



Borlaug Global Rust Initiative

Cd. Obregón, Sonora, Mexico, March 17-20, 2009

Poster Abstracts



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The abstracts were edited by Dr. Robert McIntosh, Honorary Associate at the Plant Breeding Institute of the University of Sydney.

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Theme 1:

Rust Race Analysis & Surveillance

1. Genetic Diversity of Wheat Stem Rust Pathogen (*Puccinia graminis* f. sp. *tritici*) Isolates from Ethiopia as Revealed by Microsatellites

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Puccinia graminis f. sp. *tritici* (*Pgt*) causes stem rust, which is a major production constraint of wheat in many warmer countries, including Ethiopia. The pathogen is known to have high genetic and virulence variability throughout the world and has gained evident importance today due to the appearance of race Ug99 that overcomes the widely used resistance gene *Sr31*. Although recent studies indicated high virulence diversity in Ethiopia, the genetic structure of the pathogen is not known in Ethiopia and in most east African countries, where highly virulent races like Ug99 have originated. The present study employed simple sequence repeat (SSRs) markers to determine the genetic structure of *Pgt* isolates sampled in three different regions of Ethiopia. The assays showed high genetic diversity within each population (0.600 - 0.718). On the other hand, the genetic distance between populations was very low (0.08 – 0.315). Cluster analysis placed all isolates, except one, in a single cluster. This, coupled with a low coefficient of genetic differentiation (0.107), indicated an absence of genetic differentiation among populations. The high gene flow among populations (10 per generation) was attributed to the absence of population sub-division. Overall, the pathogen population of Ethiopia is characterized by a high genetic diversity and homogeneity across regions, suggesting that the Ethiopian *Pgt* populations did not evolve independently, and are parts of a larger pathogen genetic pool with a common ancestor. Such phenomena are reminders that the pathogen in Ethiopia can easily adapt to deployed stem rust resistance genes and fungicide treatments. Hence, the agricultural research and development system needs to deploy cultivars possessing “horizontal” resistance to attain durable stem rust control.

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2. Wheat Rusts Survey and Virulence of *Puccinia graminis* in Ethiopia

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Wheat (*Triticum* spp) rust surveys were conducted in the main season (June-November) of 2007 and off-season (April-August) of 2008 in the Oromia, Amhara and Southern Nations and Nationalities Peoples regions of Ethiopia. Five hundred sixty two wheat fields in the main season and 76 wheat fields in the off-season were assessed for rust diseases. The mean prevalence of stem rust (*Puccinia graminis*) for the three regions was 30.4%, leaf rust (*P. triticina*) 64.4%, and for yellow (stripe) rust (*P. striiformis*) 47.2% in the main season, whereas the prevalence of stem rust was 14.5% and leaf rust 37% in the off-season. The overall mean stem, leaf and yellow rust incidences in the main season were 16, 40 and 24.9%, whereas the severities were 8.2, 11.2 and 9.9%, respectively. The incidences and severities of the three rusts were low in the off-season. Among the improved bread wheat cultivars sown, Kubsa (with pedigree Atila), Meda Walabu (TL/3/Fn/TA/Nar59*2/4/Bil'S'), Tuse (Cook/VEE'S'//Dove'S'/Seri), and Galema (4777(2)//FKN/GB/3/PvN'8') were affected by all three rusts. Stem rust samples isolated from these and other cultivars were variable. Of 23 pathotypes identified, 37% were virulent for *Sr31*, 48% were virulent for *Sr36*, and about 4% of isolates were virulent for both *Sr31* and *Sr36*. These virulent stem rust isolates were collected from wheat fields in the southeastern, central, western and northern parts of Ethiopia. Gene *Sr24* was effective against all isolates.

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3. *Puccinia striiformis* f. sp. *tritici* Race Changes in the United States

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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is most frequently destructive on wheat in the western United States and has become more frequently epidemic in the Great Plains and southeastern U.S. states since 2000. Races of the pathogen have been determined every year from infected leaf samples of wheat and grasses, collected throughout the U.S., on seedlings of a set of 20 wheat differential genotypes. From 2000 to 2008, a total of 117 races were detected, of which 79 were first detected during this period. The predominant races, which were first detected in 2000, were the group with basic virulences to Lemhi (*Yr21*), Heines VII (*Yr2*, *YrHVII*), Lee (*Yr7*, *Yr22*, *Yr23*), Fielder (*Yr6*, *Yr20*), Express (*YrExp1*, *YrExp2*), AVS/6**Yr8* (*Yr8*), AVS/6**Yr9* (*Yr9*), Clement (*Yr9*, *YrCle*), and Compair (*Yr8*, *Yr19*). This race group continues to evolve into new races with additional virulences to differential genotypes, including Chinese 166 (*Yr1*), Moro (*Yr10*, *YrMor*), Paha (*YrPa1*, *YrPa2*, *YrPa3*), Druchamp (*Yr3a*, *YrDru*, *YrDru2*), Produra (*YrPr1*, *YrPr2*), Yamhill (*Yr2*, *Yr4a*, *YrYam*), Tye (*YrTye*), Tres (*YrTr1*, *YrTr2*), and/or Hyak (*Yr17*, *YrTye*). From 2000 to 2003, the predominant races were PST-78 (virulent on wheat differential genotypes Lemhi, Heines VII, Lee, Fielder, Express, AVS/6**Yr8*, AVS/6**Yr9*, Clement and Compaie) and PST-80 (the same virulences plus virulence on Produra). In 2004 to 2006, the most predominant race throughout the U.S. was PST-100 (the same virulences as PST-80 plus virulences on Yamhill and Stephens). Starting in 2006, races with the virulences of PST-100 or similar races plus virulence to *Yr1* became predominant in California, and PST-114 with combined virulences of PST-100 and virulence to *Yr10* became predominant in the Pacific Northwest. Over the nine-year period, races with more virulences became increasingly predominant, indicating that races with more virulences have advantages over those with fewer virulences.

4. Population Structure of Wheat Disease Pathogens Causing Epiphytotics in Southern Russia

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The north Caucasus region, the main grain crop producing region in Russia, loses annually 450 – 1,050 Kg/hectare of wheat. A major reason for such large losses is the presence of fungal diseases, the most widespread and injurious among them being leaf rust (caused by *Puccinia triticina*), yellow (stripe) rust (*P. striiformis*) and stem rust (*P. graminis*). Leaf rust is detected every year; but the occurrence of yellow rust and stem rust has increased in recent years.

The Laboratory for Cereal Immunity to Fungus Diseases of the All-Russian Institute of Biological Plant Protection has long-term experience in population and immuno-genetic research of the “wheat – rust pathosystem” in developing methodological foundations for development of resistant cultivars and improved crop protection.

The principles of host : parasite systems formulated by Vavilov, Zhukovsky, Flor and others form the basis of the research. One of the research areas is the study of rust virulence.

Wheat field investigations in 2008 indicated average levels of yellow rust development in different agroclimatic zones of the North Caucasus, varying between 1 and 5%. Leaf rust occurred at 1 to 10%, and stem rust was in the range of 1%, mainly in the southern foothills.

Virulence analysis of the wheat yellow rust pathogen population in the North Caucasus region showed that it included isolates virulent to 12 of the 16 of the differentials being used. Isolates virulent to the lines with genes *Yr5*, *Yr24*, *Yr26*, and *YrSP* were not detected; isolates virulent on lines with *Yr10* and *Yr17* were detected at the rate of 5%; lines with *Yr15*, *Yr27* and *Yr32* at 5-10%; those with *Yr1*, *Yr8* and *Yr9* at 10-25%; on carriers of *Yr6*, *Yr7*, *Yr18* and *YrA* – at more than 25%.

The stem rust pathogen population included isolates virulent to 30 of the 42 carriers of defined resistance genes. Clones virulent to testers with *Sr7a*, *9b*, *9e*, *11*, *12*, *21*, *24*, *25*, *29*, *30*, *35*, and *WLD* were not

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detected; isolates virulent to genes *Sr9a*, *33*, *Sr36* (*Tt1*) and *Dp2* at the rate of 5%; those virulent to *Sr5*, *8a*, *13*, *17*, *23*, *27*, *31*, *32* and *37* at 5 to 10%; those virulent to *Sr9d* (*Sr1*), *6*, *7a*, *8b*, *9g*, *14*, *15*, *20*, *22*, *26*, *36c* at 10 to 25%; and those virulent to *Sr9d* (*Sr1*), *10*, *16*, *19*, *Tt2* (*37*) at more than 25%.

In the leaf rust pathogen population, clones virulent to testers with *Lr9*, *19*, *24*, *29*, *41*, *42*, and *43+24* were not detected. At the same time, high frequencies of clones virulent to lines with *Lr1*, *2c*, *3*, *3ka*, *10*, *11*, *14a*, *14b*, *16*, *17*, *23*, *26*, *28*, *30*, *33*, *40*, and *B* (more than 40%) were detected. Isolates virulent to testers with *Lr52* (*LrW*) and *Lr45* were present at the rate of 2-3%.

The research results of the rust fungal population structure can be applied in the selection of the wheat cultivars, selection for resistance to specific pathogen races, cultivar recommendation and resistance sources, and recommendations on chemical protection of individual wheat cultivars.

5. Variability in Responses to *Puccinia graminis* pers. f. sp. *tritici* on Different Host Plants

ES Skolotneva, SN Lekomtseva

Parasitic fungi need to keep up with changing environments that are comprised of the natural environment, specific biochemistry and resistance systems of the host plant. Consequently, the genomes of parasitic fungi evolved to be highly flexible. Stem rust (caused by *P. graminis* f. sp. *tritici* (Pgt)) is a dangerous pathogen that infects wheat and some grasses. This pathogen is distributed worldwide, including Russia. There is wide genetic variability within this *formae specialis*. Pgt was collected from barberry, wheat, barley and wild graminaceous species in various regions of Russia (Central Region, Northern Caucasus, Western Siberia) between 2001 and 2005. A total of 309 monoklonal clones were isolated and multiplied on a susceptible wheat genotype. The Shannon diversity

index (Shannon's index) was used to evaluate diversity of race composition of populations depending on the season, host plant and geographical zone. In 2001-2005 race composition of Pgt was very diverse; 43 pathogenic races, 2-3 of which dominated in each year, were identified. The frequencies of other races were less than 8%. We classified these races as rare. The percentages of rare races varied from season to season. The highest diversity of fungal races was observed in the 2001 and 2002 seasons which were relatively favorable for the development of wheat stem rust. The race composition on various host plants in Central Russia (Moscow region) revealed that the Pgt clones obtained from barberry were the most diverse. Our results suggested that the sexual process contributed to the diversity of Pgt on wheat in this region, as well as to the variability and race composition of samples collected from wild cereals. Evaluations of the responses of isogenic wheat lines indicated that in 2001-2005 most of them, excluding those with *Sr11*, *Sr9b* and *Sr13*, were resistant.

Using isozyme and randomly amplified polymorphic DNA (RAPD) markers we performed an analysis of Pgt isolates from various grasses and barberry. Pgt isolates clearly segregated into three groups: one from barberry and the others from *Elytrigia* and *Hordeum*. RAPD analysis showed that the genotypes of isolates collected from barberry (Central Russia) clustered into a distinctive stable (bootstrap index up to 94%) group. By contrast, clusters of the MDG pathotypes of the "barberry" isolates were more similar to isolate groups from grasses, probably indicating that the pathotypes occurring on barberry and grasses are different from those occurring on wheat. Analysis of MDH phenotypes revealed a geographic variation among the isolates collected from different grass species. On the other hand, RAPD profile-based groups of Pgt isolates were independent of their geographic origins. The particular host plants determined the structure of RAPD diversity. These results could suggest there are several trends of Pgt variability at the molecular level.

