

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+ cooperators 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-B1a1*, *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.

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 potyvirus 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 (19°C and 20–26°C). 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 20–26°C, 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 19°C with no synergistic interaction, whereas both viruses accumulated at moderate levels at 20–26°C and induced mild to moderate disease synergism in doubly infected Mace when compared to Arapahoe and Tomahawk. Co-infections in Mace at 20–26°C 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 *Puccinia 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*), MLDS (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 above-ground 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, Zeleny 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.