1R	0	L	4/6	

Table 1. Field observations on a *Triticum monococcum* subsp. *monococcum* collection for leaf rust, stem rust, barley yellow dwarf virus, and heading date in 2010. For most accessions, at least two replications were evaluated. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	Leaf rust		Stripe rust		Barley yellow dwarf		Heading date	Country of origin
	26/5/10	2/6/10	26/5/10	2/6/10	13/5/10	26/5/10		
142	5R	10R	0	0	L	L	1/6	Bosnia–Herzegovina
	1R	10R	0	1R	M	M	31/5	
	20R	20MR	1R	5R	M	M	29/5	
	10R	10R	0	1R	L	M	1/6	
1988	1R	5R	0	1R	M	M	1/6	United Kingdom
	20R	25MR	0	10MR	L	M	3/6	
	5R	15R	0	5R	H	H	1/6	
	5R	30MR	0	5R	L	L	2/6	
	5R	20MR	0	15R	L	L	5/6	
2024	10R	10MR	0	5R	M	H	31/5	Turkey
	20MR	20MR	5MR	5MR	H	H	31/5	
2025	5R	15R	0	5MR	M	H	31/5	Turkey
	20R	10R	1R	5R	M	H	28/5	
2026	10R	15R	0	1R	M	M	2/6	Turkey
	30R	40R	0	5R	M	H	5/6	
2027	1R	15R	0	0	L	L	4/6	Turkey
	—	—	—	—	H	H	—	
	5R	10R	5MR	15MR	M	M	2/6	
2028	5R	15MR	0	5R	M	M	31/5	Turkey
	5R	5R	0	1R	M	M	30/5	
2029	10R	15R	1R	1R	M	H	30/5	Turkey
2030	30R	25MR	1R	5R	L	M	2/6	Spain
	10R	10R	5R	10R	M	H	30/5	
2031	20R	20MR	0	5R	L	L	31/5	Spain
	10R	10MR	1R	5R	M	M	28/5	
2032	30R	25MR	1R	5R	L	M	1/6	Spain
	20R	20MR	0	5R	L	M	4/6	
2033	1R	15MR	0	1R	M	M	31/5	Portugal
	5R	5R	0	1R	M	M	30/5	
2034	1R	20MR	0	1R	M	H	31/5	Bosnia–Herzegovina
	1R	5R	5R	5R	M	M	29/5	
2035	10R	20MR	0	1R	L	L	4/6	Hungary
	15R	15MR	0	1R	M	M	3/6	
2036	5R	25MR	0	5R	M	M	31/5	Hungary
	10R	20R	0	1R	M	M	29/5	
2037	5R	5R	1R	0	L	L	4/6	Albania
	10R	10R	0	1R	L	M	3/6	
2038	5R	10MR	0	5R	M	H	3/6	Albania
	5R	10R	0	1R	M	M	3/6	
2039	1R	15MR	0	5R	H	H	3/6	Albania
	15R	20R	0	1R	M	M	3/6	
	5R	10R	0	15R	M	H	4/6	
2701	5R	30MR	1R	5R	L	L	1/6	Romania
	10R	15R	0	1R	L	M	3/6	
2702	10R	20MR	0	5R	L	M	31/5	Italy
2703	5R	15R	5R	5R	M	H	31/5	USA
	5R	20MR	1R	5MR	H	H	29/5	
2704	15R	20MR	1R	5R	H	H	2/6	United Kingdom
	10R	20R	1R	1R	H	H	2/6	
2705	30R	25MR	0	10R	L	M	28/5	United Kingdom
2706	10R	30MR	5R	5R	H	H	1/6	United Kingdom
2706	15R	15MR	0	1R	M	M	5/6	
2707	5R	20R	0	0	L	L	4/6	United Kingdom
	15R	15MR	0	1R	M	M	5/6	
2708	10R	25MR	0	10R	L	L	28/5	Former USSR
	10R	25MR	0	5R	M	H	1/6	
2709	20R	30MR	10MR	15MR	L	L	28/5	Spain
2710	20R	15MR	10R	10MR	0	M	3/6	Unknown
	5R	25MR	20MR	1R	L	L	4/6	

Table 1. Field observations on a *Triticum monococcum* subsp. *monococcum* collection for leaf rust, stem rust, barley yellow dwarf virus, and heading date in 2010. For most accessions, at least two replications were evaluated. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	Leaf rust		Stripe rust		Barley yellow dwarf		Heading date	Country of origin
	26/5/10	2/6/10	26/5/10	2/6/10	13/5/10	26/5/10		
2711	10R	20R	0	5R	L	M	4/6	Serbia
	5R	25MR	0	15MR	L	M	2/6	
	5R	20R	0	5R	M	H	3/6	
2712	30R	30MR	0	5R	M	H	1/6	Serbia
	30R	30MR	0	5R	M	H	1/6	
	5R	30R	1R	5R	M	H	5/6	
2713	20R	NT	0	NT	H	H	1/6	Hungary
	5MR	20MR	10MR	1R	H	H	4/6	
2714	20R	20MR	1R	10R	M	M	31/5	Albania
	20MR	20MR	5MR	5R	H	H	2/6	
	5R	30R	0	5R	L	M	2/6	
2715	30R	40MR	1R	5R	M	H	31/5	Germany
	10MR	30MR	0	15R	H	H	2/6	
2716	5R	20MR	1R	5R	M	M	2/6	United Kingdom
	1R	30MR	0	10R	L	M	31/5	
2717	20R	30MR	1R	5R	M	H	5/6	Austria
	30R	35MR	5R	10R	L	M	5/6	
2718	20R	25MR	0	5R	L	M	3/6	Azerbaijan
	15R	30R	0	5R	M	M	31/5	
2719	1R	30MR	5R	10R	M	M	14/5	Germany
	5R	30MR	10MR	5R	M	H	14/5	
	1R	1R	5MR	10M	L	L	31/5	
	10R	30MR	20MR	10R	M	H	16/5	
	5R	25MR	15MR	20MR	L	M	1/6	
2720	10R	15MR	0	5R	M	H	4/6	Germany
	20R	30MR	5R	5MR	H	H	3/6	
2722	10R	15R	0	1R	L	L	3/6	Former USSR
	15R	15R	0	1R	L	L	4/6	
2723	10R	25MR	1R	5R	M	H	3/6	Germany
	5R	30MR	1R	10R	M	M	3/6	
	10R	30MR	0	10R	0	M	30/5	
2724	10R	10R	10MR	5R	M	H	28/5	United Kingdom
	5R	10R	0	5R	L	M	31/5	
2725	10R	15MR	0	5R	L	L	28/5	Japan
4447	30R	35MR	1R	5R	L	M	5/6	Reduced-height mutant
	30R	40MR	0	5R	L	L	5/6	
10418	30R	35MR	0	10R	H	H	4/6	Turkey
	15MR	20MR	5MR	5MR	H	H	3/6	
10555	15R	15MR	0	5R	L	M	5/6	Serbia
	10R	20MR	5MR	5R	M	H	5/6	
10556	5R	25MR	10R	10MR	M	H	3/6	Serbia
	20R	25MR	10M	5R	M	H	3/6	
10557	5R	10MR	0	1R	L	L	3/6	Albania
	5R	10R	0	10R	M	H	2/6	
10558	1R	10MR	1MR	10MR	L	M	28/5	Bulgaria
	20R	25R	20MR	10R	H	H	30/5	
10559	5R	15MR	5R	5R	L	M	5/6	Romania
	5R	10R	0	1R	H	H	5/6	
10560	20R	25MR	0	5R	L	M	5/6	Romania
	15R	15MR	0	5R	M	H	5/6	
10561	30R	35MR	5R	10R	L	L	3/6	Romania
	10R	20MR	1R	10MR	H	H	5/6	
10562	15R	20MR	0	5R	L	M	5/6	Romania
	15R	20MR	0	5R	L	L	5/6	
10563	15R	25MR	0	5R	M	H	5/6	Romania
	10R	35MR	1R	5R	H	H	5/6	
10564	30R	30MR	1R	5R	H	H	5/6	Romania
	5R	35M	5MR	10MR	H	H	5/6	
10565	5R	10MR	0	5R	H	H	5/6	Romania
	15R	15MR	0	1R	L	M	3/6	

Table 1. Field observations on a *Triticum monococcum* subsp. *monococcum* collection for leaf rust, stem rust, barley yellow dwarf virus, and heading date in 2010. For most accessions, at least two replications were evaluated. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	Leaf rust		Stripe rust		Barley yellow dwarf		Heading date	Country of origin
	26/5/10	2/6/10	26/5/10	2/6/10	13/5/10	26/5/10		
10566	30MR	30MR	0	5R	M	H	4/6	Romania
	20R	25MR	5R	10MR	M	H	4/6	
10567	30R	30MR	0	5R	L	L	1/6	Turkey
	15R	15R	0	1R	L	L	4/6	
10568	10R	20MR	0	5R	L	M	5/6	Italy
	5R	5R	0	1R	M	M	3/6	
10569	20R	25MR	1R	5R	M	H	5/6	Germany
	20R	40MR	1R	5MR	M	M	1/6	
10571	10MR	25MR	0	5R	M	H	31/5	Asia Minor
	10R	10MR	0	1R	L	L	30/5	
10573	10R	10R	0	10R	L	L	29/5	Asia Minor
	10R	15R	5R	10MR	L	L	30/5	
10574	1R	25R	1R	5R	M	H	5/6	Belgium
	10R	10MR	5R	5R	M	H	2/6	
10575	20R	25R	5R	5R	L	M	5/6	Italy
	15R	10R	0	1R	M	M	3/6	
10576	5R	25MR	0	10MR	M	H	5/6	Italy
	15R	15R	0	1R	M	M	5/6	
10577	10MR	20MR	5MR	20MR	L	M	2/6	Germany
	10R	15R	5R	5MR	L	M	3/6	
10578	5R	25MR	0	5R	L	M	4/6	Balkans
	10R	10R	0	1R	M	H	4/6	
10579	20MR	40MR	1R	10R	M	H	5/6	Germany
	20R	30MR	0	5MR	L	M	5/6	
10580	10R	20MR	0	5R	M	H	1/6	Germany
	15R	30MR	0	10MR	L	M	5/6	
10581	30R	30MR	1R	5R	L	L	5/6	Austria
	20R	25MR	5R	5R	L	L	5/6	
10582	25R	25MR	0	5R	L	M	5/6	Austria
	10R	25MR	0	5R	M	M	5/6	
10583	30R	30MR	0	1R	L	L	5/6	Austria
	10R	25MR	0	5R	L	L	4/6	
10584	20R	25MR	1R	5R	L	M	5/6	Austria
	20R	20R	5MR	5MR	M	H	5/6	
10585	5R	10R	5R	1R	L	L	4/6	Kosovo
	10R	10R	5R	5R	L	L	5/6	
10586	10R	30MR	1R	20MR	L	M	29/5	Turkey
	5R	25MR	0	15MR	L	M	3/6	
10587	20R	20MR	10R	10MR	M	H	28/5	Montenegro
	10R	10R	1R	5R	M	M	29/5	
10588	5R	15MR	5R	5MR	L	M	3/6	Turkey
	15R	15R	0	5R	L	L	3/6	
10589	10R	25MR	0	10R	O	L	4/6	Unknown
	20R	30MR	0	5R	L	L	5/6	
10590	30R	30MR	10R	10R	L	M	3/6	Turkey
	25R	25MR	10MR	10MR	L	M	5/6	
10591	5R	20MR	5R	5MR	H	H	3/6	Turkey
	25R	25MR	0	1R	M	H	5/6	
10593	20MR	40MR	1R	10R	M	H	29/5	Turkey
	15MR	30MR	5MR	10MR	L	H	28/5	
10594	10R	35MR	0	5R	L	M	31/5	Turkey
	10R	25MR	0	1R	L	L	1/6	
10595	10MR	35MR	5R	10R	L	H	3/6	Turkey
	15MR	30MR	5R	5R	L	M	2/6	
10598	40R	25MR	0	5R	M	M	1/6	Turkey
	1R	10R	0	1R	L	L	5/6	
10623	5R	10R	0	1R	M	M	5/6	Albania
	10R	20R	0	10MR	L	M	5/6	
10624	5R	10R	0	0	L	L	5/6	Albania
	1R	15MR	0	5R	L	L	5/6	

Table 1. Field observations on a *Triticum monococcum* subsp. *monococcum* collection for leaf rust, stem rust, barley yellow dwarf virus, and heading date in 2010. For most accessions, at least two replications were evaluated. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	Leaf rust		Stripe rust		Barley yellow dwarf		Heading date	Country of origin
	26/5/10	2/6/10	26/5/10	2/6/10	13/5/10	26/5/10		
10625	10R	15R	0	5R	L	M	3/6	Albania
	10R	20R	0	1R	L	L	4/6	
10626	10R	30MR	0	5R	L	L	5/6	Unknown
	10R	25R	0	5R	0	L	5/6	
10627	15R	25MR	0	5R	L	M	3/6	Unknown
	20R	30MR	0	5MR	0	L	5/6	
10628	25R	35MR	10MR	1R	L	M	4/6	Unknown
	30R	40MR	5MR	10MR	M	H	4/6	
10629	30R	35MR	5MR	5MR	L	H	5/6	Balkans
	10R	15R	5MR	10MR	M	H	5/6	
10630	5R	10MR	5R	10MR	M	H	5/6	Unknown
	5R	15R	10MR	20MR	0	L	5/6	
10631	10R	35MR	1R	5R	M	H	5/6	Unknown
	20R	25R	0	1R	L	L	4/6	
10632	10R	30MR	0	1R	L	M	4/6	Romania
	10R	15R	5MR	10MR	L	L	5/6	
10634	20R	30MR	0	1R	L	M	5/6	Italy
	25R	25MR	0	5R	0	L	4/6	
10635	20R	25MR	0	1R	L	M	5/6	Georgia
	10R	15R	5R	5R	L	M	4/6	
10636	15R	25MR	0	1R	L	L	5/6	Georgia
	5R	15MR	0	1R	L	M	5/6	
10637	20MR	30MR	5R	5MR	M	H	5/6	Unknown
	30R	30MR	0	15MR	L	L	5/6	
10639	15R	35MR	0	5MR	L	M	3/6	Unknown
	20R	25MR	5R	5MR	L	L	5/6	
10640	30R	45MR	0	5MR	L	M	5/6	Germany
	15MR	30MR	5R	5MR	L	H	4/6	
10641	20R	30MR	0	1R	0	L	1/6	Unknown
	10R	25MR	1R	5R	L	M	5/6	
10642	15R	15MR	0	1R	M	M	1/6	Unknown
	15R	15R	0	1R	0	L	5/6	
10643	20R	25MR	0	1R	M	M	5/6	Unknown
	20R	20R	5R	5R	L	M	4/6	
10644	10R	15R	10R	10MR	L	H	6/6	Unknown
10645	20R	25MR	5R	10MR	0	L	5/6	Unknown
	20R	30MR	1R	5R	L	M	5/6	
10646	20R	30MR	0	1R	L	M	6/6	Unknown
	15R	40MR	0	5R	L	M	6/6	

Table 2. Field observations on a collection of *Triticum* and *Aegilops* species for leaf and stem rust, barley yellow dwarf, and heading date in the 2009–10 growing seasons. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf {BYD) and powdery mildew (PM) incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	2010							2009							Species	Country of origin
	Leaf rust		Stripe rust		BYD		HD	Leaf rust			BYD		PM	HD		
	5/26	6/2	5/26	6/2	5/13	5/26		5/21	6/1	6/5	5/21	6/1	5/21			
10	5R	NT	0	NT	M	H	17/5	0	1R	5MR	0	H	0	23/5	timopheevii	Iraq
18	5M	10M	10M	20MR	L	M	24/5	1R	1R	1R	H	H	0	24/5	timopheevii	Iraq
39	5MR	NT	5R	NT	M	H	24/5	1R	5R	10MR	M	H	0	23/5	timopheevii	Iraq
49	30M	30M	10MR	15MR	H	H	27/5	5R	30R	50M	0	H	0	25/5	timopheevii	Azerbaijan
89	40M	NT	20MR	NT	H	H	29/5	1R	10MR	35M	H	H	0	24/5	turgidum	Turkey
109	20MS	30M	10M	20M	M	H	17/5	10R	40MS	50S	L	H	0	24/5	turgidum	Syria
122	—	—	—	—	—	—	—	5R	30MR	40MS	H	H	0	24/5	turgidum	Syria
129	10R	20MR	1R	5R	H	H	25/5	5R	20M	40MS	H	H	0	23/5	turgidum	Israel
149	15R	25MR	5R	5MR	M	H	23/5	1R	40MR	35MS	L	H	0	23/5	timopheevii	Iraq
169	20M	25M	10R	10MR	M	H	17/5	0	10MR	10MR	L	H	0	22/5	timopheevii	Iraq
183	30R	30MR	5R	10MR	M	H	28/5	0	5R	5R	M	H	M	26/5	aegilopoides	Iran
	10R	25MR	1R	5R	L	M	2/6									
	20R	25MR	5R	10R	L	M	2/6									

Table 2. Field observations on a collection of *Triticum* and *Aegilops* species for leaf and stem rust, barley yellow dwarf, and heading date in the 2009–10 growing seasons. TA# indicates the accession number in the Wheat Genetic and Genomic Resources Center Gene Bank. The leaf and strip rust screening data is described in detail on p. 238. For barley yellow dwarf {BYD) and powdery mildew (PM) incidence; H = high, M = medium, L = low, and 0 = no disease; — = missing data. The country of origin for the accession is listed if known.