6. Occurrence of Wheat Rusts in Turkey During the 2008 Growing Season

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The rusts are major diseases of wheat in Turkey and they can cause significant yield losses in years with suitable conditions. However, rust prevalence changes from year to year and from region to region depending on climatic conditions. This study was conducted to monitor the occurrence of rusts in different parts of Turkey in 2008. Survey trips were conducted covering the Marmara, Aegean, Thrace, East Mediterranean, Southeast Anatolia, Central Anatolia, East Anatolia and Mid-Blacksea regions. Two hundred and forty two wheat fields were examined for the presence of stripe rust, leaf rust and stem rust. The frequencies of infected plants were recorded and severities were estimated using the Modified Cobb scale. Seventy one fields were infected with rusts. Of these, 60 were infected with stem rust, 6 with leaf rust, and 9 with stripe rust. In some fields, more than one rust was present. In 2008 Turkey suffered from severe drought which was so severe that some fields were not harvested. Stem rust was most prevalent in inner parts of Black Sea region. Severities of rust diseases were therefore non-significant. However, their occurrences under such dry conditions indicate that they keep their potential to cause severe losses.

This study was conducted as part of the project 'Determination of Races of Wheat Stem Rust (*Puccinia graminis* f. sp. *tritici*) and Resistant Wheat Genotypes Against Common Races in Turkey, No:106O331' financed by the Scientific and Technical Research Council of Turkey (TUBITAK).

7. Evolution of the Leaf Rust Pathogen on Durum Wheat in Northwestern Mexico

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CIMMYT-derived durum wheat (*Triticum turgidum* var *durum*) germplasm was highly resistant to leaf rust (caused by *Puccinia triticina*) to prevalent race BBB/BN in Mexico until 2000. However, a large portion of the germplasm was susceptible in Chile and North Africa. A new race, detected in northwestern Mexico in 2001, was virulent on more than 80% of the germplasm, including the most popular cultivar Altar C84. This race was designated BBG/BN. Apparently a single gene mutation towards virulence on *Lr11* was observed, but virulence to the undesignated gene in Altar indicated the possibility of an exotic origin. During the same year a variant, designated as BCG/BN, was identified with an unnecessary virulence for resistance gene *Lr26* present in the 1B.1R translocation in bread wheat (*T. aestivum*). In 2008 leaf rust was observed on previously resistant durum cultivars Jupare C2001 and Banamichi C2004. Single pustule isolates indicated the presence of a new race designated BBG/BP, which evolved through a single mutation in race BBG/BN for virulence to the complementary resistance genes *Lr27+Lr31* present in Gatcher, Jupare C2001 and Banamichi C2004, and adult plant resistance gene *Lr12*. A variant isolate of race BBG/BP, designated as CBG/BP, with additional virulence for *Lr3* present in CIMMYT durum 'Storlom' was also identified. Although virulence to *Lr3*, *Lr12* and *Lr27+Lr31* is known to occur in *P. triticina* races predominant on bread wheat, this is first time that we identified such virulences in races predominant on durum wheat. Since the introduction of BBG/BN in Mexico in 2001, this durum *P. triticina* race has continued to evolve and defeat race-specific resistance genes commonly present in both durum and bread wheat.

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8. Wheat Rusts in India - Pathogenic Changes

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Surveys and surveillance of wheat rusts began in India in 1930 and the rust pathotyping was done at the Wheat Rust Laboratory, Shimla. Since then pathogenicity surveys have detected many changes in the rust pathogens. The changes can generally be divided into two periods, viz. the pre-Mexican influence period (referred to as first period) and the post Mexican influence period (second period). *Puccinia graminis tritici* from the first period was virulent on plants with *Sr9d* and *Sr9g* and local durums and cultivated emmers, except Khapli, were susceptible. However, Khapli was resistant. The second period witnessed acquisitions of virulences for *Sr5*, *8a*, *9b*, *11*, *13* and *14* (Khapli), *24*, *25*, and *28*. Most of the changes were for *Sr5*, *9b*, *11*, and *13* whereas there were a few for *Sr24* and *Sr25*. Some of these changes could be attributed to the introduction of cultivars carrying corresponding resistance genes (like Kalyansona and Sonalika), whereas others were not related to host genotypes. Leaf rust in the first period was avirulent for most of the named genes. The second period witnessed changes for many genes including *Lr1*, *2a*, *3*, *10*, *13*, *20* and *26*. The most common changes were observed for *Lr23*, *26* and *13* and more recent changes to virulence for *Lr9*, *19* and *28* were not related to the introduction of varieties with the corresponding resistance genes. For stripe rust, pathogen was virulent for *Yr6* and *7* in the first period, and in the second period, the pathogen acquired virulences for many genes including *Yr2*, *A*, *4b*, *9*, *25* and *27*. Some of these changes were related to the introduction of varieties such as Kalyansona (*Yr2*), Sonalika (*YrA*), Veery#5 (*Yr9*), and PBW343 (*Yr9+27*), but other changes such as those corresponding to *Yr4b* and *Yr25* could not be related to host genotypes.

9. Effective Rust Resistance Genes in Wheat under Moroccan Conditions

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In order to evaluate the effectiveness of leaf rust and yellow (stripe) rust resistance genes, a set of leaf rust and a set of yellow rust differentials were grown under field conditions and tested for rust resistance in three contrasting locations (Meknès, Douyet and Annoceur). The sowing date was around the end of November in plots of two 0.5 m rows 30 cm apart. The rust diseases were scored during grain filling according to the modified Cobb scale coupled with reaction types to calculate coefficients of infection (CI). During the 2006-07 season, yellow rust was the most prevalent disease at all three sites. Leaf rust was observed only at Meknès. Since yellow rust precedes leaf rust in time of appearance, the latter could not be scored on lines that were highly susceptible to the former. The coefficients of infection for yellow rust ranged from 0 to 50, 0 to 80, and 0 to 90 at Annoceur, Douyet and Meknès, respectively. Lines possessing *Yr1*, *Yr5*, *Yr10*, *Yr15*, *Yr17*, *YrSP*, and to some extent, *Yr8*, were highly resistant at the three sites, whereas lines with *Yr18* and *Yr27* exhibited some interaction with sites. They were highly effective at Meknès, moderately so at Annoceur, and less effective at Douyet. Lines carrying *Yr9*, *Yr7*, *Yr6* and *YrA* were susceptible at all three sites. At Meknès, the coefficient of infection for leaf rust ranged from 0 to 80. The line carrying *Lr23+* exhibited immunity and that carrying *Lr20* exhibited only traces of pustules. The lines carrying *Lr21*, *29* and *34* exhibited co-efficients of infection (CIs) of 5. Lines carrying separately *Lr10*, *12*, *13*, *14a*, *14b*, *15* and *28* exhibited CIs of no more than 10. In contrast, lines carrying the slow rusting character were completely immune towards leaf rust. These lines were also free of yellow rust. Moreover, many combinations of *Lr* genes, such as the combination *Lr10*, *Lr27+Lr31*, *Lr34*, gave very good levels of leaf rust resistance. It is of interest to mention that the lines carrying *Yr1*, *Yr5*, *Yr10*, *Yr15*, *Yr17* or *YrSP*, that were highly resistant to yellow rust, were also resistant to leaf rust, as well as having high agronomic scores.

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10. Survey of Wheat Diseases in Morocco During the 2007-08 Growing Season

A Ramdani

There are many biotic constraints to wheat production in Morocco. Leaf rust, septoria leaf blotch, and to some extent, yellow (stripe) rust are the most damaging diseases on wheat. The objective of this survey was to assess the prevalence, incidence and severity of wheat diseases across Morocco in order to produce a multi-layered map. Such a map is a very useful tool to tailor breeding objectives and for more objective deployment of the available commercial cultivars. This survey, which is planned to be ongoing, is also the backbone of pre-breeding activities dealing with disease resistance. The survey also permits collection of pathogen samples for determination of genetic diversity and virulence phenotyping. The survey was carried out during the first half of April, 2008, in the Chaouia, Abda, Doukkala and Sais areas when the growth stages of the wheat crop ranged from milk to physiological maturity. In the area of Middle Atlas, the survey was carried out during the second fortnight of June, 2008, also corresponding to the milk to physiologically mature stages. The data recorded were host species, growth stage, visual assessment of grain yield, and incidences and severities of the main diseases from which the prevalences were computed.

In order to avoid a biased assessment of the importance of necrotrophic foliar diseases separately, namely Septoria leaf blotch, Septoria glume blotch and tan spot (yellow spot), because of the similarity of symptoms and the scarcity of fruiting bodies (pycnidia), we assessed the complex, hereafter named Septoria-like-diseases (SLD). A total of 96 fields were inspected, the numbers for each being 43, 22, 30 and 1 fields for bread wheat, durum, barley and triticale, respectively.

This survey revealed that the most prevalent diseases on both bread and durum wheats were Septoria-like diseases, leaf rust and, to some extent, yellow rust and stem rust. Powdery mildew and common bunt were less prevalent and were detected only on bread wheat. Overall, 63% and 59% of bread wheat and durum wheat fields, respectively, were infected by SLD, while leaf rust was detected in 79% and 64% of fields, respectively. Stem rust was detected on 16% and 9% of bread wheat and durum fields, respectively; and yellow rust was detected on 9% of fields for both species. The survey provided information on the potential threat of the various diseases, although their severities in 2008 were not high because of the unfavorable environmental conditions.

INRA Morocco, Ville Nouvelle, BP Meknès, Morocco

11. Diverse Stem Rust Races Found in a Single Field in Washington, USA

M Rouse¹, S Stoxen¹, L Szabo^{1,2}, X Chen³, Y Jin^{1,2}

In 2007, a spring barley field in northeastern Washington State was severely infected by stem rust and a bulk sample was collected. Preliminary testing on wheat stem rust differentials suggested that the sample consisted of many different virulence types. To further characterize the virulence types, we derived 83 single-pustule isolates: 63 isolates from Line E wheat, 15 from Hiproly barley, and 5 from Prolific rye from inoculation with urediniospores collected from the sample. All isolates were race-typed in two replicates on the 20 North American stem rust differential lines and eight supplemental wheat lines, viz. Line E, Chinese Spring, LMPG-6, Little Club, Rusty, Morocco, Federation, and Gabo, most of which are considered to be widely susceptible to *Puccinia graminis tritici*. Twenty seven races were identified from the 83 isolates. The most frequently identified races included BBBB, JCBBB, and QHMJC. The supplemental lines further differentiated the isolates because isolates within each of the races frequently displayed different reactions on the supplemental lines. It is likely that this population consisted of several *formae speciales* in addition to *P. graminis* f. sp. *tritici*. The isolates were genotyped with 20 SSR markers. Our results demonstrated the vast diversity of stem rust races present at this location. This population is likely derived from the sexual cycle of *P. graminis*. Barberry is widely distributed in the region.

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Theme 2: New Sources of Rust Resistance for Wheat

12. A Survey of Genetic Variation for Adult Plant Stem Rust Resistance Among the A.E. Watkins Collection of Hexaploid and Tetraploid Wheat Genotypes

HS Bariana, UK Bansal, H Miah, AK Toor, F Hussain, RF Park

The pathotype 'Ug99' of the wheat stem rust pathogen was first detected in Uganda in 1999. Since its first detection, it has produced variants with added virulence for Sr24 and Sr36. A strategic global effort was undertaken to tackle this menace through deployment of genetic resistance in new wheat cultivars. The identification and characterisation of diverse sources of resistance is essential to combat the threat posed by new variants of pathogens. We studied genetic variation for stem rust resistance among the AE Watkins collection of hexaploid and tetraploid wheat genotypes. A specific attempt was made to identify new sources of durable minor gene controlled adult plant stem rust resistance. Tests on these genotypes under field conditions, followed by seedling tests with the same pathotype (s) of the stem rust pathogen, indicated the presence of minor (non- hypersensitive) genes for resistance in both hexaploid and tetraploid genotypes. Genotyping using Sr2-linked molecular markers enabled identification of genotypes that lacked Sr2 and carried as yet uncharacterised adult plant resistance gene (s). These putative new sources of resistance were crossed with susceptible cultivars to develop mapping populations for genetic characterisation of the resistance. Bulked segregant analysis will be performed to identify genomic regions that control adult plant resistance in some selected genotypes.

13. Sources of Resistance to Stem Rust Race Ug99 in Wild Tetraploid Wheat Accessions

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Stem rust caused by *Puccinia graminis* f. sp. *tritici* race TTKS commonly known as "Ug 99" is becoming a serious threat to wheat production worldwide. To cope up with the rapidly changing stem rust pathogen, new sources of seedling and adult plant resistances might be sought from the wild relatives of cultivated tetraploid wheat. A total of 1,524 wild tetraploid wheat accessions were evaluated against the prevailing Syrian stem rust population under field conditions at the International Center for Agricultural Research in the Dry Areas (ICARDA), Tel Hadya, Aleppo, Syria.

Two hundred and thirty eight accessions with adult plant resistance were selected for further seedling and adult plant assessments at the Debre Zeit Research Center, Ethiopia; a reputed 'hotspot' site for stem rust epidemics on tetraploids. The accessions were exposed to a mixture of isolates comprising Ug99 and a local bulk of urediniospores collected from hexaploid and tetraploid wheats. About 37% and 36% of the accessions showed resistance to stem rust at the seedling and adult growth stages, respectively. About 15% exhibited resistance at both the seedling and adult plant stages, leaving 21% with adult plant resistance only. This preliminary result indicated that wild tetraploid wheats could be potentially important sources of resistance to the prevailing stem rust races including Ug99. Some accessions have been selected for repeat testing to confirm the results. Crosses between these and elite bread wheat and durum varieties have also been initiated. Further ongoing genetic and genomic studies using these accessions should identify and characterize the resistance genes and reveal potentially new stem rust resistance genes for deployment in both durum and bread wheat breeding.

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14. SSR-Genotyping Of *Triticum aestivum* x *T. timopheevii* Introgression Lines and Mapping of Genes for Leaf Rust Resistance

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Twenty-four leaf rust resistant *T. aestivum* x *T. timopheevii* hybrid lines were developed using five common wheat cultivars. The resistances were analyzed using microsatellite markers specific for *T. aestivum* and *T. timopheevii*. Microsatellite analysis revealed two major areas of introgression of the *T. timopheevii* genome: chromosomes of homoeological groups 2 and 5. Translocations were detected in the 2A and 2B chromosomes in 11 lines. The length of the translocated fragment in the 2B chromosome was identical in all hybrid lines and did not depend on the parental wheat variety.

The hybrid line 842-2 was used for detailed characterization of introgression and mapping of loci determining resistance to leaf rust. Molecular analysis using 350 specific short sequence repeat (SSR) markers identified genes from the *T. timopheevii* genome in chromosomes 1A, 2A, 2B, 5A, 5B, and 6B. An F₂ mapping population of line 842-2 crossed with common wheat cultivar Skala was used for analysis of association of phenotypic and genotypic data. Adult plant leaf rust resistance was determined by loci in chromosomes 5B and 2A. The major locus transferred from *T. timopheevii* chromosome 5G mapped to the microsatellite interval *Xgwm408* – *Xgwm1257* controlled 72% of the phenotypic diversity in leaf rust response. The other, less effective gene was located on chromosome 2A at a distance of 10 cM from *Xgwm312*, accounted for 7% of the trait expression. Microsatellite markers located near these loci may be used for the transfer of these valuable genes to new lines and cultivars.

15. Association Mapping of Loci Conferring Resistance to Race TTKSK in Cultivated and Wild Barley Germplasm

BJ Steffenson¹, J Roy¹, H Zhao¹, Y Jin²

The threat that race TTKSK (Ug99) poses to wheat worldwide is well known and documented. However, this race also threatens barley throughout the world, including those cultivars carrying the durable rust resistance gene *Rpg1*. To identify and map loci conferring resistance to race TTKSK, we are using an association mapping approach in both cultivated (Barley Coordinated Agricultural Project or BCAP) and wild (Wild Barley Diversity Collection or WBDC) *Hordeum* germplasm. BCAP accessions were genotyped with 1,536 SNP markers and WBDC with 3,072 SNP and 558 DArT markers. Marked variation in the germplasm was observed in response to race TTKSK at the seedling stage, with some accessions exhibiting a high level of resistance. Association mapping analyses of BCAP germplasm identified resistance QTL on chromosomes 1H, 2H, 3H, 5H and 7H ($p=2.01E-07$ to $8.00E-04$, $r^2=1.4$ to 2.4%). The QTL on chromosome 5H was coincident with the previously identified resistance gene complex *rpg4/Rpg5*. In the WBDC germplasm, QTL for resistance were identified on all seven chromosomes ($p=0.000$ to 0.002, $r^2=2.9$ to 7.4%). Several identified QTL on chromosomes 5H and 7H were coincident with those found in the same region of the BCAP germplasm. Additionally, QTL were found coincident with both *Rpg1* on chromosome 7H and *rpg4/Rpg5* on chromosome 5H. This work documents the power of association mapping for identifying and mapping stem rust resistance loci in cultivated and wild *Hordeum* germplasm.

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16. R-Genes *Rpg4* and *Rpg5* are Required for Resistance to Stem Rust Race TTKSK in Barley

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We characterized a 70 kbp genomic region from barley containing two stem rust resistance genes, *rpg4* and *Rpg5*, conferring resistance to *Puccinia graminis* f. sp. *tritici* (*Pgt*) pathotypes QCCJ, MCCF and TTKSK (Ug99), and *P. g. f. sp. secalis* (*Pgs*) isolate 92-MN-90. *Rpg5* is a novel R-gene containing a nucleotide binding site (NBS)-leucine-rich repeat (LRR) domain in combination with a serine threonine protein kinase (STPK) domain. The predicted RPG5 protein has two putative transmembrane sites, possibly involved in membrane localization and potentially presenting the LRR domain outside the cell, while the NBS and STPK domains remain intracellular. High-resolution mapping, allele and recombinant sequencing identified *rpg4* as encoding an actin depolymerizing factor-like protein (ADF2). Both *Adf2* and *Rpg5* appear to be essential for resistance against the *Pgt* pathotypes, but not the *Pgs* isolate. A possible hypothesis for *Adf2* gene function is that it might be modified by fungal invasion, activating *Rpg5* to initiate signal transduction pathways resulting in resistance. An alternative hypothesis is that *Adf2* controls actin networks that may be redirected by the fungus to obtain nutrients from the plant via a haustorial-plant interface. If the *adf2* gene is inactive or inappropriately active, the actin network required to feed the fungus might fail leading to resistance. The recessive nature of *rpg4* makes the alternative hypothesis appealing. Study of the *rpg4/Rpg5* locus may provide insight into how stem rust maintains its biotrophic life style on its host to possibly be utilized in disease management strategies.

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17. Slow Rusting Resistance to Stripe Rust and Leaf Rust in Indian Wheat Genotypes Under Artificially Inoculated Conditions

MS Saharan, AK Sharma

Stripe (yellow) rust and leaf (brown) rust of wheat are important wheat diseases worldwide, including India. Slow-rusting resistance is a useful type of rust resistance. Sets of wheat genotypes in advanced breeding trials numbering 220 (150 advanced entries and 70 checks), 247 (180 advanced lines and 67 checks) and 228 (154 advance lines and 74 checks) were inoculated with bulked prevalent pathotypes of *Puccinia striiformis tritici* (Indian designations 67S8, 47S102, 46S103, 70S69, 46S119, 78S84) and *P. triticina* (Indian designations 12-2, 77-2, 77-5, 104-2) at Karnal during the 2005-06, 2006-07 and 2007-08 crop seasons, respectively. The rust intensities recorded at equal intervals were computed to relative Area Under the Disease Progress Curve (AUDPC) values, and the genotypes were categorized into four groups. Group I included genotypes exhibiting AUDPC values <1% of the susceptible checks Bijaga Yellow (AUDPC 2,000) for stripe rust and Agra Local (AUDPC 2,000) for leaf rust. Genotypes exhibiting AUDPC values for stripe rust in the range of 1-100, 101-200 and 201-500 were allocated to: Group II (2 genotypes in 2005-06, 15 in 2006-07, 16 in 2007-08); Group III (12 genotypes in 2005-06, 27 in 2006-07, 14 in 2007-08); and Group IV (48 genotypes in 2005-06, 57 in 2006-07, 27 in 2007-08). Similarly, of 220 genotypes evaluated during 2005-06 for leaf rust, 39, 5 and 9 genotypes were placed in Groups II, III and IV, respectively. During 2006-07, of 99 genotypes evaluated for leaf rust, 5, 27 and 22 were placed in Groups II, III and IV, respectively. During 2007-08, 13, 9 and 17 genotypes were in the Groups II, III and IV, respectively. Thirteen (WH 542, HD 2932, K 9107, HS 295, PBW 373, PBW 502, MACS 3313, GW 1189, NIDW 295, VL 882, VL 804, RAJ 3765 and HD 2833) and eight genotypes (HS 490, VL 829, HD 4717, PBW 175, PBW 373, WH 542, HUW 234 and MP 1203) generated AUDPC values of 101-500 (groups III and IV) for both rusts during 2006-07 and 2007-08, respectively. Group III and IV genotypes were characterized as partially resistant as these genotypes exhibited AUDPC values less than 50% of the checks.

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18. Identification of Chromosomal Regions Determining Leaf Rust, Yellow Rust and Stem Rust Resistances in CIMMYT Germplasm Through Association Mapping

SA Herrera-Foessel¹, RP Singh¹, J Crossa¹, J Burgeno¹, S Bhavani¹, J Huerta-Espino², S Dreisigacker¹, PK Singh¹ and D Singh¹

A historical set of 170 bread wheat (*Triticum aestivum*) lines originating from the CIMMYT 1st, 6th, 10th, 20th and 24th elite spring wheat yield trials (ESWYT) were evaluated for resistance to leaf rust (LR) (caused by *Puccinia triticina*) and stripe rust (YR) (*P. striiformis* f. sp. *tritici*) in field trials established in Mexico in 2007, and to stem rust (SR) (*P. graminis* f. sp. *tritici*) in Kenya in the off- and main seasons in 2008 under high disease pressure using prevalent races. In addition, leaf rust resistance genes present in these wheat lines were postulated from seedling reaction data obtained in the greenhouse using 13 Mexican *P. triticina* races. The ESWYT set was used previously for identifying genomic regions associated with resistance to the three rusts and other traits utilizing phenotypic data collected between 1979 and 2004, and genotypic data generated through Diversity Array Technology markers (DARs) (813 in total) together with 831 other markers. In this study, association analyses were conducted using new rust data and the previously available genotypic data. We used the mixed model for association analyses incorporating the relationship matrix comprising the coefficients of parentage among lines and the population structures. This increases the power of detecting more reliable marker-trait associations. Results reveal that markers identified to be associated with resistance to all three rusts were located on chromosome arms 1AS, 1AL, 3BS, 3BL, 4AL, 4BL, 5BS, 5BL, 6BS, 7AS, 7BL, and 7DS. Additional markers associated with rust resistance were located on the short arms of 1B (LR, YR), 2A (YR), 2B (SR), 2D (LR), 4B (LR, SR), 4D (LR), 5A (YR), 6A (SR), 7B (SR), and on the long arms of 1B (YR, SR), 1D (YR, SR), 2A (SR), 2B (LR, SR), 3A (LR, SR), 5A (LR), 6A (LR, SR), and 7A (LR, SR). The identified genomic regions carrying resistance genes are being verified through further genetic analyses.