TA #	2010							2009							Species	Country of origin
	Leaf rust		Stripe rust		BYD		HD	Leaf rust			BYD		PM	HD		
	5/26	6/2	5/26	6/2	5/13	5/26		5/21	6/1	6/5	5/21	6/1	5/21			
186	30R	30MR	15MR	20MR	M	H	30/5	0	5R	1R	L	H	0	26/5	aegilopoides	Iran
	15R	25MR	5R	15MR	L	M	3/6	0	5MR	5MR	0	H	0	26/5		
	15R	20MR	5R	5MR	M	M	2/6									
196	5MR	25MR	5MR	10MR	L	M	24/5	0	5R	5R	L	H	L	26/5	aegilopoides	Iran
	10R	30MR	5MR	5MR	L	M	24/5									
	5R	25MR	0	5R	L	L	31/5									
199	5R	15MR	5MR	5MR	0	L	3/6	0	1R	1R	L	M	0	1/6	aegilopoides	Azerbaijan
203	5R	15MR	5R	5MR	0	M	31/5	1R	5MR	5R	H	H	0	23/5	aegilopoides	Iraq
	10MR	30MR	5MR	10MR	L	M	23/5									
	5R	15MR	1R	5R	0	L	28/5									
206	10R	30M	5MR	10MR	M	M	23/5	0	5MR	15MR	M	H	0	26/5	aegilopoides	Iraq
	5R	10MR	1R	5R	M	L	25/5	0	10M	5R	M	H	0	26/5		
	5R	15MR	0	5R	0	0	28/5									
215	5R	15MR	5R	5MR	H	H	15/6	1R	5R	5M	M	H	0	25/5	aegilopoides	Iraq
	5R	15MR	10R	15MR	L	L	25/5									
	5R	25MR	1R	5R	L	L	24/5									
223	5MR	20M	5MR	10MR	M	H	15/5	0	1R	5MR	L	M	L	22/5	aegilopoides	Iraq
	5MR	25MR	5R	5MR	L	M	27/5									
	10R	25MR	5MR	20MR	L	L	28/5									
237	5R	10R	5MR	5MR	L	L	17/5	0	5R	5R	L	H	0	25/5	aegilopoides	Iraq
	5R	10R	1R	5MR	0	L	27/5									
	5R	15R	1R	5R	L	L	24/5									
249	10R	35MR	1R	10MR	L	M	24/5	0	10R	10MR	M	H	0	26/5	aegilopoides	Iraq
289	5R	15MR	1R	10R	L	L	24/5	0	1R	5MR	L	H	L	17/5	aegilopoides	Iraq
300	5R	25MR	5R	5R	L	M	25/5	0	5R	5R	L	H	0	26/5	aegilopoides	Iraq
326	5R	15R	0	10R	L	L	30/5	0	1R	10M	L	M	L	26/5	aegilopoides	Iraq
	5R	25MR	1R	5R	L	L	30/5									
	5R	15MR	1R	5R	L	L	30/5									
349	10MR	25M	5MR	10MR	M	H	30/5	0	10R	25MR	L	H	0	26/5	aegilopoides	Iraq
389	5R	15MR	1R	5M	L	M	23/5	0	1R	5MR	L	M	0	18/5	aegilopoides	Iraq
396	15R	25MR	0	10R	L	M	30/5								aegilopoides	Iraq
	20R	30MR	0	5R	L	L	30/5									
	10R	15R	0	5R	0	L	29/5									
399	5R	15MR	5R	5R	L	M	24/5	1R	5R	5MR	L	H	0	24/5	aegilopoides	Iraq
419	5R	30MR	1R	5R	M	M	13/5	0	1R	10MR	L	H	L	17/5	aegilopoides	Iraq
439	5MR	15MR	1R	5R	L	M	25/5	1R	1R	20M	L	H	0	25/5	aegilopoides	Iraq
527	20R	20M	0	10MR	0	L	2/6								aegilopoides	Turkey
	15MR	15MR	0	5R	0	L	1/6									
	10R	20MR	0	5R	0	L	2/6									
709	20R	—	5MR	NT	L	M	15/5	10R	10MR	10R	L	H	0	22/5	urartu	Turkey
739	5R	30M	15MR	20MR	L	M	15/5	0	5R	5MR	L	H	0	17/5	urartu	Turkey
789	10R	25MR	0	5R	L	L	15/5	0	1R	5R	L	H	0	18/5	urartu	Lebanon
799	10R	20M	1R	10R	L	L	27/5	0	1R	5MR	L	H	0	24/5	urartu	Lebanon
810	15R	30MR	5R	10MR	L	H	17/5	5R	NT	NT	M	H	0	18/5	urartu	Turkey
819	5R	NT	40M	NT	M	M	13/5	0	5R	20MR	O	H	0	17/5	urartu	Turkey
829	20R	30MR	10MR	20MR	L	L	5/6	1M	1R	20MR	L	M	0	3/6	urartu	Armenia
879	20R	20R	5R	5R	L	L	27/5	0	5R	20MR	L	H	L	25/5	aegilopoides	Iraq
909	10R	NT	25M	NT	M	H	24/5	0	1R	1MR	L	M	0	23/5	timopheevii	Iraq
991	30M	40M	5MR	20MR	H	H	23/5	5MR	50MS	60S	H	H	H	26/5	turgidum	Turkey
1009	30M	30M	10MR	25M	H	H	23/5	10M	10M	50MS	H	H	H	26/5	turgidum	Turkey
1019	10R	40MS	20MR	20M	M	H	30/5	10MR	60MS	70S	M	H	0	26/5	turgidum	Turkey
1339	10R	15R	5R	5R	L	M	28/5	0	1R	5MR	L	H	0	25/5	aegilopoides	Iraq
1369	15MR	NT	20MR	NT	H	H	28/5	0	1R	5R	L	H	L	17/5	aegilopoides	Iraq
1489	10MR	15MR	5MR	5MR	L	M	24/5	0	1R	1M	L	H	0	18/5	timopheevii	Iraq
1528	5R	25MR	1R	5R	M	M	27/5	0	10MR	15MR	L	H	0	25/5	timopheevii	Iraq
1569	20MR	20MR	10R	10MR	M	H	30/5	0	5R	10R	M	H	0	26/5	timopheevii	Armenia
1579	10R	25M	15MR	5R	M	M	12/5	0	NT	30MR	H	H	0	16/5	tauschii	Unknown
1599	10R	30MR	15MR	15MR	L	M	15/6	0	1R	1R	L	H	0	17/5	tauschii	Iran

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TA #	2010							2009							Species	Country of origin
	Leaf rust		Stripe rust		BYD		HD	Leaf rust			BYD		PM	HD		
	5/26	6/2	5/26	6/2	5/13	5/26		5/21	6/1	6/5	5/21	6/1	5/21			
1669	10MR	20M	5R	5R	M	M	25/6	0	1R	1R	M	H	M	24/5	tauschii	Azerbaijan
1689	30S	NT	70S	NT	0	L	12/5	0	30MS	NT	H	H	0	5/15	tauschii	Japan
1702	10R	10MR	10MR	15MR	0	L	14/5	0	5R	5MR	L	H	0	16/5	geniculata	Romania
1729	10R	10R	15R	15MR	M	H	23/5	1R	10R	10M	L	H	0	23/5	triuncialis	Turkey
1749	5R	25R	0	5R	M	M	13/5	0	1R	1R	M	H	0	17/5	triuncialis	Afghanistan
1769	10R	NT	15MR	NT	M	M	13/5	0	1R	5R	0	M	0	17/5	triuncialis	Iran
1771	5R	5R	1R	1R	L	L	27/5	0	0	1R	L	H	0	25/5	speltoides	Turkey
1789	5R	15MR	0	1R	L	L	25/5	0	1R	5R	0	M	0	24/5	speltoides	Iraq
1794	5R	NT	1R	NT	M	M	11/5	5R	1R	1R	0	H	0	5/15	neglecta	Iraq
1799	5R	20MR	1R	10R	L	L	17/5	0	1R	5R	0	L	0	23/5	geniculata	Turkey
1819	5R	10MR	5R	5R	L	L	14/5	0	5R	5R	L	M	0	17/5	geniculata	Japan
1823	10R	NT	15MR	NT	L	M	12/5	0	5R	NT	L	H	0	16/5	umbellulata	Turkey
1826	5R	20MR	0	5R	0	L	25/6	0	1R	5R	0	H	0	24/5	umbellulata	Turkey
1833	10R	NT	5R	NT	M	M	12/5	1R	1R	NT	H	H	0	12/5	umbellulata	Iran
1843	5R	15R	0	1R	L	L	30/5	0	1R	10MS	L	M	0	26/5	cylindrica	Turkey
1859	25M	30M	20MR	20M	L	M	24/5	0	25MR	50M	L	H	0	25/5	cylindrica	Turkey
1868	5R	25MR	1R	5R	L	L	15/5	1R	1R	5R	L	H	0	21/5	neglecta	Japan
1874	50S	NT	20MS	NT	H	H	14/5	10MR	40MS	40M	M	H	0	17/5	crassa	Iran
1875	60S	NT	10MR	NT	M	M	13/5	10M	NT	NT	H	H	0	5/15	crassa	Iran
1878	NT	NT	NT	NT	H	H	14/5	5M	50MR	60MS	L	H	0	17/5	vavilovii	Turkey
1881	40MS	NT	30MS	NT	0	M	15/5	10M	NT	NT	M	H	0	16/5	crassa	Afghanistan
1883	70MS	25MR	30M	35M	M	M	14/5	5M	50M	60M	H	H	0	17/5	vavilovii	Italy
1906	20MR	NT	30MR	NT	M	M	14/5	15M	30MR	NT	L	H	0	17/5	caudata	Turkey
1909	60MS	NT	15M	NT	M	H	27/5	0	30M	40MR	L	H	0	25/5	caudata	Turkey
1960	5MR	NT	0	NT	H	H	10/5	1R	NT	NT	H	H	0	12/5	biuncialis	Israel
1963	10R	NT	5R	NT	M	M	14/5	0	10MR	5R	0	H	0	14/5	biuncialis	Canada
1965	10R	10R	1R	1R	L	M	28/5	0	5R	1R	L	M	0	26/5	comosa	Turkey
1967	5R	10MR	1R	1R	0	L	30/5	0	0	5R	0	M	0	25/5	comosa	Greece
1972	20R	NT	20MR	NT	H	H	11/5	1R	NT	NT	H	H	0	14/5	biuncialis	Turkey
1983	NT	NT	NT	NT	M	H	12/5	1R	10R	NT	L	H	0	13/5	kotschyi	Egypt
1989	10R	25MR	10MR	15MR	H	H	15/6	1R	5R	30MS	M	H	0	23/5	ventricosa	England
1991	5R	15MR	5MR	10MR	L	M	15/6	0	1R	1R	M	H	0	21/5	biuncialis	Turkey
1993	20MR	25MR	10MR	20MR	L	H	25/5	0	15R	30M	H	H	0	22/5	ventricosa	Romania
1996	NT	NT	NT	NT	M	H	12/5	0	NT	NT	M	NT	0	22/5	sharonensis	Israel
2004	5R	30MR	1R	5R	M	M	25/6	0	1R	NT	M	H	0	23/5	aegilopoides	Turkey
	5R	35MR	1R	10MR	L	L	28/5									
	10R	30MR	0	10MR	L	L	25/6									
	5R	30MR	1R	10MR	L	L	27/5									
2061	5R	5MR	1R	1R	L	L	15/5	0	10MR	5R	L	H	0	18/5	geniculata	Morocco
2074	10R	NT	1R	NT	L	M	27/5	0	25M	10R	0	M	0	24/5	biuncialis	Turkey
2084	10MR	35MR	5R	25M	L	M	28/5	1R	NT	NT	H	H	0	23/5	columnaris	Turkey
2102	5R	15MR	5MR	5MR	0	L	25/6	0	1R	5R	L	M	0	25/5	comosa	Greece
2104	5R	20MR	0	5R	L	L	30/5	0	5R	5R	L	H	0	26/5	comosa	Greece
2108	20MR	25MR	10R	10R	M	H	28/5	0	5MR	5R	L	H	0	24/5	columnaris	Turkey
2115	30MS	NT	25M	NT	M	H	15/6	0	30M	30M	L	H	0	18/5	juvenalis	Canada
2142	10R	10R	5R	10MR	H	H	10/5	0	1R	5R	H	H	0	12/5	villosa	Croatia
2202	20M	NT	5MR	NT	M	H	5/21	1R	40MR	50M	L	H	0	24/5	cylindrica	Romania
2211	20MR	NT	30M	NT	L	M	25/6	0	1R	5MR	M	H	0	23/5	ventricosa	Spain
2216	40S	NT	60S	NT	M	H	15/6	20M	60M	NT	H	H	0	18/5	crassa	Kyrgyzstan
2304	5R	10MR	1R	1R	L	L	30/5	0	5R	5R	0	M	0	26/5	triuncialis	Turkey
2319	30M	30MS	25M	30M	L	M	15/5	1R	15MR	40MS	M	H	0	17/5	crassa	Turkey
2322	10R	NT	10MR	NT	M	M	14/5	0	5R	5R	L	M	0	17/5	triuncialis	Turkey
2344	10R	10R	30M	40M	0	L	30/5	0	5R	NT	H	H	0	23/5	searsii	Syria
2348	5R	30MR	0	5R	M	M	17/5	0	5R	5R	M	H	0	18/5	speltoides	Israel
2369	5R	5R	1R	1R	L	L	27/5	0	1R	1R	L	M	0	26/5	tauschii	Russia
2399	30M	30MR	20M	25MR	L	H	12/5	1R	20MR	NT	H	H	0	18/5	tauschii	Afghanistan
2429	30MS	NT	20M	NT	M	H	14/5	5R	NT	NT	H	H	H	14/5	tauschii	Afghanistan
2601	15MR	15MS	20MR	20M	M	M	23/5	0	10MR	30MS	H	H	H	26/5	aestivum	Turkey
2602	14R	15MR	0	5R	M	H	5/6	0	20R	15MS	L	M	0	4/6	aestivum	UK

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TA #	2010							2009							Species	Country of origin
	Leaf rust		Stripe rust		BYD		HD	Leaf rust			BYD		PM	HD		
	5/26	6/2	5/26	6/2	5/13	5/26		5/21	6/1	6/5	5/21	6/1	5/21			
2619	10R	15MR	5R	5R	L	L	28/5	0	5R	10R	0	L	0	25/5	triuncialis	Turkey
2661	10MR	NT	0	NT	M	M	10/5	0	5MR	5MR	L	H	0	12/5	biuncialis	Syria
2686	10R	10R	1R	5R	0	L	30/5	1R	1R	5MR	M	H	0	25/5	uniaristata	Russia
2688	5R	25MR	1R	10MR	M	M	28/5	0	5R	15MR	L	H	L	25/5	uniaristata	Greece
2774	5R	10R	20MR	25MR	L	L	30/5	0	1R	1R	L	M	0	5/20	speltoides	Turkey
2783	10R	20R	5R	5R	M	M	28/5	0	5R	1R	L	M	0	24/5	biuncialis	Bosnia
2790	10R	10R	5R	15MR	L	L	23/5	0	1R	10R	M	H	0	18/5	neglecta	Bosnia
2799	10R	30MR	5R	5MR	L	M	28/5	0	10MR	10R	M	H	0	24/5	cylindrica	Turkey
2805	10R	25MR	20MR	25MR	M	H	28/5	1R	10MR	10M	M	H	0	18/5	turgidum	Unknown
10059	30M	NT	10MR	NT	H	H	12/5	0	10R	NT	L	H	0	5/15	biuncialis	Turkey
10069	30MR	35M	30MR	30M	M	H	15/5	15R	15M	4OM	0	H	0	18/5	tauschii	Afghanistan
10099	25M	NT	20M	NT	M	H	25/5	1R	30MR	60M	L	H	0	24/5	tauschii	Armenia
10339	30MS	35MS	20MR	20M	M	M	30/5	20M	60M	60MS	M	H	0	22/5	crassa	Tajikistan
10348	20MR	30MR	5MR	20MR	L	M	15/6	1R	10R	20R	L	H	0	23/5	cylindrica	Tajikistan
10372	5R	15MR	5R	5R	L	L	15/6	0	5R	5R	L	H	0	18/5	triuncialis	Tajikistan
10426	30MR	35M	15MR	20MR	M	H	14/5	0	5MR	40MS	H	H	0	18/5	aestivum	Turkey
10570	10MR	20MR	10R	15MR	M	M	28/5								aegilopoides	Switzerland
	10R	20MR	0	5R	M	H	31/5									
10572	10MR	30MR	10MR	15MR	M	H	15/5								aegilopoides	Iran
	15M	15MR	10R	15MR	L	M	14/5									
10592	10R	20MR	5R	10MR	L	M	29/5								aegilopoides	Turkey
	5R	10MR	5MR	10MR	L	M	30/5									
10596	20MR	30MR	10R	10MR	M	H	3/6								aegilopoides	Turkey
	25R	25MR	0	10R	L	M	5/6									
10597	30R	40MR	5MR	10MR	L	H	3/6								aegilopoides	Turkey
	20R	30MR	0	5R	O	L	5/6									

MINNESOTA

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Wheat rusts in the United States in 2009.

Wheat stem rust (*Puccinia graminis f. sp. tritici*). Texas. The first report of wheat stem rust in 2009 was of low levels found on spelt wheat and barley planted as a windbreak for watermelons in Hidalgo County along the Rio Grande Valley in southeast Texas on 23 March. Low levels of wheat stem rust were found on flag leaves and stems in McNair 701 disease-detection plots in irrigated nurseries at Beeville and Castroville in south Texas on 9 April. The pustules developed from spores that were likely rain deposited approximately 10–14 days earlier. On 22 April, stem rust was developing slowly on susceptible cultivars (McNair 701), a few winter wheat lines, and on a winter triticale (Tamcale 5019) in the Castroville irrigated plots in south Texas. On 27 April, a few pustules of wheat stem rust were found in the McNair 701 stem rust trap plot at College Station in central Texas. In early May, wheat stem rust was found on the susceptible cultivar McNair 701 at McGregor and College Station and in plots of susceptible cultivars at Bardwell and Giddings in central Texas. On 6 May, low levels of stem rust were found in a field in Jones County in northwest Texas. In late June, low levels of stem rust were reported in a Texas Panhandle wheat plot.

Oklahoma. In late May, low levels of stem rust were found in plots of two susceptible cultivars at Stillwater, Oklahoma.

Kansas. In late May, low levels of stem rust were found in plots in Reno County in south-central Kansas. In early June, low levels of wheat stem rust were found on the susceptible hard red winter cultivar Winterhawk in central Kansas plots in Ellsworth and Stafford counties. On 3 June, low levels of wheat stem rust also were found on Winterhawk in plots at Belleville in north-central Kansas. In all cases, the infections were concentrated in small foci with lesions on both stems and leaves.

Colorado. In late June, low levels of stem rust were found on the varieties Winterhawk and Bill Brown in northeastern Colorado plots.

Nebraska. On 9 June severe levels of stem rust were found on a susceptible line in the Lincoln, Nebraska breeding nursery. In late June, severe levels of stem rust were found in a susceptible triticale in an irrigated nursery in Mead, Nebraska. Severe levels of stem rust also were observed on wheat and triticale in the Lincoln nursery. In late June, high levels (20% severity) of stem rust were found in susceptible winter wheat fields at the hard dough maturity stage in Nuckolls and Franklin counties in south central Nebraska.

South Dakota. During the second week in July, low levels of stem rust were found on an experimental line in a regional nursery near Brookings, South Dakota.

North Dakota. On 10–11 August, trace levels of wheat stem rust were found in plots of susceptible wheat in eastern and central North Dakota. In late July, no stem rust was found at the Minot plots in west-central North Dakota.

Minnesota. On 13 July, high levels of wheat stem rust were found on susceptible winter wheat near maturity in plots at Rosemount in southeastern Minnesota. Also on 13 July, light levels of wheat stem rust were found on an 'old timer', susceptible spring wheat cultivar Baart in plots at Rosemount, Waseca, and Lamberton experiment stations in southern Minnesota. On 29 July, trace levels of stem rust were found on Baart rust trap plots at Morris, in west-central Minnesota.

Louisiana. In early April, a center of stem rust was found in a disease detection plot of Panola at the Jeanerette experiment station in southern Louisiana. Severities ranged from trace to 40% in a '2 m x 2 m' foci. On 8 April, severe levels of stem rust were found in several wheat plots at the Winnsboro experiment station in northeastern Louisiana. The rust had not spread evenly across the nursery. Weather conditions had been ideal for rust development with adequate moisture (rain, dew, and fog) and ideal temperatures across much of Louisiana. On 22 April, low levels of wheat stem rust were found in the Crowley plots in south-central Louisiana on the susceptible cultivar Panola and other varietal trial entries. The cultivars matured rapidly and, therefore, rust did not have much time to increase. In early May, wheat stem rust was increasing in plots at Winnsboro in northeast Louisiana. Many of the soft red winter wheats had severities of 40 to 60%.

Alabama. On 21 April, low to moderate levels of stem rust were found in a plot of the susceptible cultivar McNair 701 at Headland in southeastern Alabama. By early May, severe levels of stem rust were found in the plots.

In summary, during the early spring of 2009, low levels of stem rust were found in susceptible plots of barley and soft and hard red winter wheat in many southern states.

Arkansas. In early May, wheat stem rust was found in plots in Crawford and Pope Counties (northeastern Arkansas) on Delta King 9577 and Panola, respectively. In the southeastern part of the state, light levels of stem rust were found in a field.

Tennessee. In late May, moderate levels of wheat stem rust were found in a field near Jackson in west central Tennessee. This is the most stem rust seen in this area in the last 30 years.

Missouri. In early June, a stem rust collection was made in soft red winter wheat in Barton County in southwestern Missouri. On 8 July, high levels of stem rust were found in a field of mature winter wheat in Harrison County in northwestern Missouri. Incidence was 100% and severity was more than 40%. The grain was severely shriveled, likely resulting in a significant yield loss in this field.

Illinois. In early June, low levels of stem rust were found in plots in Madison, Champaign, and Montgomery Counties in southern Illinois. In late June, moderate levels of stem rust were found in plots in DeKalb County in north-central Illinois.

Indiana. In early June, low levels of wheat stem rust were found on a commercial cultivar in research plots in Posey, Spencer, and Vanderburgh Counties in southwest Indiana.

Michigan. On 23 June, low levels of stem rust were reported in wheat research plots in Lenawee County in southeastern Michigan. On 10 July, low levels of stem rust were found in soft winter wheat plots in Ingham and Saginaw counties in central Michigan.

Wisconsin. In late July, low levels of wheat stem rust were found in a soft red winter wheat plot in Door County in northeastern Wisconsin.

In summary, during July and August, low levels of wheat stem rust were found in susceptible winter wheat and spring wheat plots from northeastern Wisconsin through Minnesota to central North Dakota. Stem rust was not observed on any current wheat cultivars in research plots or in fields in this area.

Idaho. On 23 June 23, 20% rust severities were reported in a spring wheat field close to barberry bushes (alternate host of wheat stem rust) in Latah County, Idaho. Plants with rust pustules were 20 feet from the bushes. Spring wheat and barley crops were planted later this year so stem rust will likely develop more than in the last two years in the Palouse region. On 7 July, low levels of stem rust were found on an experimental line at the soft dough growth stage in the soft white winter wheat nursery in Aberdeen, Idaho.

Washington. Between late July and late August, a large number of stem rust samples collected from nursery plots in Whitman and Steptoe counties in Washington.

California. In early August, stem rust infection was observed on barley plants in Sonoma county, California. This was the first observation of stem rust on barley in the state of California in recent years.

This year there were more stem rust reports on susceptible cultivars in the winter wheat-growing area than recent years. The crop matured slower than normal, which allowed more stem rust than normal to develop.

Preliminary race identifications. In 2009, race QFCSC was identified as the predominant race in states of east of Rocky Mountains. This common race 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 QFCSC. A second race, RFCSC, was found in low frequencies from OK, IL, IN, NE, and MN. This race was first isolated from Texas in 2007. Virulence of race RFCSC is identical to that of race QFCSC except for virulent to *Sr7b*, a likely mutant of race QFCSC.

From stem rust collections made in a spring wheat field in Latah County, Idaho, preliminary race-typing identified the following Pgt races: JCCDC, QFCDC, QFCJC, QFCNC, QFCSC , QCMNC, QFMNC, and SCCSC. These races are relatively avirulent to most wheat cultivars east of the Rocky Mountains. However, race SCCSC has virulence to *Sr9e* and *Sr13*, a resistance gene combination that has served as the main component of stem rust resistane in durum cultivars of the northern Great Plains.

From stem rust collections made in Steptoe and Whitman counties, Washington, preliminary race typing identified 17 races, including BCCSC, GCCDB, GCCDC, GCCNC, GFCSB GFCNC, LCCJB, LCCSC, QCCDC, QCCNC, QFCDC, QFCNS, QFCJC, QFCSB, QFCSC, QCMSC, HCCJC, and MCCJB. Similar to the races in ID, these races are relatively avirulent to the majority of wheat cultivars east of the Rocky Mountains.

The diverse races in the Palouse region bordering Idaho and Washington are likely a part of a sexual population known to be present in the region due to the presence of common barberry plants and other *Berberis* spp. From the races identified in the 2009 season, virulence to *Sr9g*, *Sr10*, and *Sr17* appeared fixed in the population. Virulence frequencies were high to *Sr5*, *Sr8a*, *Sr9a*, *Sr9d*, *Sr13*, *Sr21*, and *SrMcN* and were low to *Sr7b*, *Sr9e*, and *Sr36*.

The 2009 U.S. stem rust observation map and results of race identification to date can be found at the CDL website (http://www.ars.usda.gov/Main/docs.htm?docid=9757).

Stem rust on barberry. In mid-May, light pycnial infections were found on common barberry bushes growing in south central Wisconsin. In late May, moderate numbers of aecial infections were found on susceptible barberry bushes growing in southeastern Minnesota and Wisconsin. Aecial infections on common barberry from Latah County, Idaho, were observed in mid June. In mid-July, light aecial infections were found on four common barberry bushes near Colville, in Stevens County, Washington. Infection occurred mostly on young fruits. This is the first time stem rust infections were observed on common barberry bushes located in this area.

Aecial infections from western Idaho, eastern Washington, southeastern Minnesota, and south-central Wisconsin were identified as rye stem rust. Three wheat races, BCCBC, BLBBB and GCCJC, were recovered from aecial collections from Idaho, Washington, and Wisconsin.

New barberry/stem rust web resource. In addition to the CDL's Barberry and stem rust pages, APHIS has created a new website for their Barberry/Black Stem Rust program. The page can be found at http://www.aphis.usda.gov/plant_health/plant_pest_info/barberry/index.shtml.

Wheat leaf rust. Texas. In mid-February, low levels of leaf rust were found in central Texas. In late February, leaf rust was observed in irrigated plots in south Texas at Castroville. The most severe leaf rust was found on the Jagger (*Lr17* resistance), Jagalene (*Lr24*), and TAM 112 (*Lr41*) cultivars. By mid-March, leaf rust was severe in the plots. The rust in these irrigated plots was much more severe than in the past two years. In late February, low levels of leaf rust were found on the lower leaves of wheat growing in irrigated fields in the Rio Grande Valley. Dryland fields had lower incidences of leaf rust. In early March, low levels of leaf rust were found in southern and central Texas fields. By mid-March, leaf rust was severe on susceptible cultivars in the College Station nursery in central Texas. The severe drought in the 2008–09 winter throughout much of Texas limited rust development. Mid-March rains improved conditions for rust development in Texas.

In early April, susceptible varieties Overley (*Lr41*), Jagalene (*Lr24*), and Jagger (*Lr17*) growing in nurseries at Castroville, Beeville, College Station, and McGregor, Texas, had 60% leaf rust severities on lower leaves. In more resistant cultivars, such as Fuller and Fannin, lower infection severities were observed. Fields in southern Texas were under drought stress, and rust was found only in irrigated plots in the region. During the first week in April, low to moderate levels of leaf rust were noted in central Texas fields (Fig. 1).

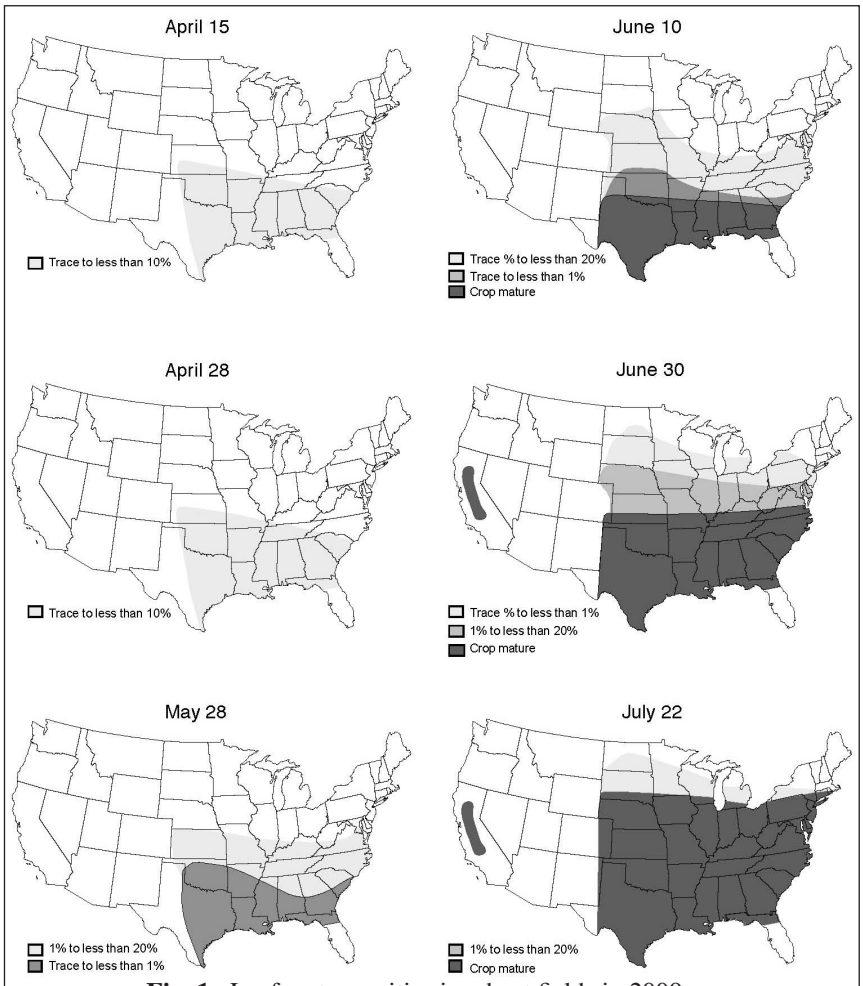

Fig. 1. Leaf rust severities in wheat fields in 2009.

In early May, high levels of leaf rust were found in plots of susceptible wheat while low levels were found in fields in central and northern Texas. In late May, low levels of leaf rust were found in fields in the Rolling Plains, the Texas Panhandle, and North Texas High

Plains fields. In much of Texas, drought-like conditions hampered the crop and rust development. These Texas locations provided less rust inoculum for areas further north than usual.

Oklahoma. In mid-February, leaf rust was at trace to low levels in Oklahoma plots. In mid-March, low levels of leaf rust were found throughout Oklahoma. The most severe leaf rust was in early-planted Jagalene. In late April, only low levels of leaf rust were observed in Oklahoma. In 2008, by late April, leaf rust was much more prevalent and severe throughout Oklahoma.

In early May, leaf rust was found in the canopy of Jagalene (*Lr24*) and Jagger (*Lr17*) plots at Stillwater, Oklahoma. Leaf rust was at the 15% severity level on flag leaves and at the 40–65 MS/S level on leaves below the flag. By early May, leaf rust increased with the ideal temperatures and abundance of free moisture. In mid-May, high levels of leaf rust were found on flag leaves of susceptible cultivars Jagger and Jagalene in the Stillwater plots. By late May, the incidence and severity of rust throughout Oklahoma increased dramatically. Leaf rust approached severity levels in the 65–90% range during the last week in May at locations where leaves were still green. In early June, high severity (60%) levels of wheat leaf rust were found in fields of Jagalene, Jagger, and Overley throughout north-central Oklahoma. In most cases, the rust arrived too late to cause significant rust losses.

Kansas. In mid-February, traces of wheat leaf rust that overwintered were found in a southeast Kansas field. In late February, traces of leaf rust were detected in northeastern Kansas plots near Manhattan. In mid-March, low levels of leaf rust were found in an eastern Kansas field.

In early April, leaf rust was at low levels throughout south-central and central Kansas. In early April, the lower leaves of the wheat in northeastern Kansas plots naturally deteriorated with age taking some of the over wintering leaf rust with it. Despite this decrease in incidence, leaf rust was still found at trace levels in research plots of susceptible cultivars. In late April, leaf rust remained at low levels throughout south-central and central Kansas. There were no reports of leaf rust in western Kansas in late April.

In mid-May, low levels of leaf rust were found on flag leaves in north-central Kansas plots and fields. The rust infections originated from spores from rust infected wheat further to the south, which were deposited with rainfall.

In early June, high severity (60%) levels of wheat leaf rust were found in fields of Jagalene, Jagger, and Overley in southeastern and south-central Kansas (Fig. 1, p. 248). Some fields had been sprayed with fungicide to control the rust. In unsprayed fields, leaf rust caused yield losses in susceptible varieties in south central and central Kansas. In varietal plots in south-central Kansas, leaf rust was low in the resistant cultivars Fuller, Santa Fe, and Art. In western Kansas, rust severity was less than 5% on most leaves. In early June, in north central Kansas fields of Overley, etc., leaf rust severities on flag leaves were increasing because of the ideal conditions for rust development. These areas provided more rust inoculum for areas further north. Losses due to leaf rust for 2009 in Kansas were estimated to be 1.37%. This estimate is considerably lower than the 20-year average of nearly 4%. The reduced losses due to leaf rust in 2009 were likely due to less leaf rust being produced in drought and freeze damaged wheat fields in Texas and Oklahoma.

Colorado. In early June, low levels of leaf rust were widespread in northeastern Colorado plots and by late June, severe levels of leaf rust were found in the same plots.

Nebraska. In early June, low levels of leaf rust were found in fields and plots in southeastern and the central Panhandle of Nebraska. In plots at Lincoln, severities ranged up to 80% in plots of the susceptible cultivar Overley (*Lr41*). In late June, high levels of wheat leaf rust were found in susceptible winter wheat fields from southern to northwestern Nebraska. In early July, high levels of wheat leaf rust were found in plots of susceptible wheat cultivars in the Nebraska Panhandle.

South Dakota. In early June, leaf rust was found on winter wheat at very low levels in the mid-canopy of several fields in southeastern South Dakota. In late June, low levels of wheat leaf rust were found in plots and fields of susceptible winter wheat cultivars in southern South Dakota. In early July, leaf rust was limited to only the most susceptible winter wheat cultivars in fields and plots in South Dakota. During the third week in July, leaf rust was at trace levels in spring wheat fields throughout eastern South Dakota.

North Dakota. In late June, trace levels of leaf rust were found in a plot of the susceptible winter wheat Jagalene in Dickey County in southeastern North Dakota. In early July, leaf rust was limited to only the most susceptible winter wheat cultivars in fields and plots in North Dakota. On 13 July in susceptible winter wheat plots in Ramsey County in southeastern North Dakota, 10–40% leaf rust severities were found on the flag leaves at the soft dough stage. Fungicide application at the flowering growth stage had effectively controlled leaf rust at this North Dakota location. During the third week in July, leaf rust was at trace levels in spring wheat fields throughout North Dakota. Low to moderate levels of leaf rust were found in plots of susceptible spring wheat cultivars in eastern and central North Dakota on 10–11 August. Increased amounts of leaf rust were found in plots of the cultivars Knudson and Briggs, which were highly resistant in previous years. No leaf rust was observed on cultivars with *Lr21*, e.g., Faller, Glenn, Steele, RB07, and others. Leaf rust was at trace levels on susceptible cultivars at Minot and Langdon in mid-August.

Minnesota. In late June, low levels of wheat leaf rust were found in plots and fields of susceptible winter wheat cultivars in west-central Minnesota. In early July, leaf rust was limited to only the most susceptible winter wheat cultivars in fields and plots in northwestern Minnesota. In plots of unsprayed susceptible spring wheat, high levels of leaf rust were found at Rosemount, Waseca, Lamberton, and Morris on 13–15 July. On 29 July, wheat leaf rust was severe in plots of susceptible cultivars at Morris in west-central Minnesota, whereas leaf rust was low on currently grown cultivars. In late July, leaf rust was not observed in susceptible wheat plots in northwest Minnesota or in the northern tier of counties in North Dakota.

Northern Plains. In 2009, wheat leaf rust was widespread, but cool and dry conditions in May and June delayed the arrival and drastically slowed the development of wheat leaf rust. The loss of many winter wheat fields in North and South Dakota due to winterkill also removed a susceptible early source of leaf rust in this region. Many of the wheat fields in the spring wheat region were treated with fungicide, which reduced losses due to leaf rust and Fusarium head blight.

Louisiana. In early March, infection levels of wheat leaf rust were much lower than normal in southern Louisiana. During the fourth week in March, low to moderate levels were found in plots and fields throughout Louisiana. Growers sprayed with fungicides to control the leaf rust. In late March, weather conditions were ideal for rust development with considerable moisture (rain, dew and fog) and ideal temperatures across Louisiana for a couple weeks. In mid-April, wheat leaf rust was severe on many susceptible lines and cultivars in the Louisiana plots.

In early May, high levels of leaf rust were observed in susceptible wheat plots in central and northeastern Louisiana. Significant levels of leaf rust were found in fields of LA841 in northern Louisiana. This cultivar has occupied a large portion of the acreage in the region for the last five years and has the *Yr17*/*Lr37*/*Sr38* gene complex. The *Yr17* gene appears to still be effective against stripe rust in the region, but virulence on *Lr37* exists in the current leaf rust population.

Arkansas. In early March, low levels of wheat leaf rust were found in southwest Arkansas. In early April, low levels of wheat leaf rust were reported across southern Arkansas.

In early May, low levels of leaf rust were reported throughout northern Arkansas fields. In mid May, high levels of leaf rust were reported on a few susceptible lines and cultivars throughout Arkansas plots. Leaf rust was at lower levels than the past several years in Arkansas plots and fields. Little leaf rust over wintered in Arkansas and less rust arrived from southern locations (i.e., south Texas and Louisiana).

Mississippi. In mid-March, leaf rust was found on wheat in southern Mississippi plots. In early May, moderate levels of leaf rust were found in central Mississippi plots.

Alabama. In mid-April, leaf rust severities ranged from 1 to 70% in wheat varietal plots in Fairhope and Headland in southern Alabama. In early May, high levels (60–80%) of leaf rust were found in plots of susceptible wheat in central Alabama and in fields in southwestern Alabama. Leaf rust from this area provided leaf rust inoculum for northern wheat areas.

Georgia. In mid-March, leaf rust was found on the lower leaves of the most susceptible soft red winter wheat lines at the Plains nursery in southern Georgia. In early May, high levels of leaf rust were found in plots while low levels were found in fields in southwestern Georgia.

Illinois. In early June, low levels of leaf rust were found in fields and severe levels were found in plots of soft red winter wheat in southern Illinois. In mid-June, moderate levels of leaf rust were found in soft red winter wheat plots in east-central Illinois. In late June, low levels of leaf rust were found in north-central Illinois plots.

Indiana. In early June, low levels of leaf rust were found in fields in southwest and east-central Indiana. In southwest Indiana plots, infection on the flag leaves ranged from 5–15% severity on Pioneer 25R47.

Michigan. In mid-June, moderate levels of leaf rust were found in southeastern Michigan soft red winter wheat plots. In late June, low levels of leaf rust were found in southwestern Michigan plots.

Wisconsin. In mid-June, moderate levels of leaf rust were found in southeastern Wisconsin soft red winter wheat plots. In early July, high levels of leaf rust were found in fields of susceptible soft red winter wheat in Door County in north-eastern Wisconsin.

South Carolina. In mid-April, low to moderate levels of leaf rust were observed in plots at Blackville in south-central South Carolina.

North Carolina. In mid-May, severe levels of leaf rust were found on susceptible lines and cultivars in plots and light levels in fields in eastern North Carolina. Much of the acreage had been sprayed for wheat diseases.

Virginia. In mid-May, severe levels of leaf rust were found on susceptible lines and cultivars in plots and low levels in fields in northeastern Virginia. Many of the wheat fields had been sprayed for wheat diseases.

Maryland. In mid-May low levels of leaf rust were found in plots on the Delmarva Peninsula. Only a few pustules developed on the flag leaves, but conditions were good for continued development. Much of the acreage had been sprayed for wheat diseases.

Delaware. In mid-June, low levels of leaf rust were found in Delaware winter wheat plots and fields.

New York. On 22 May, low levels of leaf rust were reported in Monroe County west of Rochester and along Lake Ontario. In mid-June, low levels of leaf rust were found in central and western New York winter wheat plots and fields.

California. During the second week in May, leaf rust was detected in plots in the nursery at Davis and by the third week in May 60% severities were reported in susceptible lines.

Washington. In late June, low levels of leaf rust were observed in wheat nurseries at Mt. Vernon and Walla Walla.

Ontario, Canada. Low levels of leaf rust (trace to 3%) were found in southwestern Ontario fields in late June.