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19. Resistance to Wheat Stem Rust in Triticale (*X Triticosecale*)

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Triticale (*X Triticosecale*) is an amphiploid between wheat (*Triticum aestivum*) and rye (*Secale cereale*) developed as a crop in the late 20th century, and it is grown commercially mostly in Europe, China, Australia and South Africa. Triticale is an excellent source of resistance to wheat stem rust as several stem rust resistance genes have been described. A collection of 567 triticale accessions from 21 countries was evaluated at the seedling stage for resistance to several races of *Puccinia graminis* f. sp. *tritici* with broad virulence ranges, including TTKSK, TRTTF, and TTTTF. A high frequency of resistance to race TTKSK was observed; 417 (73.5%) exhibited low infection types ranging from 0; to 2. Based on infection types, we postulated genes *Sr27*, *SrSatu* and other known or predicted *Sr* genes of rye origin. Accessions exhibiting resistance to races TTKSK, TRTTF, and TTTTF were further characterized for reaction to other races in the TTKS lineage and additional US races. Several resistant accessions from diverse geographic origins and exhibiting different infection types were selected as parents to develop crosses in an attempt to determine the genetic control of resistance to race TTKSK.

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20. Characterisation of a Leaf Rust Resistance Gene Transferred into Wheat from *Aegilops speltoides*

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Wheat leaf rust can be controlled by host resistance. Relatives and progenitors of wheat have been abundant sources of leaf rust resistance (*Lr*) genes. Effective *Lr* genes were transferred from *Aegilops speltoides* to wheat by J. Dvorak and D. Knott. Subsequently, P. Dyck produced a near-isogenic line (RL6161) carrying this gene in a Thatcher background. To further characterise the resistance in RL6161, agronomic, quality and genetic tests were undertaken. Compared to the recurrent parent (Thatcher), RL6161 showed no penalty in yield or quality that sometimes accompanies alien transfers. Monosomic analysis placed the *Lr* gene on chromosome 1B. A doubled-haploid population from the cross Thatcher / RL6161 was tested with microsatellite markers specific to chromosome 1B and the results showed that the *Ae. speltoides* DNA carrying the *Lr* gene was linked to markers on the long arm. Preliminary mapping data showed that recombination occurred between the *Ae. speltoides* and wheat DNA. Therefore, lines with reduced introgression size can be identified and used as sources of resistance in breeding populations. Whereas the uniqueness of the resistance in RL6161 is not known, it is possible that the resistance gene is *Lr51*, or an allele, since *Lr51* was also transferred from *Ae. speltoides* to wheat chromosome 1BL. Experiments to demonstrate the relationship between the two resistance sources are in progress.

21. Mapping of New Sources of Resistance to *Puccinia graminis* f. sp. *tritici* Race Ug99

S Bhavani¹, RP Singh¹, J Huerta-Espino², D Singh¹, Y Jin³

One of the best approaches to alleviate the threat from *Puccinia graminis tritici* race Ug99 (TTKSK) is to identify and characterize sources of resistance within the available wheat (*Triticum aestivum*) breeding materials and commercial cultivars. Genes identified can then be deployed in combinations. Identification of molecular markers tightly linked to resistance genes can aid their pyramiding, and allow selection of plants without the need for disease screening. This is especially important with Ug99 and its derivatives, which are absent in many countries. F₃ and F₄ populations derived from the crosses of susceptible PBW343 with three resistant parents with race-specific resistance genes were developed and characterized for reaction to TTKSK in the greenhouse at USDA-ARS CDL, St. Paul, MN; and, during 2008, in the field at Njoro, Kenya, where the *Sr24* virulent Ug99 variant. Bulk-segregant analysis was performed to identify marker trait associations and the linked markers were used for genotyping lines clearly identified in field trials as homozygous resistant and homozygous susceptible. Genomic regions with 3 putative new resistance genes, temporarily designated as *SrA*, *SrB* and *SrC* were identified. Gene *SrA* was mapped on chromosome 3DL (linked markers, *Xgwm52*, *Xgwm341*) of Milan/Sh47/3/Thb/CEP7780//Sh4/Lira/4/Sh4/Chil, *SrB* on chromosome 3BS (*Xgwm566*, *Wmc231*) of Ning9415/3/Ures/Bow//Opata/4/Ningmai 7, and *SrC* on chromosome 5DL (*Xgwm292*, *Xgwm212*) of Chen/Ae.Sq//2*Weaver/3/Oasis/5*Borl95. Like several other characterized stem rust resistance genes, the three new resistance genes provide moderate levels of resistance at the seedling and adult stages. Further studies to confirm the results and development of targeted mapping populations to identify closely linked markers are under progress.

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22. Allosyndetic Recombinants of the *Ae. peregrina*-Derived *Lr59* Translocation in Common Wheat

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The wild relatives of wheat constitute a valuable source of rust resistance genes that can be utilized in breeding. Translocation of desirable genes from wild species inevitably results in co-transfer of un-needed alien chromatin. The *Lr59* translocation appears to involve the complete long arm of chromosome 1A. An attempt was made to replace some of the *Aegilops peregrina* chromatin with wheat chromatin through induction of homoeologous chromosome pairing by deleting *Ph1*. Resistant testcross F1 plants were characterized for the presence of three mapped wheat microsatellite loci and a newly discovered SCAR locus that maps to the *Lr59* translocation. Within the mapped region primarily single crossovers occurred, as expected with homoeologous chromosome pairing. Overall, the recombination data were reflective of comparatively regular pairing of highly homoeologous chromosome region. Strong segregation distortion resulted in the recovery of an abnormally high frequency of recombinants. Eight of the 160 resistant recombinants had recovered wheat chromatin at each of the four marker loci and apparently retained comparatively short terminal segments of foreign chromatin. The latter plants were used in a search that identified 12 anonymous AFLP loci that could be used for continued mapping. The data obtained suggested reduced homoeology between 1AL and the *Lr59* translocation in the distal chromosome regions, most likely due to the presence of a paracentric inversion. Up to six or seven of the eight shortest recombinants may have been produced through crossing over within an inversion loop and are thus genetically imbalanced. Development and field evaluation of near-isogenic lines of five of the eight recombinants will be necessary to identify those that retained the shortest balanced translocations.

23. Stem Rust Resistance in *Triticum monococcum* Germplasm

M Rouse¹, B Steffenson¹, Y Jin^{1,2}

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, has been effectively controlled through the use of genetic resistance. The recently identified race TTKSK (Ug99) possesses virulence to many resistance genes that have been used in wheat breeding worldwide. One strategy to aid breeders in developing resistant varieties is to provide resistance genes transferred from wild relatives to wheat. Stem rust resistance genes *Sr22* and *Sr35*, derived from *Triticum monococcum* are effective against race TTKSK. In order to identify additional genes from this relative of wheat, we screened 1,062 accessions of *T. monococcum* deposited in the National Small Grains Collection against TTKSK and two additional races with broad virulence. We identified 625 accessions (58.85%) with resistance to TTKSK with infection types ranging from 0 to 2+. Among these resistant accessions, 90 accessions (8.47% of the total) were also resistant to TTTTF and TRTTF. Results from the preliminary screening suggested that new resistance genes are likely to be present in *T. monococcum*. These resistant accessions are being characterized further by testing with additional stem rust races. Crosses among selected resistant *T. monococcum* accessions have been initiated to determine the number and allelic relationships of stem rust resistance genes.

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24. Toropi, a Source of Leaf Rust Resistance Genes in Wheat

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Leaf rust is one of the most prevalent diseases in wheat and is found almost everywhere wheat is grown. The most cost effective method to control leaf rust is resistance. Sixty one leaf rust resistance loci have been formally designated. Most leaf rust resistance genes are race-specific. Some adult plant sources and resistance genes have provided more durable protection than many genes expressed at the seedling stage. Toropi, a Brazilian cultivar released in 1965, and grown extensively for 15 years, has maintained its resistance for over 40 years. Two complementary recessive genes on chromosomes 1AS and 4DS were identified when *P. triticina* virulence phenotype LCG-RS was used as the test culture. The objective of our study was to identify, characterize, and fine map the leaf rust resistance genes in Toropi. Resistant lines derived from crosses between Toropi and susceptible parent IAC 13-Lorena, and both parents, were inoculated at the seedling and adult stages with isolates of six *P. triticina* pathotypes (BBBD, TDBG, TBBJ, MGBJ, MBDS, MBRJ) and with a mixture of pathotypes. The results achieved to date demonstrated that Toropi has at least one race-specific seedling resistance gene and three adult plant resistance genes, two of which are non-specific-race specific. Crosses between Toropi and Thatcher are being made to develop a new mapping population to better characterize the source of resistance present in Toropi and to map the resistance genes.

25. Sources of Resistance to the Ecuadorian Yellow Rust Population in Bread Wheat Germplasm of CIMMYT

J Ochoa, E Falconí

Resistance to yellow (stripe) rust (caused by *Puccinia striiformis* f. sp. *tritici*) (YR), the major threat to bread wheat (*Triticum aestivum*) in commercial varieties in Ecuador, has been ineffective so far. New sources of resistance available in CIMMYT germplasm, the basis of the Ecuadorian breeding program, should be efficiently exploited. With this consideration and taking the advantage of the rapid evolution of YR in Ecuador, systematic selection and characterization of the resistance sources in CIMMYT germplasm were carried out at INIAP, near Quito, Ecuador. In 1995, 104 of 2,812 CIMMYT lines were selected with disease severity equal to, or lower than, 30%. These lines, together with modern Ecuadorian cultivars were evaluated at the seedling and adult stages to the races 110 E207, 198 E10 and 7 E8 in 1996, 1997 and 2000, respectively. As a group these races carry the individual virulences identified so far in Ecuador. Most of the lines, initially selected, were susceptible to at least one of the races, whereas 32 lines carried effective levels of resistance to all three races. In the following years, the responses of some of the promising lines or derivatives were monitored in the field, and in year 2008, also at the seedling stage. Effective seedling resistances were identified in Milan, Catbird, Corrydon, SW89.3243, SW89-1862, Chuanha 118 and Child, among which at least the resistances in Milan and Catbird have remained effective over many years. Similarly, the adult plant resistances in Chum 18 and Tinamou were confirmed to be effective, and results indicated that PF74354, IAN8/FINK'S', ALUCAN/YMI#6, ALDAN/IAS58 might also have adequate resistance. Residual resistance levels in Burrion, NANJING8331/3/SUZ10//ALD/PVN and GZ156/NAC//PSN/URES as well as of the commercial cultivars INIAP-Altar and INIAP-Quilindaña are comparatively high. These studies identified new and different types of resistance which will help in improving the management of YR in Ecuador.

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26. Attempts to Remove Gametocidal Genes Co-Transferred With Rust Resistance from *Aegilops speltoides*

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Transfers of rust resistance genes from *Aegilops speltoides* are often accompanied by completely linked gametocidal (*Gc*) genes that preclude their commercial utilization. Two such introgressions, S13 (with resistance genes *LrS13*; *YrS13* and *SrS13*) and S24 (with *SrS24*), were studied with the aim to separate the *Gc* and resistance genes. Evaluation with western Canadian pathotypes of *Puccinia triticina* and *P. graminis* f. sp. *tritici* races showed that the S13 genes are worth exploring, whereas the *SrS24* source is susceptible to one Canadian pathotype. Attempts to remove *Gc* genes were nonetheless continued with both introgressions as it also provided for a better understanding of *Gc* mechanisms. An attempt to rid S24 of *Gc* genes through homologous chromosome pairing and rigorous selection for increased fertility was unsuccessful and the fertilities of the better selections could not be maintained in subsequent generations. The S13 introgression was mapped to chromosome 3A with the use of wheat marker loci following which allosyndetic pairing induction was attempted. This produced seven putative primary recombinants. Following microsatellite mapping, the best recombinant (04M127-3) was identified. Resistance in this recombinant had exchanged a small region of intercalary donor chromatin for wheat chromatin, but was still associated with somewhat reduced *Gc* effects. Selection 04M127-3 was crossed with wheat and then testcrossed. The progeny yielded a total of 35 resistant progeny, all of which were secondary recombinants. Microsatellite and DArT markers showed that the recombinants were similar, and that in each, a major portion of the *Ae. speltoides* chromatin was replaced with wheat chromatin. Both *YrS13* and *SrS13* were lost together with the exchanged chromatin. Preliminary

indications are that the *Gc* system had largely broken down in some of the secondary recombinants; however, these need to be characterized further to find the most useful recombinant for continued exploitation. The nature of the recombinants produced in the two S13 experiments suggests that a complex multigenic interaction governs the gametocidal response, explaining why it is so difficult to dismantle. However, it appears possible to completely separate the gametocidal genes from *LrS13*.

27. New Sources of TTKSK Resistance Derived from *Thinopyrum* and *Aegilops* Species

SS Xu¹, Y Jin²

Several stem rust resistance genes derived from *Thinopyrum* and *Aegilops* sources are highly effective against race TTKSK (Ug99) of *Puccinia graminis* f. sp. *tritici*. We evaluated and characterized the seedling resistances to TTKSK of 62 wheat lines derived from crosses of common wheat or durum with the grass species *Th. junceum*, *Th. intermedium*, *Th. bessarabicum*, *Th. elongatum*, *Th. ponticum*, *Ae. caudata*, and *Ae. speltoides*. Thirty four wheat-alien species derivatives had resistance to TTKSK. Comparisons of the wheat-alien species derivatives and their parental lines for reactions to different stem rust races suggested that several lines, including seven wheat-*Th. intermedium* amphiploids, one wheat-*Th. ponticum* amphiploid, six durum-*Ae. speltoides* amphiploids, one wheat-*Th. junceum* disomic addition line, two wheat-*Ae. caudata* disomic addition lines, and a wheat-*Th. bessarabicum* 7J disomic addition line, may carry novel genes for TTKSK resistance. These lines will be useful for introducing the resistance genes into wheat. Research efforts are currently underway to introduce the resistance genes into wheat genomes through *ph1b*-induced homoeologous recombination.

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28. Haplotyping New Sources for Stem Rust Resistance in Wheat Using Available Markers

LX Yu, ME Sorrells

Stem rust is one of the most serious diseases of wheat. The recent emergence of wheat stem rust race Ug99 threatens global wheat production. The development of durable and effective disease resistant wheat varieties is our primary goal. To develop and optimize markers for stem rust resistance, a survey of available stem rust resistance genes including those conferring resistance to Ug99 has been completed in our group. All mapped major stem rust resistance genes were characterized for source, markers available, current research activities, and prioritized for this project (<http://rustopedia.get-traction.com/traction>). We screened 58 markers for 23 stem rust resistance genes among 24 randomly selected wheat lines. About 80% of the markers showed PCR products. Of those amplified, 75% showed polymorphism. We then performed haplotyping analysis with selected polymorphic markers among 248 wheat lines. To date, 15 markers associated with major resistance genes, including Sr1A1R, Sr2, Sr9a, Sr13, Sr17, Sr22, Sr24, Sr32, Sr36, Sr40 and Sr44 were analyzed. Preliminary analysis of haplotyping data from 15 markers, using PCR amplicons, generated a group of haplotypes among the diverse wheat lines. Phylogenetic analysis using the same data showed 3 major and 12 minor clusters. More markers will be used for haplotyping stem rust resistance among those wheat lines, and statistical tools such as association and regression may provide a way for Sr genotypic prediction.

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29. Molecular and Pathological Characterization of Slow Rusting Against Leaf Rust in Common Wheat

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Rust diseases, especially leaf rust caused by *Puccinia triticina*, are globally important fungal pathogens of wheat and may cause significant yield losses of up to 40% or more, worldwide. Due to rapid changes in pathogen races, single gene resistances are generally short lived when deployed in wheat cultivars. A more durable form of resistance, known as slow leaf rusting, has been identified and characterized in some genotypes.

Genetic studies indicate that slow rusting resistance is under polygenic control with moderate to high heritability. Such resistance, also known as adult plant resistance (APR), is controlled by minor genes. Although 10-12 slow rusting genes are present in CIMMYT spring wheats, only two such genes, *Lr34* and *Lr46*, have been characterized. Fifteen wheat genotypes, including twelve CIMMYT lines, two elite Indian wheat cultivars, HUW 234 and HUW 468, and one known leaf rust susceptible cultivar, Agra Local, were included in the present study. These lines were firstly evaluated under field conditions for disease severity, latent period and incubation period. They were subsequently evaluated under controlled laboratory conditions using a detached leaf technique with three pathotypes, designated 29R45 (12-5), 121R63-1 (77-5) and 21R55 (104-2). They were also tested in the field. Genotypes, G-5, G-11, G-12 and G-13 showed the lowest disease severities, very close to immunity, against all three pathotypes. In addition, 10 tightly linked microsatellite markers were also used to characterize the 15 lines for presence or absence of the known slow rusting leaf rust resistance genes.

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30. Quantitative Trait Loci for High-Temperature Adult-Plant Resistance to Stripe Rust And Molecular Mechanisms of the Durable Type of Resistance

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High-temperature, adult-plant (HTAP) resistance expresses when the weather becomes warm and as plants grow older, has been used successfully to control stripe rust of wheat caused by *Puccinia striiformis* f. sp. *tritici* in the Pacific Northwest and other regions of the U.S. since the 1960s when Dr. Vogel developed the semi-dwarf wheat cultivars 'Gaines' and 'Nugaines' with partial resistance. Leading cultivars with adequate levels of HTAP resistance were developed over later years. Recently, we identified and mapped several genes, or quantitative trait loci (QTL), for HTAP resistance in commercial wheat cultivars and genotypes. A major QTL (gene) in 'Alpowa' spring wheat, named *Yr39*, was mapped to the long arm of chromosome 7B. A major QTL (*Qyrlo.wgp-2BS*) in 'Louise' spring wheat was mapped on chromosome 2BS. A major QTL (*Qyr8.wgp-2DS*), tightly linked to the race-specific all-stage resistance gene *Yr8*, was mapped on chromosome 2DS in the 'AVS/6*Yr8' NIL and its donor genotype, 'Compair'. Three QTL (*Qyrex.wgp-6AS*, *Qyrex.wgp-3BL*, and *Qyrex.wgp-1BL*) were mapped on chromosomes 6AS, 3BL, and 1BL, respectively in 'Express' spring wheat. Two QTL (*Qyrst.wgp-6BS.1* and *Qyrst.wgp-6BS.2*) were mapped in 'Stephens' winter wheat. Wheat lines completely free of stripe rust were developed through molecular marker-assisted pyramiding of HTAP resistance QTL from Alpowa and Express. HTAP resistance is durable because it is non-race-specific. Transcript profiling studies using microarrays revealed that more genes are involved in non-race-specific HTAP resistance than those involved in race-specific all-stage resistance. Different HTAP resistance genes share relatively few regulated genes compared to genes controlling all-stage resistance. Broader spectra of defense genes contribute to the molecular basis of non-race-specific, and therefore, durable types of HTAP resistance.

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31. Quantitative Trait Loci for Adult-Plant Resistance to Stripe Rust in a Recombinant Inbred Line Population Derived from a Stephens x Platte Cross

M Dolores Vazquez¹, A Heesacker¹, C James Peterson¹, X Chen³, K Ammar⁴, C Mundt², JM Leonard¹, O Riera-Lizarazu¹

Stephens wheat (*Triticum aestivum* L.) has been grown commercially in the U.S. Pacific Northwest for 30 years, in part due to its durable resistance to stripe rust (caused by *Puccinia striiformis* f. sp. *tritici*). This resistance is believed to be due to a combination of genes or quantitative trait loci (QTL). The location and role of most of these loci are unknown. To better understand the genetic basis of stripe rust resistance, diversity arrays technology (DArT) and simple sequence repeat (SSR) markers were used to construct a linkage map. This map was based on 160 recombinant inbred lines (RILs) from a cross between Stephens and Platte, a stripe rust susceptible hard white winter wheat from the U.S. Great Plains. This population was also assessed for stripe rust response at four U.S. locations (Corvallis, OR; Pendleton, OR; Mt. Vernon, WA; and Whitlow, WA) and at one location in Mexico (Toluca, MX). Quantitative trait analysis revealed loci that were significant across environments on chromosomes 2A, 4B, and 7A, explaining 15, 20, and 16% of the phenotypic variance, respectively. The QTL on chromosome 4B was contributed by Platte and was significant in the Oregon locations, Toluca, Mexico, and Whitlow, WA. QTL on chromosomes 1A and 5A gave resistance only at the two Washington locations. These results indicated that QTL of moderate effect contribute to resistance in this population and that there were QTL x environment interactions. Because our linkage map is based mostly on DArT markers, additional genotyping is ongoing to identify breeder-friendly markers for marker-assisted selection. A more thorough assessment with additional phenotypic data is ongoing.

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32. Genetic Analysis of Wheat Leaf Rust Resistance Associated with the Solid Stem Trait

BD McCallum¹, FR Clarke², RE Knox², RM De Pauw²

The solid stem trait conditions resistance to wheat stem sawfly (*Cephus cinctus* Nort.) which causes major losses in some areas. Improved resistance to wheat leaf rust (*Puccinia triticina*) was observed when the solid stem character was transferred into wheat from a synthetic hexaploid, *Triticum turgidum* L. var. durum cv. Golden Ball/*Triticum tauschii*. The solid stem trait was backcrossed into the cultivar AC Elsa and lines with solid stem were more leaf rust resistant than the recurrent parent. To investigate the genetic basis of this resistance both AC Elsa and an AC Elsa backcross line with solid stem were crossed to the leaf rust susceptible cultivar Thatcher. The F₁s were backcrossed to Thatcher. Preliminary results suggest that AC Elsa has two seedling resistance genes, whereas the AC Elsa backcross solid stem line has three. However, both backcross populations appeared to have only one main resistance gene effective in adult plant field trials. This effective gene is likely *Lr34* based on marker and phenotypic data. Additional genes in the solid stem AC Elsa backcross line enhanced the level of rust resistance in progeny with *Lr34*, but were not effective in isolation.