Leaf rust race identifications. In 2009, 41 races of wheat leaf rust were described in the United States (Table 1, pp. 252-253). Races MLDSD (28.9%), TCRKG (16.8%), TDBGG (14.4%), MCTSB (7.4%), and MFPSB (4.9%) were the five most common races. Races MLDSD (*Lr9*, *Lr17*, *Lr41*/*Lr39* virulence), TDBGG (*Lr24* virulence), and MFPSB (*Lr17*, *Lr24*, and *Lr26*) were most common races in the Great Plains region. Races TCRKG (*Lr26*, *Lr11*, and *Lr18* virulence) and MCTSB (*Lr11*, *Lr17*, and *Lr26* virulence) increased in 2009 and were found mostly in the southeastern states.

Races with virulence to genes *Lr24*, *Lr26*, *Lr17*, and *Lr41*/*Lr39* that are present in the hard red winter wheat were common in the Great Plains region (Table 2, p. 254). Races with virulence to *Lr24*, *Lr26*, *Lr11*, and *Lr18* that are present in the soft red winter wheat were common in the southeastern states. Races with virulence to *Lr16* that is present in the hard red spring wheat were at low frequencies in the Great Plains region. Races with virulence to *Lr21* that is present in hard red spring wheat was not detected (http://www.ars.usda.gov/Main/docs.htm?docid=10493).

Lr gene postulations of current soft red winter, hard red winter, and hard red spring wheat cultivars are available in a searchable database at: http://160.94.131.160/fmi/iwp/cgi?-db=Lr%20gene%20postulations&-loadframes.

Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*). Texas. During the fourth week in March, low levels of stripe rust were found in southeastern Texas. The severe drought during the winter throughout much of Texas limited rust develop-

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2009 identified by virulence to 19[a] lines of wheat with single genes for leaf rust resistance. [a] Lines tested were Thatcher lines with genes *Lr1, Lr2a, Lr2c, Lr3a, Lr9, Lr16, Lr24, Lr26, Lr3ka, Lr11, Lr17, Lr30, LrB, Lr10, Lr14a, Lr18, Lr21, Lr28,* and winter wheat lines with gene *Lr41*.

Pheno-type	Virulences	AL, AR, GA, LA, MS, NC, SC		MD, NY, PA, VA		IL, MI, WI		OK, TX		KS, NE		MN, ND, SD		AZ, CA		ID, WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBQB	B,10	0	0	0	0	0	0	0	0	0	0	0	0	4	33.3	0	0	4	0.7
CCPMB	3,26,3ka,17,30,B,18	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
FCPNB	2c,3,26,3ka,17,30,B,14a	0	0	0	0	0	0	2	1.2	0	0	0	0	0	0	0	0	2	0.3
MBBJG	1,3,10,14a,28	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MBDSB	1,3,17,B,10,14a	1	0.6	0	0	0	0	0	0	0	0	0	0	2	16.7	0	0	3	0.5
MBGJG	1,3,11,10,14a,28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	20	2	0.3
MBPTB	1,3,3ka,17,30,B,10,14a,18	2	1.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MBRKG	1,3,3ka,11,30,10,14a,18,28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	1	0.2
MBTSB	1,3,3ka,11,17,30,B,10,14a	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.2
MCDSB	1,3,26,17,B,10,14a	12	7.3	0	0	0	0	2	1.2	0	0	0	0	5	41.7	0	0	19	3.2
MCGDG	1,3,26,11,14a,28	2	1.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MCPQG	1,3,26,3ka,17,30,B,10,28	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MCPSB	1,3,26,3ka,17,30,B,10,14a	5	3	0	0	0	0	2	1.2	2	2.9	0	0	0	0	0	0	9	1.5
MCRJG	1,3,26,3ka,11,30,10,14a,28	0	0	1	1.7	0	0	0	0	0	0	0	0	0	0	0	0	1	0.2
MCRKG	1,3,26,3ka,11,30,10,14a,18,28	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MCTSB	1,3,26,3ka,11,17,30,B,10,14a	21	12.8	11	18.3	6	20	2	1.2	2	2.9	2	2.6	0	0	0	0	44	7.4
MDBJG	1,3,24,10,14a,28	0	0	12	20	0	0	0	0	0	0	0	0	0	0	0	0	12	2
MFBJG	1,3,24,26,10,14a,28	0	0	8	13.3	0	0	0	0	0	0	0	0	0	0	0	0	8	1.4
MFGJG	1,3,24,26,11,10,14a,28	0	0	2	3.3	0	0	3	1.8	0	0	0	0	0	0	0	0	5	0.8
MFPSB	1,3,24,26,3ka,17,30,B,10,14a	6	3.7	2	3.3	4	13.3	6	3.6	6	8.8	5	6.4	0	0	0	0	29	4.9
MLDSD	1,3,9,17,B,10,14a,41	12	7.3	2	3.3	1	3.3	80	47.3	38	55.9	35	44.9	1	8.3	2	20	171	28.9
NBBKG	1,2c,10,14a,18,28	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
PBBHG	1,2c,3,10,18,28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	50	5	0.8
PCMJG	1,2c,3,26,3ka,30,10,14a,28	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
SBBGG	1,2a,2c,10,28	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	1	0.2
TBBJG	1,2a,2c,3,10,14a,28	2	1.2	0	0	0	0	0	0	3	4.4	2	2.6	0	0	0	0	7	1.2

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2009 identified by virulence to 19[a] lines of wheat with single genes for leaf rust resistance. [a] Lines tested were Thatcher lines with genes *Lr1, Lr2a, Lr2c, Lr3a, Lr9, Lr16, Lr24, Lr26, Lr3ka, Lr11, Lr17, Lr30, LrB, Lr10, Lr14a, Lr18, Lr21, Lr28,* and winter wheat lines with gene *Lr41.*

Pheno-type	Virulences	AL, AR, GA, LA, MS, NC, SC		MD, NY, PA, VA		IL, MI, WI		OK, TX		KS, NE		MN, ND, SD		AZ, CA		ID, WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
TBGJG	1,2a,2c,3,11,10,14a,28	2	1.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	9	5.5	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	10	1.7
TCDSB	1,2a,2c,3,26,17,B,10,14a	0	0	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
TCJDB	1,2a,2c,3,26,11,17,14a	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.2
TCQJG	1,2a,2c,3,26,3ka,11,10,14a,28	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.2
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	70	42.7	4	6.7	17	56.7	5	3	1	1.5	2	2.6	0	0	0	0	99	16.8
TCTJG	1,2a,2c,3,26,3ka,11,17,30,10,14a,28	2	1.2	2	3.3	0	0	0	0	0	0	0	0	0	0	0	0	4	0.7
TDBGB	1,2a,2c,3,24,10	0	0	0	0	0	0	2	1.2	0	0	0	0	0	0	0	0	2	0.3
TDBGG	1,2a,2c,3,24,10,28	4	2.4	0	0	0	0	43	25.4	9	13.2	29	37.2	0	0	0	0	85	14.4
TDBJG	1,2a,2c,3,24,10,14a,28	8	4.9	2	3.3	2	6.7	7	4.1	3	4.4	0	0	0	0	0	0	22	3.7
TDRKG	1,2a,2c,3,24,3ka,11,30,10,14a,18,28	0	0	0	0	0	0	4	2.4	0	0	0	0	0	0	0	0	4	0.7
TFBGG	1,2a,2c,3,24,26,10,28	0	0	0	0	0	0	4	2.4	0	0	1	1.3	0	0	0	0	5	0.8
TFBJG	1,2a,2c,3,24,26,10,14a,28	3	1.8	0	0	0	0	0	0	2	2.9	0	0	0	0	0	0	5	0.8
TJBGG	1,2a,2c,3,16,24,10,28	0	0	0	0	0	0	2	1.2	2	2.9	2	2.6	0	0	0	0	6	1
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,14a,28,41	0	0	0	0	0	0	3	1.8	0	0	0	0	0	0	0	0	3	0.5
Total		164		60		30		169		68		78		12		10		591	

ment. On 27 March, low levels of stripe rust were detected in the lower canopy of susceptible Pioneer 25R78 wheat fields in Hunt, Rockwall, and Fannin counties in north-central Texas. Weather conditions were conducive for the rust to move upwards to the F-2 and F-1 leaves. Detection of stripe rust in north Texas was similar in date to 2008.

In early April, low to heavy levels of stripe rust were observed in a field of Pioneer 26R61 near College Station in central Texas. On 22 April, low levels of stripe rust were found on a few winter wheat lines in the irrigated nursery at Castroville, Texas (Fig. 2, p. 255). Stripe rust was extremely light and hard to find in the nursery at College Station.

Oklahoma. In early June, severe levels of stripe rust were found in a field in the Panhandle of Oklahoma. The rust arrived so late that it did not affect the wheat yield.

Kansas. On 22 May, stripe rust was observed at trace levels in Saline County (central Kansas). In early June, low levels of stripe rust were observed in Reno county (central Kansas) and Sumner county (south-central Kansas) plots of cultivars known to be susceptible to stripe rust. Lesions were 2 to 3 cm long and actively producing spores suggesting that the infections had taken place at least three weeks earlier. On 8 June, several small foci of stripe rust were found in the susceptible cultivars 2137, TAM 110, and TAM ll2 in northwest Kansas. A few stripe rust lesions were identified on cultivars previously identified as moderately resistant. This observation on the MR cultivars has been reported late in the growing season the past two years. Losses to stripe rust were light in Kansas in 2009.

Colorado. In early June, low levels of wheat stripe rust were found at Julesburg, in northeastern Colorado plots.

Table 2. Number and frequency (%) of isolates of *Puccinia triticina* in the United States in 2009 virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance gene	AL, AR, GA, LA, MS, NC, SC		MD, NY, PA, VA		IL, MI, WI		OK, TX		KS, NE		MN, ND, SD		AZ, CA		ID, WA		Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	164	100.0	58	96.7	30	100.0	167	98.8	68	100.0	78	100.0	8	66.7	10	100.0	583	98.6
Lr2a	102	62.2	10	16.7	19	63.3	72	42.6	20	29.4	36	46.2	0	0.0	0	0.0	259	43.8
Lr2c	102	62.2	14	23.3	19	63.3	74	43.8	20	29.4	36	46.2	0	0.0	5	50.0	270	45.7
Lr3	164	100.0	58	96.7	30	100.0	168	99.4	68	100.0	78	100.0	8	66.7	10	100.0	584	98.8
Lr9	12	7.3	2	3.3	1	3.3	83	49.1	38	55.9	35	44.9	1	8.3	2	20.0	174	29.4
Lr16	0	0.0	0	0.0	0	0.0	2	1.2	2	2.9	2	2.6	0	0.0	0	0.0	6	1.0
Lr24	21	12.8	26	43.3	6	20.0	74	43.8	22	32.4	37	47.4	0	0.0	0	0.0	186	31.5
Lr26	123	75.0	40	66.7	27	90.0	26	15.4	13	19.1	10	12.8	5	41.7	0	0.0	244	41.3
Lr3ka	117	71.3	28	46.7	27	90.0	25	14.8	11	16.2	9	11.5	0	0.0	1	10.0	218	36.9
Lr11	109	66.5	22	36.7	23	76.7	18	10.7	3	4.4	4	5.1	0	0.0	3	30.0	182	30.8
Lr17	63	38.4	23	38.3	11	36.7	94	55.6	48	70.6	42	53.8	8	66.7	2	20.0	291	49.2
Lr30	116	70.7	28	46.7	27	90.0	25	14.8	11	16.2	9	11.5	0	0.0	1	10.0	217	36.7
LrB	60	36.6	21	35.0	11	36.7	94	55.6	48	70.6	42	53.8	12	100	2	20.0	290	49.1
Lr10	161	98.2	58	96.7	30	100.0	167	98.8	68	100.0	78	100.0	12	100	10	100.0	584	98.8
Lr14a	160	97.6	56	93.3	30	100.0	117	69.2	57	83.8	46	59.0	8	66.7	5	50.0	479	81.0
Lr18	81	49.4	10	16.7	17	56.7	10	5.9	1	1.5	2	2.6	0	0.0	6	60.0	127	21.5
Lr21	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0 0
Lr28	103	62.8	41	68.3	19	63.3	73	43.2	20	29.4	36	46.2	0	0.0	8	80.0	300	50.8
Lr41	12	7.3	2	3.3	1	3.3	83	49.1	38	55.9	35	44.9	1	8.3	2	20.0	174	29.4
Total	164		60		30		169		68		78		12		10		591	

Nebraska. In early June, trace levels of stripe rust were found in the central Panhandle of Nebraska. In late June, significant levels (40% severities) of wheat stripe rust were found in fields from Hemingford to Gordon in the northern panhandle of Nebraska (Fig. 2).

South Dakota. In early July, low levels of stripe rust were found in a spring wheat plot at the Beresford research station in southeastern South Dakota.

North Dakota. On 11 August, stripe rust was at trace levels on wheat cultivars with *Lr21*, in central North Dakota.

Montana. In early July, conditions were favorable for stripe rust development in the Gallatin Valley at the Post Research farm in Bozeman, Montana. Rust was first observed 4 June. Plots that were sprayed with fungicide had minimal disease development.

Louisiana. During the fourth week in March in northeastern Louisiana at Winnsboro, high levels of stripe rust were observed in one wheat plot; surrounding plots were relatively clean. By late March, stripe rust had not been reported in other areas of the state. In Louisiana, stripe rust epidemics usually develop in the first half of March and peak by early April when temperatures surpass the optimum for stripe rust development. In early

April, wheat rust stripe levels were lower than normal in Louisiana.

Arkansas. As of 25 March, no stripe rust had been reported in Arkansas. In mid-April, wheat stripe rust was at lower levels than in the past several years in Arkansas. Extension personnel reported light stripe rust in southwest Arkansas. In early May, no additional stripe rust was found in Arkansas. The threat of more stripe rust was low. because the wheat crop was past the most favorable time for stripe rust development and most of the acreage was planted with varieties that have resistance.

Georgia. In late March, low levels of stripe rust were found in susceptible wheat fields from southwest to south-central Georgia. During April, stripe rust developed slowly in this area, because conditions were not conducive for rust development. In early May, severe levels of stripe rust were found in susceptible cultivars at the Plains, Georgia, nursery. Stripe rust had been artificially inoculated in these plots.

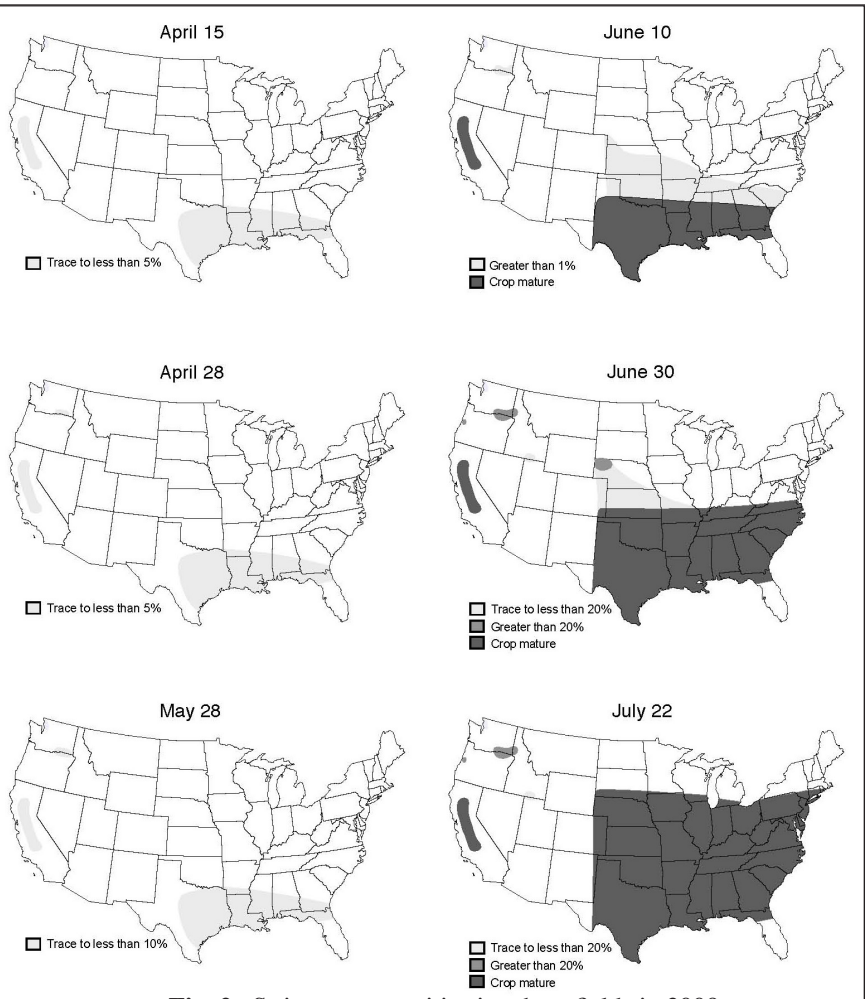

Fig. 2. Stripe rust severities in wheat fields in 2009.

Virginia. In mid-June, low levels of stripe rust were found on soft wheat cultvars in the Montgomery, Virginia nursery.

Ontario, Canada. With the cooler than usual May and June weather, wheat stripe rust in late June was more prevalent in Essex and Chatham/Kent counties Ontario (adjacent to Detroit, Michigan) than in recent years.

California. In late March, stripe rust was found in nurseries in the Sacramento and San Joaquin Valleys. From 20–23 April, high levels of wheat stripe rust were found in nurseries in the Sacramento Valley. Severities higher than 50% were observed on the susceptible wheat D6301 at Davis. During early May, conditions were conducive for rust increase and stripe rust severities of up to 60% were found in the susceptible cultivars Anza and Yecora Rojo at Colusa. The resistance of the commonly grown wheat cultivars was holding up.

Pacific Northwest. In late February, wheat stripe rust was found in the Mount Vernon area of northwestern Washington. In early April, 30% wheat stripe rust severities were reported on susceptible entries in nurseries and 2–5% severities in some Mount Vernon area fields. The rust severities were less than normal for the time of the year. In mid-June in the Mt. Vernon nursery, 80% stripe rust severities were reported in susceptible winter wheat varieties and by late June 100% severities were reported in susceptible spring wheat entries.

In mid-April, low levels of stripe rust were found in the Horse Heaven Hills area in south-central Washington and on a susceptible check in the winter wheat nursery near Walla Walla. In mid-May, foci of stripe rust (10–80% severity) were found in winter wheat nurseries in the Washington/Idaho Palouse region. In rust nurseries in Umatilla County, Oregon, stripe rust was developing on susceptible entries with 80% severities in foci. No stripe rust was found in any fields in the above area. In the Horse Heaven Hills area (Benton County) stripe rust development was under control after fungicide application.