33. A Major QTL for Leaf Rust Resistance, Widely Exploited in Durum Wheat Breeding, Maps on Chromosome 7BL

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Linkage and association mapping were used to investigate the resistance to leaf rust (*Puccinia triticina* Eriks.) from Creso and its derivatives. Creso's leaf rust resistance in durum wheat has remained effective since 1975. A Colosseo (C; resistant cultivar derived from Creso × Mexa) × Lloyd (L; susceptible) population and a panel of 164 elite accessions suitable for association mapping were tested under both seedling (greenhouse) and adult plant (open field) conditions with isolates of diverse origin. Field experiments were conducted in northern Italy (Argelato, Bologna), using inoculum of a mixture of Italian isolates, and in Mexico (El Batán and Obregon), where plants were challenged with Mexican *P. triticina* races BBG/BN and BBG/BP. Infection type responses in seedlings were recorded for isolates from Italy, central Europe, Ethiopia, Israel and Mexico. A major QTL (*R*² up to 77%) for both the adult plant and the seedling-responses was mapped in C×L on chromosome 7BL in a 5 cM interval (Maccaferri et al (2008); TAG 117:1225-1240). This chromosome region was the only one with markers consistently associated to leaf rust resistance at *P* = 0.001 in all five field trials. Candidates for the 7BL QTL include *Lr14a* (Herrera-Foessel et al. (2008) Plant Disease 92:469-473), a major hypersensitive leaf rust resistance gene introgressed from emmer wheat. Further genetic and molecular work is underway at DiSTA and PSB to fine map and eventually clone this QTL.

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34. Screening of International Wheat Germplasm for Multiple Disease Resistances in Morocco

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There are many biotic constraints to wheat production in Morocco. While leaf rust and *Septoria tritici* leaf blotch were known from early times, yellow (stripe) rust appeared in the area near the Atlas Mountains during the late 1980s. It recently spread to other cereal-growing areas, probably because of changes in virulence patterns (eg, *Yr9* is no longer effective). Hence, a search for multiple diseases resistances in wheat cultivars is a major objective. The best lines from international nurseries were screened to widen the genetic base for wheat crop improvement. Since diseases are not regularly expressed under field conditions, testing with local pathogen populations under controlled conditions was carried out for some nurseries. The objective of this study was to identify wheat lines from international nurseries that carry simultaneously adult-plant resistances to leaf rust, yellow rust, and *Septoria tritici* leaf blotch. Severities and reaction types for leaf rust and yellow rust, and pycnidial coverage for *Septoria* under field conditions, and latent period and severity of *Septoria* under greenhouse conditions, were scored. A high frequency of multiply resistant entries was observed among these accessions, reinforcing the importance of international co-operation.

35. Introgression of Resistance to Wheat Stem Rust Race TTKSK from Sharon Goatgrass into Wheat

E Millet¹, PD Olivera², BJ Steffenson²

Sharon goatgrass (*Aegilops sharonensis*) is a wild cereal endemic to the coastal plains of Israel. It is a diploid species ($2n=14$) and possesses the S^{sh} genome, which is closely related to the B genome of wheat. Sharon goatgrass exhibits a high frequency and level of resistance to a number of wheat diseases including leaf rust, stripe rust and stem rust. Many accessions of this species are also resistant to the widely virulent stem rust race TTKSK (Ug99). Gene transfer from Sharon goatgrass is not straightforward due mainly to a lack of homology between the alien and wheat chromosomes, and also to the presence in the wild species of gametocidal genes that prevent recovery of the pure wheat genetic background through backcrossing. We developed a method which combines the use of the *ph1* gene to promote pairing between homoeologous (partially homologous) chromosomes and an anti-gametocidal mutant gene to overcome the gametocidal effect. Production of wheat breeding material with a segment carrying the desired TTKSK resistance gene is under way. Selection of TTKSK resistant progenies during the transfer process will be aided by molecular markers linked to the gene.

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36. Stem Rust Resistance in *Aegilops tauschii* Germplasm

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Aegilops tauschii, the D genome donor of hexaploid wheat, has been used extensively for the transfer of agronomically important traits to wheat, including stem rust resistance genes *Sr33* and *Sr45*. In order to identify potentially new stem rust resistance genes in *Ae. tauschii* germplasm, we evaluated 530 non-duplicated accessions of *Ae. tauschii* deposited in the USDA National Small Grains Collection and Wheat Genetic and Genomic Resources Center collection, with races TTKSK (Ug99), TRTTF, TTTTF, TPMKC, QFCSC, and RKQQC of *Puccinia graminis* f. sp. *tritici*. Our preliminary results indicated that 33% of *Ae. tauschii* accessions were resistant to TTKSK with infection types ranging from ; to 2+. Based upon different compatibility phenotypes displayed to the various races by the resistant accessions, we postulated that novel resistant genes to race TTKSK are present in this species. Selected accessions are being backcrossed into wheat for the introgression of resistance to race TTKSK.

37. Resistance to Wheat Stem Rust in Spelt Wheat (*Triticum aestivum* ssp. *spelta*)

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Spelt wheat (*Triticum aestivum* ssp. *spelta*) is a hexaploid hulled wheat that was extensively cultivated in Europe until the early 1900s. This species has extensive genetic diversity, and the existence of several stem rust resistance genes were postulated by previous investigators. We evaluated a collection of 495 spelt wheat accessions at seedling stage for resistance to several races of *Puccinia graminis* f. sp. *tritici* with broad virulence, including TTKSK (Ug99), TRTTF, and TTTTF. Resistance with infection types 2 and 2+ to race TTKSK was found in 16 (3.3%) accessions. We observed a near complete association for resistance to the three races, suggesting that these spelt wheat accessions may share a common set of stem rust resistance genes. Accessions exhibiting resistance to races TTKSK, TRTTF, and TTTTF were further characterized for reaction to other races in the TTKS lineage and additional US races. Since spelt and bread wheat have the same genomic constitution (2n=6x=42; AABBDD), resistance to stem rust from spelt could be easily introgressed into bread wheat. We selected resistant accessions as parents to develop crosses in an attempt to determine the genetic basis of resistance to race TTKSK.

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38. Progress and Prospects in Discovery and Use of Novel Sources of Stem Rust Resistance

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A number of stem rust resistance genes derived from wild relatives of wheat appeared to be more effective against race TTKSK (Ug99) of *Puccinia graminis* f. sp. *tritici* than *Sr* genes of wheat origin. In an attempt to identify novel sources of stem rust resistance genes effective against TTKSK, we evaluated several cultivated and wild relatives of wheat for resistance to TTKSK and other stem rust races with broad virulence in seedling tests. Preliminary results indicated that TTKSK resistance was common, but the frequencies of resistant accessions varied between species. *Secale cereale* (533 accessions) and *Aegilops speltoides* (90 accessions) had the highest frequencies of resistance (nearly 100%). Other species having high frequencies of TTKSK resistance include triticale (74% of 567 accessions), *Ae. sharonensis* (69% of 107 accessions), *Triticum urartu* (97% of 186 accessions), and *T. monococcum* (61% of 1,020 accessions). Frequencies of TTKSK resistance in further species were: 18% in *Ae. tauschii* (114 accessions), 15% in *T. timopheevii* (298 accessions), and 17% in *T. dicoccoides* (153 accessions). Based on specific infection types to several races, known genes effective against TTKSK in some of these species were postulated. Accessions with putative new resistance genes were selected for crossing and introgressing resistances into wheat, and for developing mapping populations.

39. Wheat-Stripe Rust Interactions Involving 'Moro' Resistance

DA Gaudet¹, X Wang², B Puchalski¹, F Leggett¹, A Kuzyk¹, A Laroche¹

The wheat cultivar Moro possesses *Yr10*, which confers seedling resistance to *Puccinia striiformis* Westend. f. sp. *tritici* Eriks. race 44 E14 (European nomenclature) in Western Canadian soft white spring and winter wheats. Race CDL-29 (US nomenclature) is virulent and both races are also virulent on Fielder, but differ in aggressiveness. In a time-course study from 0 to 16 days post-inoculation (dpi), we studied compatible and incompatible stripe rust interactions in seedlings of Fielder and Moro inoculated with race 44 E14 and race CDL-29. We employed microscopy, DAB staining for detection of the oxidative burst, and qRT-PCR for expression of different PR-proteins. Penetration and early infection stages for the resistant cultivar Moro and the susceptible cultivar Fielder were similar for the first 9-10 dpi. In Moro, fungal development failed to progress beyond haustorium formation from 10-13 dpi, and the hypersensitive response occurred from 10 to 16 dpi. An oxidative burst at 6 and 14 dpi was recorded in the incompatible interaction compared to a single peak at 14 dpi in the compatible interactions. Differences in the time-course expression of the different PR-proteins were observed among treatments.

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40. Effect of Silencing Gene *Yr10* for Stripe Rust Resistance in Moro Wheat

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Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is a destructive disease of wheat worldwide and the development of resistant cultivars is the most economical control method. The *Yr10* gene in Moro wheat, that encodes a cytoplasmic NB-LRR protein containing nucleotide-binding sites (NBS) and leucine-rich repeats (LRR), imparts seedling resistance to stripe rust. Virus-induced gene silencing (VIGS) is a rapid and powerful tool to analyze the function of plant genes. We employed the barley stripe mosaic virus (BSMV)-VIGS system to study the function of different domains of the *Yr10* gene, in the resistance response in Moro wheat. A series of DNA fragments based on different domains of *Yr10* were inserted into BSMV-VIGS vectors. Moro wheat infection by *P. striiformis* following transfection with vectors was examined at the morphological, cytological and molecular levels. Susceptible responses consisting of pustule formation and symptoms of compatibility were observed in Moro leaves transfected with some of the fragments. We evaluated the expression of *Yr10* gene by probing different domains. The effects of changes in expression of *Yr10* on function of plant responses at the leaf and cellular levels will be presented.

41. Cloning And Characterization of *Avr1* Gene from *Puccinia triticina*

A Pacheco, H Zhang, DB Hays

Leaf rust is the most common, and one of the most important, cereal diseases of the world. Current leaf rust control in the U.S. consists of breeding for resistant cultivars by using identified *Lr* genes in the host. Cultivars with such genes usually become susceptible to infection due to the tremendous extant genetic diversity of the pathogen that allows it to overcome resistant cultivars in 2-4 years. Development of alternate methods of control is limited since little is known about *Puccinia* genomes and plant : pathogen interactions. Construction of a genome-wide physical map is important in order to fully understand the molecular basis of the infection mechanism of the pathogen and its interaction with the host. In an effort to discover more about the genetic potential of leaf rust in terms of AVR and VIR gene regulation, and to create future novel plant resistance breeding strategies, we have proposed a study of the pathogen genome by constructing a BIBAC library and a physical map of the pathogen. The BIBAC library is being constructed from the *P. triticina* type culture PRTUS 3 which has *AVR1* (avirulence gene corresponding to Lr1) disrupted using T-DNA mutagenesis via particle bombardment. The characterization of *AVR1* in the BIBAC library will serve as a point of reference for cloning heterologous AVR and VIR genes, and for defining their regulation and modes of inheritance and recombination.