On June 2, stripe rust on susceptible entries was found in the experimental plots near Pullman, Washington. The incidence was less than 1% and severity less than 5%. The first appearance of stripe rust near Pullman was about two weeks later than 2008. In late June, wheat stripe rust had increased rapidly (100% severities) on susceptible cultivars growing in winter wheat nurseries in the Palouse region (Whitman County, Washington, and Latah County, Idaho). At the Pendleton experiment station in Oregon, stripe rust reached 60% severity on susceptible entries. In the spring wheat nurseries, 40% severities were reported on susceptible entries. In the western Pacific Northwest area stripe rust was very

Table 3. Estimated losses in winter wheat due to rust in 2009 (T = trace).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
AL	180	55.0	9,900	0.0	0.0	1.00	100.0	0.0	0.0
AR	390	44.0	17,160	T	T	T	T	T	T
CA	315	80.0	25,200	0.0	0.0	T	T	1.0	254.5
CO	2,450	40.0	98,000	0.0	0.0	T	T	T	T
DE	67	62.0	4,154	0.0	0.0	0.00	0.0	0.0	0.0
FL	14	43.0	602	0.0	0.0	T	T	0.0	0.0
GA	250	42.0	10,500	0.0	0.0	1.00	106.1	T	T
ID	700	81.0	56,700	T	T	0.00	0.0	T	T
IL	820	56.0	45,920	0.0	0.0	1.00	463.8	0.0	0.0
IN	450	67.0	30,150	0.0	0.0	1.00	304.5	0.0	0.0
IA	22	45.0	990	0.0	0.0	0.00	0.0	0.0	0.0
KS	8,800	42.0	369,600	T	T	1.37	5,133.9	T	T
KY	390	57.0	22,230	0.0	0.0	T	T	0.0	0.0
LA	175	56.0	9,800	T	T	0.75	73.5	1.0	99.8
MD	195	60.0	11,700	0.0	0.0	T	T	0.0	0.0
MI	560	69.0	38,640	0.0	0.0	1.00	390.3	0.0	0.0
MN	45	45.0	2,025	0.0	0.0	1.00	20.5	0.0	0.0
MS	165	50.0	8,250	0.0	0.0	0.50	41.5	0.0	0.0
MO	730	47.0	34,310	T	T	1.50	522.5	T	T
MT	2,420	37.0	89,540	0.0	0.0	0.00	0.0	0.0	0.0
NE	1,600	48.0	76,800	T	T	0.70	541.4	T	T
NJ	29	51.0	1,479	0.0	0.0	0.00	0.0	0.0	0.0
NM	140	25.0	3,500	0.0	0.0	0.00	0.0	0.0	0.0
NY	105	65.0	6,825	0.0	0.0	1.00	68.9	0.0	0.0
NC	600	49.0	29,400	0.0	0.0	0.00	0.0	0.0	0.0
ND	545	48.0	26,160	0.0	0.0	2.00	533.9	0.0	0.0
OH	980	72.0	70,560	0.0	0.0	1.00	712.7	0.0	0.0
OK	3,500	22.0	77,000	0.0	0.0	6.00	4,914.9	T	T
OR	750	56.0	42,000	0.0	0.0	T	T	T	T
PA	175	56.0	9,800	0.0	0.0	T	T	0.0	0.0
SC	150	47.0	7,050	0.0	0.0	T	T	0.0	0.0
SD	1,530	42.0	64,260	0.0	0.0	1.00	649.1	0.0	0.0
TN	340	51.0	17,340	T	T	T	T	0.0	0.0
TX	2,450	25.0	61,250	T	T	1.10	681.2	T	T
UT	135	50.0	6,750	0.0	0.0	0.00	0.0	0.0	0.0
VA	210	58.0	12,180	0.0	0.0	T	T	0.0	0.0
WA	1,640	59.0	96,760	T	T	T	T	0.5	486.2
WV	5	50.0	240	0.0	0.0	T	T	0.0	0.0
WI	315	68.0	21,420	0.0	0.0	1.00	216.4	0.0	0.0
WY	132	38.0	5,016	0.0	0.0	T	T	0.0	0.0
Total above	34,469	44.1	1,521,161		T		15,475.1		840.5
U.S. % loss				T		1.00		0.06	
U.S. total	34,485	44.2	1,522,718						

Table 4. Estimated losses in spring and durum wheat due to rust in 2009 (T = trace).

SPRING WHEAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
CO	29.0	90.0	2,610	0.0	0.0	0.0	0.0	0.00	0.00
ID	530.0	77.0	40,810	0.0	0.0	0.0	0.0	T	T
MN	1,550.0	53.0	82,150	0.0	0.0	T	T	0.00	0.00
MT	2,350.0	30.0	70,500	0.0	0.0	0.5	712.1	0.00	0.00
NV	2.0	75.0	150	0.0	0.0	0.0	0.0	0.00	0.00
ND	6,300.0	46.0	289,800	0.0	0.0	1.0	2,927.3	0.00	0.00
OR	127.0	54.0	6,858	0.0	0.0	0.0	0.0	T	T
SD	1,470.0	44.0	64,680	0.0	0.0	T	T	0.00	0.00
UT	12.0	44.0	528	0.0	0.0	0.0	0.0	0.00	0.00
WA	585.0	45.0	26,325	T	T	0.0	0.0	1.00	265.90
Total above	12,955.0	45.1	584,411		T		3,639.4		265.90
U.S. % Loss				T	0.6		0.04		
U.S. Total	12,955.0	45.1	584,411						

DURUM WHEAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
AZ	124.0	100.0	12,400	0.0	0.0	0.0	0.0	0.00	0.00
CA	170.0	100.0	17,000	0.0	0.0	0.0	0.0	0.00	0.00
ID	20.0	81.0	1,620	0.0	0.0	0.0	0.0	0.00	0.00
MT	535.0	31.0	16,585	0.0	0.0	0.0	0.0	0.00	0.00
ND	1,570.0	39.0	61,230	0.0	0.0	0.0	0.0	0.00	0.00
SD	9.0	23.0	207	0.0	0.0	0.0	0.0	0.00	0.00
Total above	2,428.0	44.9	109,042		0.0		0.0		0.00
U.S. % Loss				0.0		0.0		0.00	
U.S. Total	2,428.0	44.9	109,420						

severe in nurseries in Corvallis, Oregon. In late June, no stripe rust had been observed in spring wheat fields in eastern Washington and northern Idaho. Stripe rust did not cause significant damage to the winter wheat crop in this region.

In early July, low levels of wheat stripe rust were found in spring wheat fields in the Palouse and Dayton region of southeastern Washington.

Idaho. In late June, stripe rust was moderate in winter wheat fields and plots in southeastern Idaho and northern Utah. In early July, low levels of stripe rust were found in a soft white spring wheat Jubilee plot at Aberdeen, Idaho.

In summary, stripe rust did not cause significant damage to the winter and spring wheat crop in the Pacific Northwest.

VIRGINIA

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2009 Wheat Production in the Commonwealth of Virginia.

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Growing conditions. Planting conditions in Autumn 2008 were favorable for early planting with over 20% of the state's intended acreage seeded by 20 October. The high cost of inputs influenced some growers to plant later than normal in hopes that prices would fall or fields were seeded with the intention of applying fertilizer at a later date. By 1 November, 49% of the crop was estimated as planted, which matched the 5-yr average of 50% planted by this date. Widespread rain in November provided moisture and improved groundwater supplies in many areas (Fig. 1). Although most small grain fields looked good, cool weather in November slowed crop development. Mid-winter was cooler than normal and dry, with most of the Coastal Plain region receiving two inches less precipitation than the long-term average in the month of January (Fig. 1). By February, this deficit was more than four inches and resulted in only 26% of the small grain crop rated as good or excellent. Rain in March helped make up some of this deficit ,and over 50% of the crop was rated good or better in mid-April. In May, cool, wet weather had many producers scouting fields for disease and making pesticide applications in response to threats. By the end of the month, the crop was headed but continued wet weather caused producers to be concerned over the potential for Fusarium Head Blight (FHB) as well as potential decreases in test weight due to weathering. Overall, significant FHB infection was observed in Virginia wheat fields, which lowered grain yield and grain quality. By 20 June, approximately 20% of the crop was harvested, which was significantly lower than the previous year when 44% was harvested by that date.

Fig. 1. Long-term mean and 2009 growing season statewide rain-

Disease and insect incidence and severity. Powdery mildew incidence and severity was significant at several locations in Virginia in 2009. Entries in state wheat variety trials were rated (0 = no infection to 9 = severe infection) at four locations with mean scores ranging from 0 to 8 at Warsaw, 0 to 7 at Painter, 0 to 7 at Orange, and 0 to 6 at Blacksburg, VA. The cultivar Tribute, with *Pm17*, received mean ratings of 5 at Warsaw and Painter, whereas virulence for *Pm17* was not predominant at Blacksburg and Orange where Tribute had mean ratings from 0 to 1. Leaf rust was prevalent and state wheat entries received mean ratings from 0 to 9 at Warsaw, 0 to 5 at Painter, and 0 to 2 at Blacksburg. Cultivars such as Sisson and USG3209 with gene *Lr26* and McCormick with gene *Lr24* were very susceptible to leaf rust. Race surveys conducted by the USDA–ARS Cereal Disease Lab on 38 samples from three regions in Virginia indentified 10

races among which three (MFBJG, MFGJG, MFPSC) had virulence for *Lr24* and *Lr26*, four (MCRKG, MCTSB, TCDSB, TCRKG) had virulence for *Lr26*, and two (MDBJG and TDBJG) had virulence for *Lr24*. Virulence for the widely deployed genes *Lr24* and *Lr26* was common, whereas virulence was not observed for gene *Lr9*. Stripe rust was only found at one of the seven Official Variety Test sites in 2009. Isolated infection foci were observed in wheat yield plots at Blacksburg, VA, and rust samples sent to Xianming Chen at Washington State University were identified as race PST98. Barley/cereal yellow dwarf virus infection was moderately low (0–2) at Blacksburg, VA, whereas wheat spindle streak mosaic virus infection was moderately high (0–7) in the state wheat no-till test at Warsaw, VA. *Fusarium graminearum* was severe throughout much of the state and resulted in significant losses in grain yield and quality accompanied by high DON toxin levels in some areas.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service (http://www.nass.usda.gov/Statistics_by_State/Virginia/index.asp), in 2008–09 Virginia wheat producers planted 250,000 acres (101,250 ha), down 60,000 acres (24,300 ha) from the previous year. The estimated area harvested was 210,000 acres (85,050 ha), a 25% reduction compared to the 2007–08 crop at 280,000 acres (113,400 ha). The 2009 statewide wheat yield average was 13 bu/ac (874 kg/ha) lower than the record yield 71 bu/ac (4,770 kg/ha) set in 2008, and losses due to FHB accounted for a majority of this yield difference. Overall, wheat production in 2009 was 12.2 x 10^6 bushels (331, 500 metric tons) compared with 19.9 x 10^6 bushels (541,000 metric tons) in 2008.

State cultivar tests. In the 2008–09 tests, total of 89 entries were planted at seven locations across Virginia (http://www.grains.cses.vt.edu/). The test included 45 commercial cultivars and 44 experimental lines among which seven were subsequently released as cultivars. No-till tests were conducted at Warsaw, Holland, and Shenandoah Valley and planted after corn. The released cultivars Branson, Vigoro V9723, Shirley, Progeny 185, USG 3120, Merl, Pioneer Brands 26R15, 26R20 and 26R32, NC-Yadkin, SS 520, SS-MPV 57, USG 3555, USG 3665, Coker 9553, Renwood 3434, and Vigoro V9922 all produced significantly higher yields than the overall trial average of 73 bu/ac (4,905 kg/ha). Average grain yields among the 89 entries ranged from 64 bu/ac (4,300 kg/ha) to 82 bu/ac (5,510 kg/ha). Average test weight ranged from 53.4 lb/bu (687 kg/m3) to 59.3 lb/bu (763 kg/m3) with an overall trial average of 56.3 lb/bu (725 kg/m3).

2009 Virginia Wheat Yield Contest Results. The 2009 contest was conducted statewide, and the results are presented in the table below. Average yield of all entrants was 93 bu/ac (Table 1). Congratulations to our winners.

Table 1. 2009 Virginia Wheat Yield Contest Statewide Winners.

Place	Farm	County	Yield bu/ac	Planting date	Cultivar	Rate	Row width	Previous crop	Soil type	Tillage	Total N lb/ac	Seed treatment	Herbicides	Fungicides	Insecticides
1	George Alvis, Jr.	Goochland	108.3	26/10/08	SS 560	150 lb/ac	7.5	corn	N/A	minimum	100 lb/ac, 3 apps, 6,000 gal manure	Raxil	Harmony GTXP, 0.75 oz/ac	Headline, 6 oz/ac	Warrior II, 1.5 oz/ac
2	John Black and Sons / Jon L. Black	Charles City	103.5	24/10/08	Dominion	28 sd/row ft	7.5	cotton	Pamunkey	no-till	130 lb/ac, 3 apps	Dividend Extreme	Harmony Extra, 0.75 oz/ac	Stratego, 12 oz/ac	None
3	Dennis Alvis	Goochland	96.9	1/11/08	SS 9404	150 lb/ac	7.5	corn	N/A	minimum	100 lb/ac, 3 apps	Raxil	Harmony GTXP, 0.75 oz/ac	Headline, 6 oz/ac	Warrior II, 1.5 oz/ac
4	Randy Alvis	Goochland	96.7	24/10/08	SS 8309	150 lb/ac	7.5	corn	N/A	minimum	100 lb/ac, 3 apps, 6,000 gal manure	Raxil	Harmony GTXP, 0.75 oz/ac	Headline, 6 oz/ac	Warrior II, 1.5 oz/ac

Relationships of dwarf and photoperiod insensitive genes with Fusarium head blight resistance in U.S. soft red winter wheat cultivars.

Shuyu Liu, Carl A. Griffey, Marla D. Hall, Wynse S. Brooks, Patty Gundrum, and John Seago.

Two US soft red winter wheat cultivars, Ernie and Massey, have moderate FHB resistance. Recombinant inbred line mapping populations 'Becker/Massey' (BM) and 'Ernie/Mo 94-317' (EM) were derived from them and have been screened for FHB resistance in the field in multiple years (2008 and 2009) and locations (Blacksburg and Warsaw, VA). *Rht1*, *Rht2*, and *Ppd1* segregated in both populations with *Rht8* for BM in addition. Based on field data from two years, FHB incidence, severity, and Fusarium-damaged kernels (FDK) are significantly correlated for BM (r = 0.34~0.54) and EM (r = 0.37~0.60) within year and for EM across year (r = 0.15~0.57). Height is very significantly, and negatively, related to FHB resistance for BM in 2008 (r = –0.49~–0.57) and for EM in both years (r = –0.43~–0.72), whereas heading date and flowering date are only related to FHB incidence and severity at lower significance levels in some cases (r = –0.14~–0.36) and are positively related to FDK (r = 0.15~0.23). FHB resistance QTL have been mapped onto chromosomes 4B and 4D where two major dwarf genes *Rht1* and *Rht2* reside. *Rht8* and the photoperiod insensitive gene *Ppd1* were mapped on chromosome 2D of Massey and associated with a minor QTL for FHB resistance. Further analyses showed that both *Rht1* and *Rht2* are significantly associated with FHB incidence, severity, and FDK in 2008 for BM and both years for EM. They can explain the phenotypic variations at 14 to 32% based on data from the two mapping populations in two years. However, *Rht8* is not significant in any case. *Ppd1* was significant for FHB incidence only in 2008 for BM and in 2009 for EM. It is also significant for FHB severity in both years for EM. Because FHB infection is complicated by many genetic and environmental factors, further studies are needed to clarify the effects from these genes and other morphological traits.

Release of the soft red winter wheat cultivar Merl.

Merl, developed and tested as VA03W-412 by the Virginia Agricultural Experiment Station, was released in March 2009. The name Merl was selected in honor and memory of G. Merl Longest, who served for 16 years on the Virginia Crop Improvement Association's Board of Directors as a member and three terms as president. Merl was derived from the three-way cross 'Roane/Pioneer Brand 2643//38158' (PI 619052). Merl is a broadly adapted, mid-season, moderately short, semidwarf (*Rht2*) cultivar having very good straw strength. Merl is resistant to powdery mildew and moderately resistant to stripe rust. In Virginia, Merl ranked among the top five cultivars for grain yield with a three year (2007–09) average of 5,725 kg/ha. Merl had a grain volume weight (76.4 kg hl-1) that was significantly ($P < 0.05$) higher (1.9–3.0 kg/hl) than the other top-yielding cultivars. Merl provides producers and end users in the mid to deep South, mid-Atlantic, southern Corn Belt, and Northeastern regions of the U.S. with a wheat cultivar that has high yield potential, high grain volume weight, and good milling and pastry baking qualities. A limited amount of Certified seed of cultivar Merl may be available to producers in autumn 2010.

Release of the soft red winter wheat cultivar SW049029104.

SW049029104 was developed and released by the Virginia Agricultural Experiment Station in March 2009. SW049029104 was derived from the cross '38158 (PI 619052)/Pioneer Brand 2552//Roane' and was tested under the experimental number VA04W-90. SW049029104 is a broadly adapted, high yielding, moderately short, semidwarf (*Rht2*) cultivar. This cultivar provides producers and end users in the mid to deep South, mid-Atlantic, and southern Corn Belt regions of the U.S. with a cultivar that is resistant to powdery mildew and Fusarium head blight. In the 2009 USDA–ARSUuniform Southern SRW Wheat Nursery conducted at 25 locations, SW049029104 ranked first among 40 entries for grain yield (4,889 kg/ha) and fourth for grain volume weight (73.2 kg/hl). Milling and baking quality of SW049029104 exceed those of USG 3555 and Pioneer Brand 26R61. A limited amount of Certified seed of SW049029104 may be available to producers in autumn 2010.

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A multipronged approach to develop nutritionally improved, celiac safe, wheat cultivars.

Wheat and its products are potential elicitors for two types of immune responses in human beings: the first being the immunoglobulin E (IgE)-mediated occupational responses (e.g., bakers' asthma) and the second being non-IgE-mediated responses due to ingestion of seed storage proteins of Triticeae (celiac disease). In general, wheat proteins also are poor in nutritional quality because of their imbalanced amino acid composition and deficiency of one of the essential amino acids, lysine. Among the known food allergy cases triggered by wheat and wheat products, most belong to celiac disease, constituting >24.4 million registered cases worldwide. The only effective therapy known to date is strict dietary adherence to a gluten-free diet, which often leads to nutritional deficiencies in celiac patients. In view of the above, we undertake a profound project with the ultimate objective of eliminating the prolamins from wheat grains that contain a majority of epitopes causing celiac disease. Eliminating these proteins also will address the issue of imbalance in the amino acid profile of wheat proteins.

Mapping and cloning of barley and wheat DEMETER homologues. DEMETER (DME) and its functional homologues ROS1, DML1, and DML2 were recently characterized from *Arabidopsis* and rice. DEMETER encodes a 5-methylcytosine DNA glycosylase that is involved in demethylation of genomic DNA in tissue and developmental specific manner as a short-patch, base excision repair pathway. Both the barley mutant Risø 1508 (lys3a) and *Arabidopsis* dme mutants prevent demethylation of gene promoters (von Wettstein 2009). We first identified a barley homologue (TA38047) of AtDME and designed primers to amplify it from barley genomic DNA and cDNA. The amplified product was used as probe to hybridize with the high-density filters of a barley BAC library. Gel-blot analyses allowed identification of a single BAC clone harboring the *HvDME* gene, which was then subcloned and sequenced to obtain full-length HvDME sequence and verified by cDNA sequencing. We used the barley DEMETER sequences (genomic DNA and cDNA) to identify wheat ESTs showing homology with the gene. The ESTs were assembled in contig. These ESTs were derived from ten different wheat cultivars, including 11 from Chinese Spring (CS), five from Recital, and four from Thatcher. The EST assembly was carefully examined for the presence of homoeologous sequence variants (HSVs) that allowed partitioning of the EST-contig into three sub-contigs. These sub-contigs virtually represent clusters of different homoeologous copies of the gene. We used these HSVs to tag our primers at their 3' ends, which allows us to amplify specific products from different subgenomes of bread wheat. We tested the primers on a complete set of nulli-tetrasomic lines, with CS as a control, to localize them to specific chromosomes and test their specificity. One of the primer pairs was assigned unambiguously to wheat chromosome 5B. We used the same set of primers on the genomic DNA of nulli-tetrasomic lines for group-5 chromosomes, deletion lines for long and short arms of chromosome 5B, and an interstitial deletion line *ph1b* to assign one of the DEMETER homoeologues (TaDME-B1) to a subchromosomal region. The analysis allowed localization of TaDME-B1 to the subcentromeric bin of 5BL, bracketed on either side by deletion break points of 5BL-12 (proximal) and 5BL-2 (distal). Two STS primers, derived from the RFLP probes co-localizing with the *lys3a* gene, also were localized to chromosome 5B using wheat aneuploid and deletion stocks. The subgenome specific primers developed as above were used to screen a CS genomic DNA library, leading to the identification of seven BAC clones that are currently being sequenced to get full-length gDNA sequences of wheat DEMETER homoeologues. HvDME genomic DNA and cDNA sequences also were blasted against CS genomic DNA sequences released recently in the public domain (http://www.cerealsdb.uk.net/search_reads.htm). More than 200 sequences showing similarity with HvDME were identified and are currently being utilized to assemble a contig spanning the whole gene sequence. The contig will be examined manually to identify subgenome-specific patterns and to develop specific primers for the D genome of bread wheat.

Establishment of a novel transformation procedure based on microspore culture and electroporation of binary Ti-vectors. We established a novel transformation procedure, where haploid microspores at uninucleate stage were selected, harvested, and purified by density-gradient centrifugation before transformation. The microspores were then transformed with binary Ti-vectors by electroporation using suitable transfection media followed by co-cultivation with ovaries on suitable culture media for induction of embryogenesis. The microspore-derived embryoids were then transferred to the selection media to weed out the nontransformants, and the survivors from there were selected using visible markers to eliminate false positives. Only the selected plantlets obtained from the true-transformants were then treated with colchicine to induced chromosome doubling leading to the production of doubled-haploid, homozygous transgenic lines. Three binary test plasmids were used to optimize the electroporation conditions with genes expressed and monitored in developing transformed embryoids, young seedlings, and maturing plants: (1) pJH271 and (2) pRBOV-hySFi-GFP expressing the green fluorescing protein GFP with the CaMV 35S promoter and (3) pYW300 expressing the *Trichoderma harzianum* endochitinase that can be monitored by UV-induced fluorescence upon cleavage of 4-methylumbelliferyl-β-D-N,N',N''-triacetylchitotrioside substrate. The transformants obtained using each of above three binary vectors were tested for their respective visual phenotypes and with gene specific primers for the integration of respective transgenes in their nuclear genomes. Both of the above genotypic and phenotypic screens confirmed the integration of transgenes in the nuclear genome of the transformants.

Silencing wheat DEMETER genes using artificial microRNAs (amiRNAs) and hairpin constructs. We have amplified a 981-bp fragment of bread wheat covering the active site of DEMETER and a 300-bp fragment from the N-terminal first exon (covering the bipartite nuclear localization signal). These fragments were analyzed by the Web MicroRNA Designer (WMD: http://wmd3.weigelworld.org/cgi-bin/webapp.cgi) for the most suitable sequences for amiRNAs. For the fragment covering the active site region, eight sequences were suggested suitable, and for the fragment spanning the N-terminal domain, only one sequence was suggested suitable by the software. From the suggested sequences, we selected three sequences, two from the active site region (DME1 and DME2) and one from the N-terminal domain (TADMEStart) for constructing the first amiRNAs. The artificial miRNA-containing precursors of the DME1, DME2, and TADMEStart have been generated on the pNW55-OsaMIR528 of *Oryza sativa* following fusion PCR reactions. These amiRNAs will

be expressed under the control of the D-Hordein (D-Hor) promoter of barley and/or HMW-glutenin (HMWg) promoter of wheat and will be cloned in pGreen binary vector. Similarly, hairpin constructs were designed from the above two DEMETER fragments and will be incorporated in pHELLSGATE vector using homologous recombination. The hairpin constructs will be expressed under the control of D-Hor and/or HMWg promoters.

Cloning and expression of prolyl endopeptidase. Prolyl endopeptidase (PREP) or prolyl oligopeptidase is a cytosolic enzyme that belongs to a distinct class of serine peptidases. The enzyme cleaves peptide bonds at the C-terminal side of proline residues. Its activity is confined to action on oligopeptides of less than 10 kDa. The PREP enzyme has been shown to decrease the propensity of gluten-containing wheat products by detoxifying the peptides causing celiac disease. In view of the above, we used the PREP sequence of *Flavobacterium meningosepticum*, optimized its codon composition, had it synthesized by GenScript Inc., U.S., and cloned it in pUC57 using the *Eco*RV restriction site. The insert cloned in pUC57 was flanked by the restriction sites of *Eco*RI and *Apa*I, these restriction sites were specifically selected to digest the plasmid and to take out the insert, which will then be cloned in the Pichia expression vectors using the same restriction sites (pPICZ A, Invitrogen Inc., U.S.). The above experiment will allow us to test the PREP functionality and activity in the eukaryotic system (yeast). Once the codon optimized PREP sequence is tested for its functionality and activity in the yeast, it will be introduced in wheat under the control of HMWg promoter through our microspore transformation technique. The transforments thus obtained will then be examined for PREP activity and gluten content.

***In vitro* examination of DEMETER activity.** We were able to obtain full-length sequences of DEMETER from barley mutant Risø 1508 (lys3a) and its parent variety Bomi. Wild type and mutant DEMETER cDNA clones were expressed in *E. coli* with a his-tag. The resultant proteins will be purified on a Ni2+-NTA column, and their activity tested with methylcytosine containing double-stranded oligonucleotides. The recombinant protein expressed in *E. coli* is used to raise antibodies against the DEMETER protein, which is used in quantification of DEMETER protein in TILLING mutants.

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The mission of the Western Wheat Quality Laboratory 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 cultivars 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. 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 currently are researching the genetic basis for noodle dough color stability. Bettge currently is researching the influence of oxidative gelation on flour end-use functionality. As such, he is developing a laboratory-scale method for pancake-making in order to provide an end-use test for flour functionality in batter systems.

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Table 1. Wheat descriptors with data currently in GRIN (February 2009).

Descriptor	Years	Location	Accessions evaluated
DISEASE DESCRIPTORS			
Barley Yellow Dwarf Virus	1985–92	Davis, CA	2,287
Barley Yellow Dwarf Virus	1988–94	Urbana, IL	17,517
Soilborne Mosaic Virus	1985–89	Urbana, IL	6,587
Soilborne Mosaic Virus	2000	Manhattan, KS	4,998
Leaf Rust	1983–89, 1991–95	Manhattan, KS	38,751
Leaf Rust – Adult	2000	Manhattan, KS	5,000
Stripe Rust – Adult	1984–2005	Mt. Vernon, WA	47,540
Stripe Rust – Adult	1984–2005	Pullman, WA	37,676
Stripe Rust – PST 17	1984–2005	Pullman, WA	24,662
Stripe Rust – PST 20	1984–95	Pullman, WA	12,508
Stripe Rust – PST 25	1984–95	Pullman, WA	1,682
Stripe Rust – PST 27	1984–95	Pullman, WA	14,511
Stripe Rust – PST 29	1984–95	Pullman, WA	14,259
Stripe Rust – PST 37	1984–2005	Pullman, WA	17,252
Stripe Rust – PST 43	1984–2005	Pullman, WA	16,285
Stripe Rust – PST 45	1984–2005	Pullman, WA	17,217
Stripe Rust – PST 78	2000–05	Pullman, WA	4,277
Stripe Rust – PST 80	2004–05	Pullman, WA	2,998
Stripe Rust – PST 100	2004–05	Pullman, WA	5,892
Stem Rust – Adult	1987–94	Rosemount, MN	8,078
Stem Rust – Adult	1987–94	St. Paul, MN	19,141
Stem Rust – HJCS	1987–92	St. Paul, MN	4,342
Stem Rust – QFBS	1987–92	St. Paul, MN	8,639
Stem Rust – QSHS	1987–92	St. Paul, MN	4,455
Stem Rust – RHRS	1987–92	St. Paul, MN	4,312
Stem Rust – RTQQ	1987–92	St. Paul, MN	8,973
Stem Rust – TNMH	1987–92	St. Paul, MN	4,402
Stem Rust – TNMK	1987–92	St. Paul, MN	8,938
Stem Rust – HNLQ	1987–92	St. Paul, MN	4,705
Stem Rust – RKQS	1987–92	St. Paul, MN	4,682
Stem Rust – Genes	1987–92	St. Paul, MN	1,018
Common Bunt	1981–2004	Aberdeen, ID & Pendleton, OR	25,245
Dwarf Bunt	1978–2009	Logan, UT	20,146

Descriptor	Years	Location	Accessions evaluated
DISEASE DESCRIPTORS			
Stagonospora nodorum blotch	1970–78	Bozeman, MT	8,095
Powdery Mildew	1996–2005	Kinston, NC	13,973
Fusarium Head Blight/Scab	1998–2002	Brookings, SD	4,084
INSECT DESCRIPTORS			
Hessian Fly – B	1983–94	W. Lafayette, IN	449
Hessian Fly – C	1983–94	W. Lafayette, IN & Manhattan, KS	24,165
Hessian Fly – E	1983–94	W. Lafayette, IN & Manhattan, KS	24,149
Hessian Fly – GP	1983–94	W. Lafayette, IN & Manhattan, KS	14,441
Hessian Fly – L	1983–97	W. Lafayette, IN & Manhattan, KS	8,315
Russian Wheat Aphid – Biotype 1	1988–95, 2005	Stillwater, OK & Ft. Collins, CO	41,161
Russian Wheat Aphid – Biotype 2	2003–08	Ft. Collins, CO	14,186
Cereal Leaf Beetle	1963–70	Indiana, Michigan	16,347
AGRONOMIC–QUALITY DESCRIPTORS			
Growth Habit	1987–09	Aberdeen, ID	55,380
Lysine Content	1966–69	Lincoln, NE	10,367
Awn Color	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	27,037
Awn Type	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	30,113
Glume Color	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	27,403
Glume Pubescence	1983–97	Aberdeen, ID & Maricopa, AZ	24,312
Heading Date	1983–94	Aberdeen, ID & Maricopa, AZ	18,365
Heading Date – related to check	1999–2004	Maricopa, AZ	46,831
Kernel Color	1983–94, 2005–09	Aberdeen, ID & Maricopa, AZ	47,520
Kernels/Spike	1983–94	Aberdeen, ID & Maricopa, AZ	3,666
Kernel Weight	1983–94, 2005–09	Aberdeen, ID & Maricopa, AZ	45,947
Leaf Pubescence	1983–94	Aberdeen, ID & Maricopa, AZ	20,888
Plant Height	1983–97	Aberdeen, ID & Maricopa, AZ	21,841
Plant Height – related to check	1999–2004	Maricopa, AZ	46,841
Rachis Length	1995	Maricopa, AZ	2,512
Shattering	1983–94	Aberdeen, ID & Maricopa, AZ	10,637
Spike Density	1983–98, 2007–09	Aberdeen, ID & Maricopa, AZ	22,963
Spikelets/Spike	1995	Maricopa, AZ	2,502
Spike Type	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	22,730
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 Scott McNeil, Karla Reynolds, Carol Mortenson, Kay Calzada, and Sara Hirschi.

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 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
655954 PVPO	*Triticum aestivum* subsp. *aestivum*	HITCH	United States	Kansas
655955 PVPO	*Triticum aestivum* subsp. *aestivum*	ARMOUR	United States	Kansas
655960 PVPO	*Triticum aestivum* subsp. *aestivum*	TAM 203	United States	Texas
656377 PVPO	*Triticum aestivum* subsp. *aestivum*	ALPINE	United States	
656382	*Triticum aestivum* subsp. *aestivum*	OK RISING	United States	Oklahoma
656383 PVPO	*Triticum aestivum* subsp. *aestivum*	TOM	United States	Minnesota
656390	*X Triticosecale sp.*	X-1010	United States	Oregon
656395	*Triticum aestivum* subsp. *aestivum*	NC09MDD14	United States	North Carolina
656607	*Triticum aestivum* subsp. *aestivum*	TAMsoft 700	United States	Texas
656610	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn1*)	United States	Washington
656611	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn1*)	United States	Washington
656612	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn1*)	United States	Washington
656613	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn1*)	United States	Washington
656614	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn1*)	United States	Washington
656615	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn1*)	United States	Washington
656616	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn1*)	United States	Washington
656617	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn1*)	United States	Washington
656618	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn2*)	United States	Washington
656619	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn2*)	United States	Washington
656620	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn2*)	United States	Washington
656621	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn2*)	United States	Washington
656622	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn2*)	United States	Washington
656623	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn2*)	United States	Washington
656624	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn2*)	United States	Washington
656625	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn2*)	United States	Washington
656626	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn3*)	United States	Washington
656627	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn3*)	United States	Washington
656628	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn3*)	United States	Washington
656629	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn3*)	United States	Washington
656630	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn3*)	United States	Washington
656631	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn3*)	United States	Washington
656632	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn3*)	United States	Washington
656633	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn3*)	United States	Washington
656634	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn3*)	United States	Washington
656635	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn4*)	United States	Washington
656636	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn4*)	United States	Washington
656637	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn4*)	United States	Washington
656638	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn4*)	United States	Washington
656639	*Triticum aestivum* subsp. *aestivum*	TresNIL (*Vrn4*)	United States	Washington
656640	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn4*)	United States	Washington
656641	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn4*)	United States	Washington

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
656642	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn4*)	United States	Washington
656643	*Triticum aestivum* subsp. *aestivum*	TresNIL (*vrn4*)	United States	Washington
656753	*Triticum aestivum* subsp. *aestivum*	SHIRLEY	United States	Virginia
656754	*Triticum aestivum* subsp. *aestivum*	3434	United States	Virginia
656755	*Triticum aestivum* subsp. *aestivum*	5205	United States	Virginia
656790	*Triticum aestivum* subsp. *aestivum*	JD	United States	Washington
656791	*Triticum aestivum* subsp. *aestivum*	BABE	United States	Washington
656792	*Triticum aestivum* subsp. *aestivum*	IR14-40	United States	California
656793	*Triticum aestivum* subsp. *aestivum*	524	United States	California
656794	*Triticum aestivum* subsp. *aestivum*	IR51-8	United States	California
656795	*Triticum aestivum* subsp. *aestivum*	IR17-47	United States	California
656796	*Triticum aestivum* subsp. *aestivum*	504	United States	California
656843	*Triticum aestivum* subsp. *aestivum*	BILLINGS	United States	Oklahoma
656844	*Triticum aestivum* subsp. *aestivum*	PETE	United States	Oklahoma
656845	*Triticum aestivum* subsp. *aestivum*	AMBASSADOR	United States	Michigan
656865	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-170	Turkey	Gaziantep
656866	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-176	Turkey	Gaziantep
656867	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-180	Turkey	Gaziantep
656868	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-188	Turkey	Gaziantep
656869	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-193	Turkey	Gaziantep
656870	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-200	Turkey	Maras
656871	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-206	Turkey	Maras
656872	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-221	Turkey	Maras
656873	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-223	Turkey	Maras
656959	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn1*)	United States	Washington
656960	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn1*)	United States	Washington
656961	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn1*)	United States	Washington
656962	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn1*)	United States	Washington
656963	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn1*)	United States	Washington
656964	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn1*)	United States	Washington
656965	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn1*)	United States	Washington
656966	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn1*)	United States	Washington
656967	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn1*)	United States	Washington
656968	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn1*)	United States	Washington
656969	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn2*)	United States	Washington
656970	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn2*)	United States	Washington
656971	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn2*)	United States	Washington
656972	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn2*)	United States	Washington
656973	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn2*)	United States	Washington
656974	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn2*)	United States	Washington
656975	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn2*)	United States	Washington
656976	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn2*)	United States	Washington
656977	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn2*)	United States	Washington
656978	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn3*)	United States	Washington
656979	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn3*)	United States	Washington
656980	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn3*)	United States	Washington
656981	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn3*)	United States	Washington

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
656982	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn3*)	United States	Washington
656983	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn3*)	United States	Washington
656984	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn3*)	United States	Washington
656985	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn3*)	United States	Washington
656986	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn3*)	United States	Washington
656987	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn3*)	United States	Washington
656988	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn4*)	United States	Washington
656989	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn4*)	United States	Washington
656990	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn4*)	United States	Washington
656991	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn4*)	United States	Washington
656992	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn4*)	United States	Washington
656993	*Triticum aestivum* subsp. *compactum*	PahaNIL (*Vrn4*)	United States	Washington
656994	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn4*)	United States	Washington
656995	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn4*)	United States	Washington
656996	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn4*)	United States	Washington
656997	*Triticum aestivum* subsp. *compactum*	PahaNIL (*vrn4*)	United States	Washington
657629 MAP	*Triticum aestivum* subsp. *aestivum*	STEELE-ND	United States	North Dakota
657630 MAP	*Triticum aestivum* subsp. *aestivum*	ND 735	United States	North Dakota
657697	*Triticum aestivum* subsp. *aestivum*	BRICK	United States	South Dakota
657945	*Triticum aestivum* subsp. *aestivum*	VA04W-433	United States	Virginia
657946	*Triticum aestivum* subsp. *aestivum*	VA04W-474	United States	Virginia
657977	*X Triticosecale sp*.	Sel-002	United States	Oregon
657986 PVPO	*Triticum aestivum* subsp. *aestivum*	OGLETHORPE	United States	Georgia
657987 PVPO	*Triticum aestivum* subsp. *aestivum*	AGS CL7	United States	Georgia
657988 PVPO	*Triticum aestivum* subsp. *aestivum*	BALDWIN	United States	Georgia
657997	*Triticum aestivum* subsp. *aestivum*	NuEast	United States	North Carolina
657998	*Triticum aestivum* subsp. *aestivum*	APPALACHIAN WHITE	United States	North Carolina
658002 PVPO	*Triticum aestivum* subsp. *aestivum*	ALBANY	United States	
658007 PVPO	*Triticum aestivum* subsp. *aestivum*	JACKPOT	United States	
658008 PVPO	*Triticum aestivum* subsp. *aestivum*	AP LEGACY	United States	
658009 PVPO	*Triticum aestivum* subsp. *aestivum*	WHETSTONE	United States	
658010 PVPO	*Triticum aestivum* subsp. *aestivum*	W1104	United States	
658018 PVPO	*Triticum aestivum* subsp. *aestivum*	BARLOW	United States	North Dakota
658032 PVPO	*Triticum aestivum* subsp. *aestivum*	W980281J1	United States	
658033 PVPO	*Triticum aestivum* subsp. *aestivum*	W1062	United States	
658034 PVPO	*Triticum aestivum* subsp. *aestivum*	W1566	United States	
658035 PVPO	*Triticum aestivum* subsp. *aestivum*	LEGION	United States	
658036 PVPO	*Triticum aestivum* subsp. *aestivum*	BULLSEYE	United States	
658039 PVPO	*Triticum aestivum* subsp. *aestivum*	JENNA	United States	
658040 PVPO	*Triticum aestivum* subsp. *aestivum*	OAKES	United States	
658041 PVPO	*Triticum aestivum* subsp. *aestivum*	BRENNAN	United States	
658050 PVPO	*Triticum aestivum* subsp. *aestivum*	AGS 2020	United States	Georgia
658063	*Triticum aestivum* subsp. *aestivum*	ARS15144	United States	Washington
658064	*Triticum aestivum* subsp. *aestivum*	ARS14142	United States	Washington
658065 PVPO	*Triticum aestivum* subsp. *aestivum*	AGS 2026	United States	Georgia
658066 PVPO	*Triticum aestivum* subsp. *aestivum*	AGS 2035	United States	Georgia
658067 PVPO	*Triticum aestivum* subsp. *aestivum*	LYMAN	United States	South Dakota