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Theme 3:

Breeding Rust Resistant Wheat

42. Shortening the *Lr62/Yr42* Translocation in Common Wheat

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The *Lr62/Yr42* translocation (from *Aegilops neglecta*) in wheat consists of alien chromatin, and only the distal end of the wheat chromosome arm 6AL, including the telomere, is of wheat origin. Because the large amount of associated foreign chromatin prohibits commercial use of the resistance an attempt was made to remodel the translocation through allosyndetic pairing induction. Plants heterozygous for the translocation, but lacking the *Ph1* locus, were testcrossed with CS nullisomic 6A tetrasomic 6B (or 6D) plants. Resistant testcross F₁ progeny, were characterized with three markers (including a newly-developed SCAR marker, Sopw7) and the data were used to do a three-point genetic mapping analysis. It appeared that *Lr62/Yr42* is located towards the distal end of 6AS. Forty one recombinants were subsequently characterized with further microsatellite markers. The recombination data were complex and indicative of areas of homoeology between the wheat (CS *ph1b* mutant) and translocated chromosomes 6A; however, there was also evidence of major structural differences between the two chromosomes, including a duplication and a translocation. The structural differences led to the formation of irregular meiotic pairing structures. Single crossovers within these configurations produced complex segregation patterns that were difficult to interpret. It was, however, possible to explain the origin of the majority of recombination products, and to identify a subset of the most useful recombinants. DArT markers could be used to further discriminate among the selected recombinants and those that retain comparatively small regions of foreign DNA together with the *Lr62/Yr42* resistance genes and SCAR marker were kept for further use.

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43. Resistance to Stem Rust Race Ug99 in the Canadian Spring Wheat Cultivar 'Peace'

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is a highly destructive fungal disease of wheat. This pathogen has been effectively controlled in western Canada through resistance since the 1950s. In 1999, a new highly virulent race of stem rust was identified in Uganda. The new strain, named "Ug99", was given the North American race designation TTKSK. *In situ* screening has demonstrated that approximately 75% of Canadian wheat cultivars are susceptible to this new race of stem rust. Fortunately, two cultivars, Peace and AC Cadillac, were highly resistant to Ug99. A doubled haploid population was generated from the cross: RL6071/Peace, where RL6071 was the stem rust susceptible parent. In 2008, 189 DH lines from this population were evaluated for response to Ug99 in Kenya. RL6071 and Peace were rated: 80 S and 5 R, respectively. Disease ratings of the DH lines, ranged from 80 S to 1 R. Mendelian evaluation of the stem rust scores indicated a two-gene model ($X^2=5.51$; $0.25 < P < 0.10$; d.f.=3) of inheritance. Peace has the positive allele for the diagnostic *Lr34* DNA marker (csLVMS1) published by Spielmeier et al. (2008). It is believed that Peace carries *Lr34* and that this gene may be one of the genes responsible for Ug99 resistance in this cultivar. Molecular mapping of the Ug99 resistance in cultivar Peace is underway.

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44. Molecular Mapping of Rust Resistance Genes and Marker-Assisted Breeding in Wheat

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Molecular markers make possible the deployment of multiple rust genes in adapted elite lines. In this study we report a summary of the microsatellite tagging of a number of leaf rust, stem rust and stripe rust resistance genes from a variety of sources. Segregating Leichardt/WAWHT2071 and Sunland/Arrino populations were used for mapping *Lr13* and *Lr28* where Leichardt and Sunland were the respective sources of the resistance genes. Lines C77.19/3*77W:549-163658 and *Sr33/2*Shortim//4*3/Jacup* resistance lines were used as sources of *Sr32* and *Sr33*. F₂ and F_{2,3} populations were used for microsatellite tagging of the genes. Very closely linked SSR markers were identified for *Lr13*, *Lr28*, *Sr32* and *Sr33* on chromosomes 2BS, 4AL, 2BS and 1DS, respectively. Results from field-based studies of various mapping populations for the characterization of adult plant rust (APR) resistances from a variety of sources such as Wyalkatchem, Yitpi and Frame will also be discussed. Molecular markers for a range of other rust resistance genes (*Lr9*, *Lr19/Sr25*, *Lr24/Sr24*, *Lr34/Yr18*, *Lr46/Yr29*, *Lr47*, *Sr26* and *Sr36*) are currently being implemented for variety development and germplasm enhancement. The likely impact of these applications on wheat improvement will be discussed.

45. The Multi-State Rust Screening Nursery at Castroville, Texas, U.S.A.

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Wheat (*Triticum aestivum* L.) leaf rust (caused by *Puccinia triticina*), is a devastating foliar disease in the US Great Plains where short-lived, major gene resistances are mainly utilized. A hotspot rust screening nursery, established at Castroville, Texas, the forefront of the *Puccinia* pathway in the US, is a joint effort between Texas A&M University (TAMU), Oklahoma State University (OSU), and Kansas State University (KSU). It has grown into a 20 acre (8.3 ha) nursery has and now involves the participation of almost all wheat breeders from eight Universities and three USDA research centers across the US.

The nursery was mainly established to screen wheat for reaction to leaf rust, stem rust (caused by *Puccinia graminis* f. sp. *tritici* and stripe rust (*Puccinia striiformis*), as well as oats for reaction to crown rust (*Puccinia coronata*) and stem rust (*Puccinia graminis* f. sp. *avenae*). Heavy wheat leaf rust and oat crown rust infections are an annual event and reliable data are obtained on advanced experimental lines as well as established wheat and oat varieties. The nursery has also been utilized for selection of single plants from segregating bulks. A first look at promising resistant germplasm from CIMMYT was conducted in collaboration with OSU. This nursery has provided warnings regarding the weakening resistance of key Great Plains wheat cultivars.

Clearly, the rust screening nursery at Castroville has provided a rust screening hotspot for US breeders and has proven indispensable since its inception in 2000.

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46. Evaluation in Kenya of Global Diversity in Winter Wheat for Resistance to Stem Rust

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The International Winter Wheat Improvement Program (www.iwwip.org) is a joint project between the Ministry of Agriculture and Rural Affairs of Turkey, CIMMYT and ICARDA, and was established more than 20 years ago. The objective of the program is to develop facultative and winter wheat germplasm for the region of Central and West Asia. The materials address both irrigated and rainfed environments. IWWIP also facilitates global germplasm exchange of winter wheat by receiving breeding lines and varieties from our own and other programs, evaluating them, and distributing selected entries through the system of international nurseries. Four different international nurseries are distributed globally on an annual basis to more than 50 countries and more than 100 co-operators. Breeding for resistance to yellow (stripe), leaf and stem rust is high priority along with broad adaptation and grain quality. Due to the recent emergence of stem rust as a global threat, routine evaluation of winter and facultative germplasm in Kenya started in 2006. However, the pathogen population dynamics in Kenya and challenges with vernalization in an equatorial environment did not permit satisfactory screening until the summer cycle of 2008. Close to 700 entries representing germplasm from all continents and from major winter wheat producing countries were evaluated at KARI, Njoro, in October 2008. Two readings were taken with an interval of 10 days. Overall, 120 entries were selected with variable degrees of resistance. The evaluation data and resistant entries for the 15th and 16th FAWWON (Facultative and Winter Wheat Observation Nursery) and 10th and 11th IWWYT (International Winter Wheat Yield Trial) is available at the program web site. Additional disease data of germplasm not included in the nurseries is available from IWWIP upon request.

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47. Breeding for Rust Resistance in Winter Wheat in Szeged, Hungary

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Among the wheat rusts in Hungary, stem rust (caused by *Puccinia graminis* f. sp. *tritici*) caused large losses at the end of the 19th and the first part of the 20th centuries. Since 1950, the significance of the leaf rust (*P. triticina*) has increased steadily, and it is currently the most important wheat disease in the area. The occurrence and damage caused by yellow (stripe) rust (*P. striiformis* f. sp. *tritici*) is much less, the last epidemic occurring in 2001.

According to annual observations on near-isogenic lines in Hungary, leaf rust resistance genes *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr29*, *Lr35* and *Lr38*, and stem rust resistance genes *Sr36*, *Sr27* and *Sr31* provide effective resistances in the field. However, there is a lack of information on the effectiveness of adult resistances to yellow rust as natural infections are a rare occurrence.

We realized in the 1980s that *Sr36* provided a durable and high level resistance. As a result of extensive crosses with appropriate parental lines, *Sr36* resistance is present in a large proportion of the winter wheat varieties developed at Szeged, Hungary.

Besides the applied field research, molecular markers are increasingly being adopted in our breeding program. Tests using microsatellite markers on 220 cultivars registered in Hungary in the past 35 years showed that the frequency of *Sr31* resistance gene reached 49% (in 1994). The frequency peak for *Sr36* was 32% reached in 1983-84.

Although both *Sr36* and *Sr31* genes are still effective, the predominant use of one or the other might be dangerous.

We developed mapping populations using susceptible cultivars and leaf rust near-isogenic lines (*Lr9*, *Lr20*, *Lr29* and *Lr52*). Using these populations several RAPD, SSR and SCAR markers were identified for the genes.

Marker assisted selection was used to transfer these and other resistance genes and gene complexes (*Lr19/Sr25*, *Lr20/Sr15*, *Lr24/Sr24*, *Lr34/Yr18*, *Lr37/Yr17/Sr38*, *Lr46/Yr2*; *Lr21*, *Lr29*; *Sr36*, *Yr5*; *Yr15*) to cultivars developed at our institute.

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48. Breeding Leaf Rust Resistant Wheat Varieties in Martonvásár, Hungary

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Wheat in Hungary is threatened by all three rusts, viz. leaf rust, stem rust and stripe rust. All three diseases are capable of causing substantial economic losses, but their incidence varies due to their diverse ecological requirements. The greatest damage is currently caused by leaf rust, which infects wheat fields every year. The most environmentally sound, low cost method of controlling leaf rust is to breed and grow resistant varieties. Both traditional and molecular breeding methods are used to improve the leaf rust resistance of wheat varieties bred in Martonvásár, Hungary.

The field responses of wheat genotypes carrying designated *Lr* genes have been assessed for many years in order to determine the effectiveness of major leaf rust resistance genes. The 'Thatcher'-based near-isogenic lines, carrying single genes for resistance are sown each year. Eight NILs remain immune or highly resistant: these include lines with *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr28*, *Lr29*, *Lr35* and *Lr37*. The levels of infection on four further lines (*Lr23*, *Lr32*, *Lr3ka* and *Lr22a*) were also quite low. The line exhibiting the greatest degree of infection was the NIL carrying *Lr26*.

The segregating populations in the breeding program are tested and selected continuously under artificially inoculated conditions. A special nursery is devoted to testing the leaf rust resistance of advanced breeding lines, special genetic stocks and potential leaf rust resistance sources. The levels of resistance in the released and cultivated winter wheat varieties bred in Martonvásár, namely, 'Mv Magvas', 'Mv Marsall', 'Mv Toborzó', 'Mv Béres', 'Mv Matyó', 'Mv Vekni', 'Mv Laura' and 'Mv Lucia' at 0–20MR, are sufficient to negate the need for chemical control in farmers' fields.

Using marker-assisted selection (MAS), the resistance genes *Lr9*, *Lr24*, *Lr25*, *Lr29*, *Lr35* and *Lr37* were incorporated into four Martonvásár winter wheat varieties. A marker-assisted backcross program to track the transfer of effective *Lr* genes has begun. Wheat varieties susceptible or moderately resistant to leaf rust were crossed with NILs of 'Thatcher' each carrying a different *Lr* gene (*Lr9*, *Lr24*, *Lr25*, *Lr29* or *Lr35*) and with the variety 'Renan' (*Lr37*). Plants in the fifth backcross generation had agronomic traits resembling the recurrent parent.