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
658147 PVPO	*X Triticosecale sp*.	718	United States	California
658148 PVPO	*Triticum aestivum* subsp. *aestivum*	WB 456	United States	
658149 PVPO	*Triticum aestivum* subsp. *aestivum*	WB 523	United States	
658150 PVPO	*Triticum aestivum* subsp. *aestivum*	26R20	United States	Indiana
658151 PVPO	*Triticum aestivum* subsp. *aestivum*	25R32	United States	Indiana
658153 PVPO	*Triticum aestivum* subsp. *aestivum*	ORCF-103	United States	Oregon
658154 PVPO	*Triticum aestivum* subsp. *aestivum*	SKILES	United States	Oregon
658155 PVPO	*Triticum aestivum* subsp. *aestivum*	W000350I1	United States	
658156 PVPO	*Triticum aestivum* subsp. *aestivum*	W000570E1	United States	
658157 PVPO	*Triticum aestivum* subsp. *aestivum*	W980052N1	United States	
658158 PVPO	*Triticum aestivum* subsp. *aestivum*	W980118Q1	United States	
658159 PVPO	*Triticum aestivum* subsp. *aestivum*	W000273A1	United States	
658160 PVPO	*Triticum aestivum* subsp. *aestivum*	W000350D2	United States	
658161 PVPO	*Triticum aestivum* subsp. *aestivum*	W990117E1	United States	
658162 PVPO	*Triticum aestivum* subsp. *aestivum*	W010323D1	United States	
658163 PVPO	*Triticum aestivum* subsp. *aestivum*	W010704F1	United States	
658164 PVPO	*Triticum aestivum* subsp. *aestivum*	REDWING	United States	California
658165	*Triticum aestivum* subsp. *aestivum*	NX04Y2107	United States	Nebraska
658243 MAP	*Triticum aestivum* subsp. *aestivum*	OS9A	United States	Oregon
658244 MAP	*Triticum aestivum* subsp. *aestivum*	QCB36	United States	Oregon
658467	*Triticum aestivum* subsp. *aestivum*	UI SILVER	United States	Idaho
658468	*Triticum aestivum* subsp. *aestivum*	UICF-GRACE	Mexico	Coahuila
658496	*X Triticosecale sp*.	TCLF-AN-105	United States	California
658500 PVPO	*Triticum aestivum* subsp. *aestivum*	TAM 401	United States	Texas
658508 MAP	*Triticum aestivum* subsp. *aestivum*	USG3209	United States	Virginia
658509 MAP	*Triticum aestivum* subsp. *aestivum*	JAYPEE	United States	Arkansas
658527	*Triticum aestivum* subsp. *aestivum*	CORAL	United States	Michigan
658542 PVPO	*Triticum aestivum* subsp. *aestivum*	MOTT	United States	North Dakota
658543 PVPO	*Triticum aestivum* subsp. *aestivum*	AP BADGER	United States	
658597	*Triticum aestivum* subsp. *aestivum*	SNOWMASS	United States	Colorado
658598	*Triticum aestivum* subsp. *aestivum*	MERL	United States	Virginia
658599	*Triticum aestivum* subsp. *aestivum*	SW049029104	United States	Virginia

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2010 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11Th International Wheat Genetics Symposium held in Brisbane, Australia, and the 2009 Supplement (*Annual Wheat Newsletter* 55: 256-278) are available from the Komugi (http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp) and GrainGenes (http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/) websites. The Wheat Gene Catalog is not included as part of the proceedings and, therefore, cannot be cited as part of them.

INTRODUCTION

9. Laboratory Designators

Add to Designators:

stm Matthew Hayden
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Australia

Morphological and Physiological Traits

5. Anthocyanin Pigmentation

The genetic determinants of anthocyanin pigmentation of various tissues are largely located in the homoeologous regions in group 7, eg., 7BS (*Rc-B1*, *Pc-B1*, *Plb-B1*, and *Pls-B1*) and 7DS (*Rc-D1*, *Pc-d1*, and *Plb-D1*), and appear to be linked clusters rather than multiple alleles on each chromosome {10700}. Their relationship with genes for purple auricle and purple pericarp are still not clear.

5.2. Purple/Red auricles. Purple leaf base/sheath

Pc*/*Pls*/*Plb {10692}. 7B {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}.
ma: *Xgwm951-7B* – 6.7 cM – *Pc*/*Pls*/*Plb* – 8.2 cM – *Pp1* – 8.9 cM – *Xgwm753-7B* {10692}.

5.4. Purple/red culm/straw/stem.

Pc/Pls/Plb {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}.
ma: *Xgwm951-7B* – 6.7 cM – *Pc/Pls/Plb* – 8.2 cM – *Pp1* – 8.9 cM – *Xgwm753-7B* {10692}.

5.6. Purple glume

Pg {10692}. 2A {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}.
ma: *Xgwm328-2A* – 19.2 cM – *Pg* – 1.4 cM – *Pp3* – 5.1 cM – *Xgwm817-2A* {10692}.

5.7. Purple leaf blade

Plb {10692}. 7B {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben).
ma: *Xgwm951-7B* – 6.7 cM – *Pc/Pls/Plb* – 8.2 cM – Pp1 – 8.9 cM – *Xgwm753-7B* {10692}.

17. Dormancy (Seed)
Pre-harvest sprouting:
QTL:

Insert following the Rio Blanco entry:
'RL4452 (red-seeded, low PHS tolerance) / AC Domain (red-seeded, high PHS tolerance)': DH lines: Genes associated with falling number, germination index, and sprouting index contributing to PHS were located on chromosomes 3A, 4A (locus-2), and 4B in AC Domain and 3D, 4A (locus-1), and 7D in RL4452 {10671}.

'SPR8198 (red-seeded, PHS tolerant) / HD2329 (white-seeded, PHS susceptible)': RIL population: seven QTL located on chromosomes 2AL, 2DL, 3AL, and 3BL, the most important on 2AL and 3AL {10670}.

'Sun325B (dormant, white-seeded) / QT7475 (semidormant, white-seeded)', both parents with the chromosome 4A QTL: DH population: A QTL was located in the *Xgwm77-3B – Xwmc527-3B* interval ($R^2 = 0.19$) in the approximate region of the *R-B1* locus {10669}.

23. Frost Resistance
Fr-1.

Add as note:
Studies using *Vrn-1* induced and natural mutants suggest that differences in frost tolerance previously associated to *Fr-1* are actually pleiotropic effects of *Vrn-1* {10708}.

26. Glaucousness (Waxiness/Glossiness)
NEW: 26.3. Spike glaucousness

Spike glaucousnes is recessive {10666}.

Ws {10666}. 1AS {10666}. **bin:** 1AS1-0.47-0.86 {10666}.
v: Svenno {10666}.
ma: *BJ23702a* – 3.5 cM – *Tc95235* – 4.8 cM – *Bla* {10666}.
ws {10666}. **v:** Ciccio {10666}.

27. Glume Colour and Awn Colour

Add at end of section:

Bla1 {10666}. 1AS {10666}. **bin:** 1AS1-0.47-0.86 {10666}.
v: Svenno {10666}.
ma: *TC95235* – 4.8 cM – *Bla1* {10666}.

29. Grain Quality Parameters
29.2. Flour, semolina, and pasta colour

To the paragraph on 'Ph82-2 / Neixinag' add:
A further study confirmed major QTL on chromosomes 1RS ($R^2 = 0.319$) and 7A ($R^2 = 0.339$); minor QTL occurred on 1A and 4A {10659}.

60. Response to Photoperiod

Ppd-D1. Add note:

Jagger amplified the 414-bp band {10466} associated with daylength sensitivity, whereas 2174 amplified the 288-bp band associated with insensitivity {10665}.

63. Response to Vernalization

Replace the current preamble with:

The requirement for vernalization is particularly important for winter cereals to avoid cold injury of the sensitive floral organs during the winter. In wheat, the vernalization requirement is controlled by four major genes designated *Vrn-1*, *Vrn-2*, *Vrn-3*, and *Vrn-4*. The first three genes were identified using map based cloning approaches {10014, 10299, 10421}. The *Vrn-1* gene encodes a MADS-box transcription factor, closely related to the *Arabidopsis AP1/FRUITFULL* family, responsible for the transition of the shoot apical meristem from the vegetative to reproductive stage in wheat {10014}. Deletions in the promoter (*Vrn-A1a*, *Vrn-A1b*) {10198} or the first intron of this gene (*Vrn-A1c*, *Vrn-B1a*, and *Vrn-D1a*) {10202} are the most common sources of spring growth habit among landraces and commercial cultivars of polyploid wheat worldwide {10617, 10695, 10709}.

The *Vrn-2* locus produces two linked and related proteins designated ZCCT1 and ZCCT2, characterized by the presence of a putative zinc finger and a CCT domain {10299}. Deletions and mutations involving both the ZCCT1 and ZCCT2 genes are frequent in diploid wheat and are associated with recessive alleles for spring growth habit {10299}. Among the cultivated tetraploid and hexaploid wheat species, the *Vrn-B2* gene is generally functional, whereas the *Vrn-A2* gene is not {10710}. At least one functional copy of *Vrn-2* combined with homozygous recessive alleles at all three *Vrn-1* loci is required to confer winter growth habit in hexaploid wheat.

The *Vrn-B3* locus (formerly known as *Vrn-5* or *Vrn-B4*) is homologous to the *Arabidopsis FT* gene {10421}. This dominant allele, found in the cultibat Hope, is associated with the insertion of a transposable element in the *Vrn-B3* promoter. Natural variation at the *Vrn-A3* and *Vrn-D3* loci has been also described in hexaploid wheat {10533}. *Vrn-3* promotes the transcription of *Vrn-1* and accelerates flowering {10421}.

The *Vrn-D4* allele for early flowering was originally identified in the Australian cultivar Gabo {671} and was backcrossed into Triple Dirk to develop the isogenic line TDF {1172}. This locus was mapped on the centromeric region of chromosome 5D between markers *Xcfd78* and *Xbarc205* {10711}. Natural variation for flowering time at the centromeric region of homoeologous group-5 chromosomes has been found, so far, only in the D genome. Incorrect TDF seed stocks generated initial confusion about the existence of *Vrn-D4,* but molecular markers are now available to separate the incorrect stocks {10711}. Using genetic analyses, Iwaki et al. {10003} found the *Vrn-D4* allele for spring growth habit occurred with a higher frequency in India and neighboring regions.

Vrn-1

Add to the preamble before the first gene entry:

A polymorphism between Jagger and 2174 was associated with *vrn-A1a*. A point mutation occurred in exon 4 {10656}; 17 of 19 genotypes surveyed, including Jagalene, carried the 2174 mutation and only Jagger and Overley carried the Jagger allele {10665}.

Vrn-B1a.	**c:**	Genbank AY74603.1 {10695}.
Vrn-B1b {10695}.	**v:**	Alpowa {10695}.
	c:	GenBank FJ766015. Relative to *Vrn-B1a* (Triple Dirk B), *Vrn-b1b* has a G–C SNP at position 1,656 and a 36-bp deletion at 1,661-1,696 {10695}.
vrn-B1.	**c:**	AY747604.1 {10695}.

Vrn-1 genotypes in Pacific Northwest USA wheats are listed in {10695}.

The *Vrn3*, *Vrn4*, and *Vrn5* sections can be replaced as follows. Some references may need to be deleted as a consequence.

Vrn3 {1398}.

Replace the existing section with:

This designation was previously given to an orthologous series in homoeologous group 1 and was predicted from orthology with *Vrn-H3* (*Sh3*) in barley chromosome 1H {1455, 1316}. However, the *Vrn-H1* location proved erroneous {10421}, and any genes located in homoeologous group 1 should not be designated as *Vrn3*.

Vrn4 {279}. [Vrn5 {771, 769}, Vrn-D5 {10004}]. 5D {10002}. 5DL{10004}.

bin: Centromeric region. **i:** Triple Dirk F {10711}.

s: CS (Hope 7B) *VrnD1a* {768}.

v2: Gabo *Vrn-B1a* {1172}. Hope *Vrn-a1a* {1424}. IL47/*Vrn-A1a* {10005}.

ma: *Xgdm3-5D* – 11.5 and 4.5 cM – *Vrn4* {10004}. Located in a 1.8-cM interval flanked by markers *Xcfd78-5D* and *Xbarc205-5D* {10711}.

Vrn4 was mapped on the centromeric region of 5D between markers

Incorrect TDF seed stocks generated confusion about *Vrn-D4* existence {10711}. Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn4*. Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D.

Add:

Vrn5. The preëxisting section can be deleted, because this gene is the same as *Vrn4*.

Aneuploid and whole-chromosome substitution experiments showed that all group-1 chromosomes of wheat carry genes affecting response to vernalization {773}.

At the end of entire section add:

Stem elongation in winter wheat: In regions where wheat is used as a dual-purpose crop for grazing and grain production, a relatively long vegetative phase is required to maximize the vegetative tissue and to delay the stem-elongation phase. Variation in this attribute occurs among winter wheats such as Jagger (early stem elongation) and 2174 (late elongation).

In a 'Jagger / 2174' RIL population, QTL for stem elongation included *QSte.ocs-5A* (associated with the *Vrn-A1* locus, *Qste.ocs-1BL*, *Qste.ocs-2D* (associated with the *Ppd-D1* locus), and *Qste.ocs-6A* {1010}. In 2007, the respective R^2 values were 0.289, 0.155, 0.067, and 0.058. Jagger alleles on chromosomes 5A, 1B, and 6A promoted stem elongation, whereas the allele on chromosome 2D had a delaying effect {10665}.

Proteins

77. Proteins

77.1 Grain protein content

Enter above the heading 'Durum'

'Ning 7840 / Clark': RILs: QTL from Ning 7840 were detected on chromosomes 3AS (*Xwmc749-3AS – Xgwm 369-3AS*; R^2 = 0.9-0.11) and 4B (*Xgwm368-4B – Xwmc617-4B*, R^2 = 0.08-0.11) {10702}.

Pathogenic Disease/Pest Reaction

78. Reaction to Barley Yellow Dwarf Virus

Bdv3. **v:** Add: P98134 {10159}. **ma:** A SSR-BDV marker is described in {10159}.

Bdv3 in wheat shows distorted inheritance that varies with genetic background {10159}.

NEW SECTION. Reaction to *Bipolaris sorokiniana* DC.

Diseases: Spot blotch and common root rot

Spot blotch

QTL

'Yangmai 6 (R) / Sonalika (S)': RIL population: AUDPC was controlled by four QTL derived from Yangmai 6, i.e., *QSb.bhu-2AL* (*Xbarc353-2A – Xgwm445-2A*, R^2 = 0.148), *QSb.bhu-2BS* (*Xgwm148-3B – Xgwm375-2B*, R^2 = 0.205), *QSb.bhu-5BL* (*Xgwm67-5BL – Xgwm371-5BL*, R^2 = 0.386), and *QSb.bhu-6DL* (*Xbarc173-6D – Xgwm732-6DL*, R^2 = 0.225) {10662}.

79. Reaction to *Blumeria graminis* DC.

79.1. Designated genes for resistance

***Pm3*.** Insert the following note at the end of section:

Alleles *Pm3b*, *Pm3d*, and *Pm3f* were detected in Scandinavian cultivars using allele-specific markers {10681}.

Pm40. **v:** Yu24 {10539}; Yu {10539}; partial amphilpoid TAI7047 {10539}.
ma: Replace present entry with: *Xwmc426-7B* – 5.9 cM – *Xwmc334-7B* – 0.2 cM – *Pm40* – 0.7 cM – *Xgwm297-7B* – 1.2 cM – *Xwmc364-7B* {10539}.

Add to genotype lists: Scandinavian wheats {10681}.

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

PmCn17 {10686}. 1BS = T1BL·1RS {10686}. **v:** Chuannong 17 {10686}.
al: *S. cereale* R14 {10686}.

PmHNK {10706}. 3BL {10706}. **v:** Zhoumai 22 {10706}.
ma:*Xgwm108-3BL* – 10.3 cM – *PmHNK* – 3.8 cM – *Xwmc291-3BL* {10706}.

79.4. QTL for resistance to *Blumeria graminis*

'Bainong 64 (R) / Jinshuang 16 (S)', DH lines: Four QTL from Bainong 64: *Qpm.caas.1A*, *Xbarc148-1A – Xwmc550-1A* interval; *QPm.caas-4DL* proximal to *Xwmc331-4D*, R^2 = 0.15-0.23; *QPm.caas-6BS*, proximal to *Xbarc79-6BS*, R^2 = 0.09-0.13; and *QPm.caas-7AL*, proximal to *Xbarc174-7AL* {10680}.
'Lumai 21 (R) / Jingshuang 16 (S)', F_3 lines: Three QTL from Lumai 21: *QPm.caas-2BS*, *Xbarc98-2BS – Xbarc1147-2BS* interval, R^2 = 0.106–0.206; *QPm.caas-2BL*, *Xbarc1139-2BL – Xgwm47-2BL* interval, R^2 = 0.052–0.101; and *QPm.caas-2DL*, *Xwmc18-2DL – Xcfd233-2DL* interval, R^2 = 0.057–0.116 {10707}.

82. Reaction to *Fusarium graminearum*

82.1. Disease: Fusarium head blight, Fusarium head scab, scab

'Cansas / Ritmo': Add at end of section:
More detailed mapping led to the relocation of the 5B QTL to chromosome 1BL. The renamed *Qfhs.lfl-1BL* reduced FHB severity by 42% relative to lines lacking it {10698}. This gene also was present in Biscay, History, and Pirat {10698}.
'Soissons (relatively resistant) / Orvantis (susceptible)': Soissons carried *QFhs.jic-4D* (R^2 = 0.106-0.161) associated with *Rht-D1a* (tall allele) {10661}. FHB susceptibility tended to be associated with the *Rht-D1b* allele (10661}. Supporting studies with NILs indicated that the presence of *Rht-B1b* led to reduced type-2 resistance relative to presence of *Rht-B1b* or the tallness alleles at both loci {10661}.

82.2. Disease: Crown rot cuased by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species.

To follow the 'Kukri / Janz' entry:
'Lang (S) / CSCR6 (R)': RIL population: tested under controlled conditions with *F. pseudograminearu*m and *F. graminearum*: *Qcrs.cpi-3BL* from CSCR6, R^2 = 0.49, and *Qcrs.cpi-4B* from Lang, R^2 = 0.23 {10703}.

85. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

H18. **v:** Redland {10658}.

89. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

89.2. Sensitivity to SNB toxin

Tetraploid wheat Add to the present (2009) text:
In a reëvaluation of this work, Faris and Friesen {10688} attributed all of the variation in SNB response to the presence or absence of SnTox1.
ma: *Xbcd183-5B* – 1.2 cM – *Tsn1/Xbcd1030-5B* – 2.4 cM – *Xrz575-5B* {10688}.

90. Reaction to *Puccinia graminis* Pers.

Sr6. **bin:** 2DS5-0.47-1.00 {10657}.
ma: *Sr6* – 1.1 cM – *Xwmc453-2D* – 0.4 cM – *Xcfd43-2D* {10657}.

Sr35. **ma:** *Sr35* was mapped to a 5.1-cM interval between *XBF483299* and *XCJ656351* in diploid wheat {10712}.

Sr49 {10704}. 5BL {10704}. **v:** AUS 28011 {10704}.
ma: *Sr49 – Xwmc471-5B*L, 7.8 cM {10704}.

Genotype lists: {Add: , 10697}.

91. Reaction to *Puccinia striiformis* Westend.

91.1. Designated genes for resistance to stripe rust

Yr4. Undesignated allele. The information listed below is based on the similarity of the resistance genes in Rubric and Avalon.

YrRub {10663}. 3BS {10663}. **bin:** 3BS3-0.87-1.00 {10663}.
v: Avalon {10663}; Bolac {B008}; Emu S {10663}; Rubric AUS33333 {10663}.
ma: *Yr4* – 2.9 cM – *Xcfb3530-3B* – 2.4 cM – *Xbarc75-3B* {10663}.

The conclusion that *YrRub* is *Yr4* is based on specificity similarities and the presence of the $Xcfb3530_{150}$ and $Xbarc75_{132}$ alleles in the five genotypes listed above. The 3BS location is not consistent with that listed below for *Yr4a* and *Yr4b*.

***Yr38*.** **v:** Recombinants with shorter segments, 07M4-39, 07M4-157, and 07M4-175 are reported in {10691}.

Yr43 {10673}. 2BL {10673}. **v:** IDO377s = PI 591045 {10673}; Lolo {10673}; many IDO377s derivatives {10673}.
ma: *Xwms501-2B* – 11.6 cM – *Xwgp110-2B* – 4.4 cM – *Yr43* – 5.5 cM – *Xwgp103-2B* – 12.8 cM – *Xbarc139-2B* {10673}.

Yr44 {10673}. *YrZak* {10674}. 2BL {10674}. **v:** Zak = PI 607839 {10674}.
ma: *XSTS7/8/Yr5* – 12.7 cM – *Yr44* – 3.9 cM – *Xwgp100* – 1.1 cM – *Xgwm501-2B* {10674}.

Yr45 {10677}. 3DL {10677}. v: PI 181434 {10677}.
ma: *Xbarc6-3D* – 0.9 cM – *Xwmc656-3D* – 6.9 cM – *Xwp118-3D* – 4.8 cM – *Yr45* – 5.8 cM – *Xwp115-3D* {10677}.

This gene is highly effective and confers resistance to all North American Pst pathotypes.

Yr46 {10678}. Adult-plant resistance. 4D {10678}.
i: RL6077 = Thatcher*6 / PI 250413 {10678}.
v: PI 250413 {10678}.
ma: Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of *Yr46*) {10678}.

Yr47 {10679}. 5BS {10679}. **bin:** 5BS5-0.71-0.81.
v: AUS28183 = V336 {10679}.
ma: 5 ± 2 cM proximal to *Lr52* {10679}.

This is a seedling resistance gene (IT 1CN), effective against the main Australian groups of Pst. V336 is the original source of *Lr52*.

Yr48 {10705}. Adult-plant resistance. 5AL {10705}. **bin:** 5AL23-0.87-1.00.
v: UC1110 (S) / PI 610750 RIL 167 (R) {10705}.
ma: Co-segregated with *Vrn2*, Be495011, *Xcfa2149-5AL*, *Xgpw2181a-5AL*, *Xwmc74-5AL*, and *Xwmc410-5AL* {10705}.
Xwmc727-5AL – 4.4 cM – *Yr48* – 0.3 cM – *Xwms291-5AL* {10705}.

PI 610750 = Synthetic 205 (Croc 1 / *Ae. tauschii* // Kauz) {10705}.

Genotype list: ……., U.K. wheats {10697}.

91.2. Temporarily designated genes for resistance to stripe rust

YrC142 {10667}. 1BS {10667}. **v:** Synthetic CI142 = 'Gaza / Boy // *Ae. tauschii* 271' {10667}.
ma: Located in the *Yr24/Yr26* region close to *Xbarc187-1B* and *Xgwm273-1B* {10667}.

Although postulated to be unique this gene is likely *Yr24/Yr26*.

YrCn17 {10686}. 1BS = T1BL·1RS {10686}. **v:** Chuannong 17 {10686}.
dv: *S. cereale* R14 {10686}.

YrP81 {10696}. 2BS {10696}. **v:** P81 {10696}; Xu29 {10696}.
ma: *Xgwm429-2B* – 1.8 cM – *YrP81* – 4.1 cM – *Xwmc770-2B* {10696}.

91.3. Stripe rust QTL

'Pingyuan 50 (R) / Mingxian 169 (S)': DH population: APR: *QYrcaas-2BS* (*Xbarc13-2BS* – *Xbarc230-2BS*, R^2 = 0.05-0.09), *QYr.caas-5AL* (*Xwmc410-5AL* – *Xbarc261* – 5AL, R^2 = 0.05-0.2), *QYrcaas-6BS* (*Xgwm361-6BS* – *Xbarc136-6BS*, R^2 = 0.05 – 0.08) {10693}.

'Renan (R) / Recital (S)': RIL population: Tested for AUDPC in 1995–96 and 2005–066 with pathogen isolates avirulent and virulent, respectively, for *Yr17*: *QYr.inra-2AS.2*, (= *Yr17*), R^2 = 0.45, 1995–96; *QYr.inra-2AS.1*, R^2 = 0.9,

2005–06; *QYr.inra-2BS*, $R^2 = 0.11$ and 0.13, *QYr.inra-3Bcent*, $R^2 = 0.06$ in 2005–06; *QYr.inra-6B*, $R^2 = 0.04$ and 0.06; from Renan; and *QYr.inra-2AS.1*, $R^2 = 0.09$; *QYr.inra-3DS*, $R^2 = 0.08$ and 0.12 from Recital. Other QTL were effective only at certain growth stages {10689}.

'Express / Avocet S': RIL population: Relative AUDPC for high temperature APR was controlled by *QYrex.wgp-6AS*, $R^2 = 0.326$, interval *Xgwm334-6A – Xwgp56-6A*; *QYrex.wgp-3BS*, $R^2 = 0.274$, interval *Xgwm299-3B – Xwgp66-3B*; and *QYrex.wgp.1BL*, $R^2 = 0.094$, interval *Xwmc631-1B – Xwgp78-1B* {10672}. When rust phenotyping was based on infection type, only the 6S and 3BL QTL were evident {10672}.

92. Reaction to *Puccinia triticina*

92.1. Genes for resistance

***Lr11*.** **v:** Saluda {10699}.

***Lr13*.** **v2:** Beaver *Lr26* {1032}.

***Lr17*.**

***Lr17a*.** **v2:** Fuller *Lr39* {10699}.

***Lr26*.** **v2:** Beaver *Lr13* {10687}.

***Lr34*.** **v:** Lantian {10682}; Libellula {10682}; Strampelli {10682}.

Add to the sentence:

'STS marker csLV34 was used to confirm……in Australian cultivars {10493}' and Hungarian materials {10701}.

Add to the notes following this entry:

Diagnostic markers based on the gene sequence are reported in {10656}; AC Domain, Cappelle Desprez, H-45, Jagger, Newton, RL 6077, and H-45 do not carry *Lr34* {10656}.

***Lr39*.** **v:** Overley {10699} **v2:** Fuller Lr17a {10699}.

***Lr56*.** **v:** Recombinants with shorter segments – 07M4-39, 07M4-157, and 07M4-175 – are reported in {10691}.

Lr66 {10591}. 3A = T3A-3S^S. **v:** Correct to: 07M127-3.

Lr67 {10675}. Adult-plant resistance. 4DS {10675}.

i: RL6077 = 'Thatcher*6 / PI 250413' {10675}.

v: PI 250413 {10676}.

ma: Associated with *Xcfd71-4D* {10675}. Pleiotrophic with *Yr46*. Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of *Lr67*/*Yr46*) {10678}.

Genotype lists: Under Chinese cultivars add {…, 10682}.

Add to: ***LrZH84***. **v:** Zhoumai 11 {10682}.

92.3. QTL for reaction to *P. triticina*

'Beaver / Soissons' DH population: QTL for resistance to Australian pathotypes were located on 4-6 chromosomes over 3 years; the most consistent being 1B (T1BL·1RS), 4BS (proximal to *Xbarc20-4B*), and 5AS (*QTLBvr5AS*, proximal to *Xbarc10-5A*) and in the vicinity of *wPt-8756* and *wPt-1931* {10687}.

Add at end of section:

'TA4152-60 / ND495' DH population: Four QTL for APR, *QLr.fcu-3AL* (*Xcfa2183-3AL – Xgwm666-3AL*, $R^2 = 0.18$), *Qlr.fcu-3BL* (*Xbarc164-3BL – Xfcp544-3BL*, $R^2 = 0.19$), *Qlr.fcu5BL*, and *Qlr.fcu-6BL* (*Xbarc5-6BL – Xgwm469.2-6BL*, $R^2 = 0.12$) were from TA4152-60 and *Qlr.fcu-4DL* (*Xgdm61-4DL – Xcfa2173-4DL*, $R^2 = 0.13$) was from ND495 {10660}. The 3AL QTL conferred seedling resistance to all three races, and the 3BL gene gave race-specific seedling resistance to one race. *Qlr.fcu-3BL* was effective only in the presence of an allele associated with *Xgwm359-5DS* {10660}.

97. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

After the introductory paragraph add:

A review is provided in {10690}.

97.3. Resistance to tanspot

Tsr6 {10668}. Resistance is recessive. 2BS {10668}.

v: ND-735 {10688}.

ma: *Xwmc382-2B* – 15.3 cM – *wPt-0289* – 4.6 cM – *Tsr6* – 18.7 cM – *Xwmc-2B* {10668}.

According to {10668}, *Tsr6* should be identical to *tsc2* (see Insensitivity to tan spot toxin (chlorosis)).

96. Reaction to Soil-Borne Cereal Mosaic

SbmTmr1 {10683}. 5D {10683}. **v:** TAM 107-R7 {10683}.

SBWMV {10685}. 5D {10685}. **v:** KS96WGRC40 {10685}.
dv: *Ae. tauschii* TA2397 {10685}.
ma: *Xcfd010-5DL* – 9.5 cM – *SBWMV* – 11.1 cM – *Xbarc144-5D* {10685}.

The relationship of this gene to *Sbm1* is not known.

98. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Bt10. 6DS {10664}. **ma:** *Bt10/FSD_RSA* – 19.3 cM – *Xgwm469-6D* – 1.8 cM – *Xwmc749-6D* {10664}.

100. Reaction to *Ustilago tritic*i (Pers.) Rostrup

Utd1 {10684}. 5BS {10684}. **tv:** D93213 {10684}; P9163-BJ08*B {10684}; VIR 51658 {10684}.
ma: SCAR – 3.2 cM – *Utd1* – 5.9 cM – *Xgwm234-5B* {10684}.

102 .Reaction to Wheat Streak Mosaic Virus

Wsm1. **v:** Mace {10694}.

Genetic linkages

Chromosome 2BL

Yr5	–	*Yr44*	42 cM {10673, 10674}.
Yr5	–	*Yr43*	65.5 cM {10673}.
Yr44	–	*Yr43*	13.1 cM {10673}.

References

Updates

10159. Kong L, Anderson JM & Ohm HW 2009 Segregation distortion in common wheat of *Thinopyrum intermedium* chromosome 7B carrying *Bdv3* and development of a *Bdv3* marker. Plant Breeding 128: 591-597.

10539. Luo PG, Luo HY, Chang ZJ, Zhang HY, Zhang M & Ren ZL 2009 Characterization and chromosomal location of *Pm40* in common wheat: a new gene for resistance to powdery mildew derived from *Elytrigia intermedium*. Theoretical and Applied Genetics 118: 1059-1064.

10591. Euphytica 171: 71-85.

New

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VI. ABBREVIATIONS USED IN THIS VOLUME.

PLANT DISEASES, PESTS, AND PATHOGENS:

BYDV = barley yellow dwarf virus
BMV = barley mosaic virus
CCN = cereal cyst nematode, *Heterodera avenae*
FHB = Fusarium head blight
RWA = Russian wheat aphid
SBMV = soilborne mosaic virus
SLB = Septoria leaf blotch
TMV = *Triticum* mosaic virus
WDF = wheat dwarf mosaic
WSBMV = wheat soilborne mosaic virus
WSMV = wheat streak mosaic virus
WSSMV = wheat spindle streak mosaci virus
WYMV = wheat yellow mosaic virus
E. graminis* f.sp. *tritici = *Erysiphe graminis* f.sp. *tritici* = the powdery mildew fungus
F. graminearum = *Fusarium graminearum* = head scab fungus
F. nivale = *Fusarium nivale* = snow mold fungus
H. avenae = *Heterodera avenae* = cereal cyst nematode
P. graminis = *Polymyxa graminis* = wheat soilborne mosaic virus vector
P. striiformis* f.sp. *tritici = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus
P. triticina = *Puccinia triticina* = *P. recondita* f.sp. *tritici* = leaf rust fungus
R. cerealis = *Rhizoctonia cerealis* = sharp eyespot
R. solani = *Rhizoctonia solani* = Rhizoctonia root rot
R. padi = *Rhonpalosiphum padi* = bird cherry-oat aphid
S. tritici = *Septorai tritici* = Septoria leaf spot fungus
S. graminearum = *Schizaphus graminearum* = greenbug
St. nodorum = *Stagonospora nodorum* = Stagonospora glume blotch
T. indica = *Tilletia indica* = Karnal bunt fungus

SCIENTIFIC NAMES AND SYNONYMS OF GRASS SPECIES (NOTE: CLASSIFICATION ACCORDING TO VAN SLAGEREN, 1994):

A. strigosa = *Avena strigosa*
Ae. cylindrica = *Aegilops cylindrica* = *Triticum cylindricum*
Ae. geniculata = *Aegilops geniculata* = *Aegilops ovata* = *Triticum ovatum*
Ae. longissima = *Aegilops longissima* = *Triticum longissimum*
Ae. markgrafii = *Aegilops markgrafii* = *Aegilops caudata* = *Triticum caudatum*
Ae. speltoides = *Aegilops speltoides* = *Triticum speltoides*
Ae. tauschii = *Aegilops tauschii* = *Aegilops squarrosa* = *Triticum tauschii*
Ae. triuncialis = *Aegilops triuncialis* = *Triticum triunciale*
Ae. umbellulata = *Aegilops umbellulata* = *Triticum umbellulatum*
Ae. peregrina = *Aegilops peregrina* = *Aegilops variabilis* = *Triticum peregrinum*
Ae. searsii = *Aegilops searsii* = *Triticum searsii*
Ae. ventricosa = *Aegilops ventricosa* = *Triticum ventricosum*
D. villosum = *Dasypyrum villosum* = *Haynaldia villosa*
S. cereale = *Secale cereale* = rye
T. aestivum* subsp. *aestivum = *Triticum aestivum* = hexaploid, bread, or common wheat
T. aestivum* subsp. *macha = *Triticum macha*
T. aestivum* subsp. *spelta = *Triticum spelta*
T. militinae = *Triticum militinae*
T. monococcum* subsp. *aegilopoides = *Triticum boeoticum*
T. timopheevii* subsp. *timopheevii = *Triticum timopheevii*
T. timopheevii* subsp. *armeniacum = *Triticum araraticum* = *T. araraticum*
T. turgidum* subsp. *dicoccoides = *Triticum dicoccoides* = wild emmer wheat

T. turgidum* subsp. *dicoccum = *Triticum dicoccum*
T. turgidum* subsp. *durum = *Triticum durum* = durum, pasta, or macaroni wheat
T. urartu = *Triticum urartu*
Th. bessarabicum = *Thinopyrum bassarabicum*
Th. elongatum = *Thinopyrum elongatum* = *Agropyron elongatum*
Th. intermedium = *Thinopyrum intermedium* = *Agropyron intermedium*

SCIENTIFIC JOURNALS AND PUBLICATIONS:

Agron Abstr = Agronomy Abstracts
Ann Wheat Newslet = *Annual Wheat Newsletter*
Aus J Agric Res = *Australian Journal of Agricultural Research*
Can J Plant Sci = *Canadian Journal of Plant Science*
Cereal Chem = *Cereal Chemistry*
Cereal Res Commun = *Cereal Research Communications*
Curr Biol = *Current Biology*
Eur J Plant Path = *European Journal of Plant Pathology*
Funct Integ Genomics = *Functional Integrative Genomics*
Ind J Agric Sci = *Indian Journal of Agricultural Science*
Int J Plant Sci = *International Journal of Plant Science*
J Agric Sci Technol = *Journal of Agricultural Science and Technology*
J Cereal Sci = *Journal of Cereal Science*
J Hered = *Journal of Heredity*
J Phytopath = *Journal of Phytopathology*
J Plant Phys = *Journal of Plant Physiology*
Mol Gen Genet = *Molecular and General Genetics*
Nat Genet = *Nature Genetics*
PAG = Plant and Animal Genome (abstracts from meetings)
Phytopath = *Phytopathology*
Plant Breed = *Plant Breeding*
Plant, Cell and Envir = *Plant, Cell and Environment*
Plant Cell Rep = *Plant Cell Reporter*
Plant Dis = *Plant Disease*
Plant Physiol = *Plant Physiology*
Proc Ind Acad Sci = *Proceedings of the Indian Academy of Sciences*
Proc Natl Acad Sci USA = Proceedings of the National Academy of Sciences USA
Sci Agric Sinica = *Scientia Agricultura Sinica*
Theor Appl Genet = *Theoretical and Applied Genetics*
Wheat Inf Serv = *Wheat Information Service*

UNITS OF MEASUREMENT:

bp = base pairs
bu = bushels
cM = centimorgan
ha = hectares
kDa = kiloDaltons
m^2 = square meters
m^3 = cubic meters
μ = micron
masl = meters above sea level
me = milli-equivalents
mL = milliliters
mmt = million metric tons
mt = metric tons
Q = quintals
T = tons

MISCELLANEOUS TERMS:

Al = aluminum
AFLP = amplified fragment length polymorphism
ANOVA = analysis of variance
A-PAGE = acid polyacrylamide gel electrophoresis
APR = adult-plant resistance
AUDPC = area under the disease progress curve
BC = back cross
BW = bread wheat
CHA = chemical hybridizing agent
CMS = cytoplasmic male sterile
CPS = Canadian Prairie spring wheat
DH = doubled haploid
DON = deoxynivalenol
ELISA = enzyme-linked immunosorbent assay
EMS = ethyl methanesulfonate
EST = expressed sequence tag
FAWWON = Facultative and Winter Wheat Observation Nursery
GA = gibberellic acid
GIS = geographic-information system
GM = genetically modified
GRIN = Germplasm Resources Information Network
HPLC = high pressure liquid chromatography
HMW = high-molecular weight (glutenins)
HRSW = hard red spring wheat
HRRW = hard red winter wheat
HWSW = hard white spring wheat
HWWW = hard white winter wheat
ISSR = inter-simple sequence repeat
IT = infection type
kD = kilodalton
LMW = low molecular weight (glutenins)
MAS = marker-assisted selection
NSF = National Science Foundation
NILs = near-isogenic lines
NIR = near infrared
NSW = New South Wales, region of Australia
PAGE = polyacrylamide gel electrophoresis
PCR = polymerase chain reaction
PFGE = pulsed-field gel electrophoresis
PMCs = pollen mother cells
PNW = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada)
PPO = polyphenol oxidase
QTL = quantative trait loci
RAPD = random amplified polymorphic DNA
RCB = randomized-complete block
RFLP = restriction fragment length polymorphism
RILs = recombinant inbred lines
RT-PCR = real-time polymerase-chain reaction
SAMPL = selective amplification of microsatellite polymorphic loci
SAUDPC = standardized area under the disease progress curve
SCAR = sequence-characterized amplified region
SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis
SE-HPLE = size-exclusion high-performance liquid chromatography

SH = synthetic hexaploid
SNP = single nucleotide polymorphism
SRPN = Southern Regional Performance Nursery
SRWW = soft red winter wheat
SRSW = soft red spring wheat
STMA = sequence tagges microsatellite site
SWWW = soft white winter wheat
SSD = single-seed descent
SSR = simple-sequence repeat
STS = sequence-tagged site
TKW = 1,000-kernel weight
UESRWWN = Uniform Experimental Soft Red Winter Wheat Nursery
VIGS = virus-induced gene silencing

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IX. VOLUME 57 MANUSCRIPT GUIDELINES.

Manuscript guidelines for the *Annual Wheat Newsletter*, volume 56. The required format for Volume 57 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 44–56 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. Please include a separate .jpg or equivalent file of any graphic in the contribution. Submit by E-mail to jraupp@k-state.edu.

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The *Annual Wheat Newsletter* will continue to be available (Vol. 37–56) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.