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49. Combined Resistance to the Most Important Wheat Diseases in the Czech Republic

Alena Hanzalova, Jana Chrpova

All three rust diseases of wheat occur in the Czech Republic. Leaf rust is most frequent. The last stem rust epidemics occurred in 1972, and the last significant yellow (stripe) rust outbreak was in 1999-2001. Resistance breeding aims at combined resistance to all three rusts. Combined resistance was present in 11 of 29 tested new breeding lines recently tested. The highest resistance occurred in breeding line SG-S-469-07, followed by BR-05-082 and SG-S-316-06. On average the highest degrees of resistance were to yellow rust. Of the winter wheat cultivars registered in the Czech Republic, the highest combined resistance to all three rusts was in cultivars possessing the translocation from *Aegilops ventricosa* (*Yr17*, *Lr37*, *Sr38*). In addition to rusts, attention is also given to fusarium head blight, powdery mildew, tan spot, Septoria leaf blotch, Septoria glume blotch and BYDV (barley yellow dwarf virus). Ring tests are organized at several different locations to screen new breeding lines for resistance to the various diseases. Spreaders are inoculated when natural infection is not adequate.

50. Screening Wheat Germplasm for Resistance to Stem Rust in Georgia

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Stem rust was a major threat to wheat production in Georgia before the 1970s. However, promotion of stem rust resistant varieties, such as Bezostaiia 1, reduced its impact on production. Recently, there has been an increase in stem rust occurrence in some areas of Georgia. There is also a possibility that race Ug99 will eventually reach Georgia. Barberry is widespread in the country. Identification and promotion of rust resistant germplasm is an important strategy for wheat rust control, especially because the use of fungicides on wheat is not a common practice in Georgia. The objective of the present study

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was to identify effective rust resistance genes under the Georgian conditions and to select resistant genotypes for further utilization in breeding. The 2nd and 3rd ISRTN ICARDA-CIMMYT nurseries were tested in inoculated stem rust nurseries during 2006-7 and 2007-8 in Kobuleti, respectively. Resistance genes *Sr13*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr31* and *Sr36* were effective. However, in seedling tests, a level of virulence occurred for *Sr36* (0.3-2.9%). In 2007, the Ug99 Stem Rust Trap Nursery was planted in the Akhaltsikhe region in South Georgia, where stem rust occurs every year.

The search for resistant varieties began with screening of the Caucasian Regional Winter Wheat Nursery, which included 108 Georgian, Armenian, Azeri, Turkish and Russian varieties, for resistance to stem rust induced by inoculum collected across the entire wheat-growing area of Georgia. About 50% of entries were resistant. The same nursery was sent to Kenya for screening against Ug99. Only a few entries showed moderate resistance to Ug99, which was not confirmed after repeated testing in the following year.

The CIMMYT STEMRRS Nurseries were used to identify and promote stem rust resistance germplasm in Georgia. The 1stSTEMRRSN was tested in an inoculated rust nursery. Only 3.8% entries showed full resistance, but 70.5% were moderately resistant; the remaining 13.3% and 10.5% were moderately susceptible and susceptible, respectively. No selections were made as the nursery was planted in a non-wheat producing area where the environment was not conducive for the production of healthy grain. In the following season, the 2nd STEMRRSN was planted in the wheat-growing area, and the following lines were selected and advanced to the multiplication and agronomic assessment levels: Babax/Lr42//Babax*2/3/Brambling (6004), three sister lines of Babax/Lr42//Babax*2/3/Kuruku (6007, 6009 and 6012), Babax/Lr42//Babax*2/3/Vivitsi (6022), Croc_1/Ae.Squarrosa (205)//FCT/3/Pastor (6136), Thelin#2/Tukuru (6069), Waxwing*2/Kuruku (6086) and Canadian/Cunningham//Kennedy (6137).

The results obtained from the present study provided useful information for breeders on effective rust resistance genes and allowed for identification of resistant germplasm.

51. Wheat Breeding for Durable Rust Resistance in Pakistan

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Most of the major genes available for resistance to stem rust, leaf rust and yellow rust are currently ineffective. Wheat varieties released in Pakistan in the past possessed at least *Lr1*, *Lr10*, *Lr13*, *Lr23*, *Lr26*, *Yr9*, *Yr27* and *Sr31*. Virulences for all these genes, except *Sr31*, are widespread. Historical evidence has shown that resistances based on major genes have short duration of effectiveness whereas those based on minor genes have durability, e.g. Inqilab 91 and Lylpur 73. Numerous minor genes have been identified and it has been established that accumulations of 4-5 minor genes give resistance levels approaching immunity, whereas, 2-3 minor genes confer adequate levels of adult plant resistance (APR). At the Wheat Research Institute, Faisalabad, a project was launched in 1992-93 for the development of wheat varieties having minor gene-based resistance. Wheat germplasm was assessed for resistance by inoculating materials with diversified inocula and observing the rust development patterns for 2 or 3 years. Accessions carrying minor genes were identified and crossed following single cross, double cross, tropcross and backcross approaches for pyramiding minor genes for rust resistance. Segregating materials were evaluated in inoculated nurseries using the selected bulk method. Homozygous resistant lines selected in F_7 , were evaluated in replicated trials, in the different ecological zones of Pakistan. The most promising crosses were Wattan/2*Inqilab, Pb96/Wattan//MH97, Shalimar 88/2*Attila, Shalimar 88/ Wattan//MH97 and Luan/Kohistan. Two varieties Shafaq-06 and Lasani-08 were released to farmers and several lines having better resistance than the parents are in the pipeline. Shafaq-06 has high yield potential and durable types of resistance to yellow (stripe) rust and leaf rust. Lasani-08 has high yield potential and durable types of resistance to yellow rust, leaf rust and stem rust (including Ug99).

52. Breeding Rust Resistant Wheat Varieties in Tajikistan

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Wheat is the main staple food crop in Tajikistan and it is of increasing importance to develop high yielding varieties with disease resistance and good bread making quality. International collaboration has been established, and nurseries are received especially from the Turkey-CIMMYT-ICARDA International Winter Wheat Improvement Program (IWWIP), located in Turkey, but also more recently from Oklahoma State University in the USA.

Together with tan spot, yellow (stripe) rust is a major biotic constraint faced by wheat farmers in Tajikistan. Through a multilocation testing system, several high yielding and resistant lines were identified and are in the process of being released.

In order to test for resistance to race Ug99 in Tajik wheat germplasm a number of varieties and advanced lines were tested in Kenya in collaboration with CIMMYT. The results demonstrated a low level of resistance in Tajik germplasm, indicating an urgent need to initiate breeding activities to reduce the consequences of a possible incursion of Ug99 to Tajikistan. A collaborative project has been initiated with the Swedish Agricultural University to introgress novel genes for resistance to race Ug99 into Tajik wheat germplasm.

This paper evaluates the results of multilocation trials conducted during 2005, 2006 and 2007 through which high yielding and disease resistant lines were identified and recommended for submission to official variety testing trials. Furthermore, the paper discusses the future breeding strategy to increase the level of resistance to race Ug99 in Tajik wheat germplasm.

53. Identification of Stem Rust Resistance Germplasm in Kazakhstan

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Kazakhstan is one of the largest wheat producers in central Asia. Wheat rusts are important problems in our country. Stem rust, (pathogen, *Puccinia graminis* f. sp. *tritici*) causes considerable damage, especially in wetter years. In order to combat the menace of rust, screening of various nurseries from national and international breeding programs was initiated. The aim of the present work was to find sources of stem rust resistance and to develop disease-free germplasm. The material was screened with the predominant races in the region. Cultivar Steklovidnaya 24 was used as a susceptible check. A total of 55 wheat genotypes were included in the 2008 tests; 33 lines showed high or moderate levels of resistance in the field. Tests of the material under artificial conditions identified eight entries with stem rust immunity; viz. 86003/F9Norin10/Steklovidnaya24, 86004/F7322-MA/118-SI, 86006/F6KSI-21/Arthur, 86007/F6KSI-21/Arthur, 86018/Lawson/Currawong, 86019/Moro*2(C90)/More*2//Marcuis)2, 86022/F5Janbash/Anza, 86023/F4KLDN33/MK-3832, 86024/F4Tilek/KLDN-95. Two lines were characterized as moderately resistant; viz. 86005/F6 Progress/*T.monococcum* and 86008/F6KSI-21/97Sr25. Evaluation for agronomic traits allowed selection of 10 advanced lines with high yield potential and resistance to stem rust. Because Ug99 is virulent to the great majority of wheat varieties, we sent our promising material to Kenya for testing. Based on the results we will be able to develop cultivars possessing genes, or combinations of genes, effective against this widely virulent race of the pathogen.

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54. Employing Male Sterility Mediated Marker Assisted Recurrent Mass Selection in a Pre-Breeding Strategy for Accumulating Disease Resistance Genes

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A pre-breeding strategy based on the recurrent mass selection population developed by Stellenbosch University's Plant breeding laboratory (SU-PBL) is currently being implemented to enhance resistance against the most prevalent stem rust pathotypes occurring in the winter rainfall cereal production region of South Africa. The male sterility-mediated marker assisted recurrent mass selection (MS-MARS) scheme makes use of the dominant male sterility gene, *Ms3*, and hydroponic culturing in order to facilitate large scale hybridization of material. Male parents for this particular study were selected based on their resistance to three predominant *Puccinia graminis tritici* pathotypes, and the results obtained by molecular marker screening. The three pathotypes were 2SA88, 2SA100 and 2SA102. Markers were used to screen for the presence of *Sr2*, *Sr26* and *Sr36*. According to marker data, Kite, Songlen, Steenbras, Timgalen and Zaragoza carried *Sr2*. Only Songlen and Steenbras gave sufficient resistance to all three pathotypes. The two lines postulated to carry *Sr26*, Avocet and Eagle, both gave positive amplification for the relevant marker. The stem rust resistance reactions were also sufficient for breeding purposes. The female lines were all sourced from the SU-PBL's recurrent mass selection program. By using molecular markers for the identification of resistance gene complexes *Lr24/Sr24*, *Lr37/Sr38/Yr17* and *Sr31/Lr26/Yr9*, female lines were selected which carry all three complexes. In total 180 lines from the SU-PBL's RMS program were screened, and 11 were identified to carry all three complexes. Currently we are in the process of intercrossing the selected male and female parents.

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55. Pyramiding Slow Rusting Genes for Durable Resistance to Leaf Rust in Durum Wheat

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Variants of *Puccinia triticina* race BBG/BN, separately overcoming three resistance genes, were identified from durum wheat (*Triticum turgidum* ssp. *durum*) fields in northwestern Mexico since its introduction in 2001. Major genes available for use in breeding programs are limited and an alternative strategy is required. Previous studies indicated that slow rusting resistance in eight CIMMYT durums was determined by 2 to 3 minor genes with additive effects. Twenty-eight 4-way crosses were made between these lines with the aim of developing new germplasm with enhanced levels of resistance through pyramiding diverse minor genes. Plants in F₁ (4-way) through F₃ generations were selected for slow rusting under high leaf rust pressure at the Cd. Obregon and El Batan field sites in Mexico and spikes from selected plants were harvested as bulks. Plants in the F₄ generation were individually harvested and 1,843 advanced lines obtained, among which 106 lines with enhanced resistance, and desirable agronomic and grain characteristics were selected for non-replicated yield and leaf rust evaluation trials at Obregon during the 2007-2008 season. The best 19 lines, exhibiting near-immunity but with the presence of a few susceptible type pustules, parents and susceptible checks were evaluated for leaf rust resistance under very high disease pressure in replicated trials sown on two dates (16 May and 6 June) at El Batan during 2008. Spreader rows of susceptible cultivar 'Banamichi C2004', sown as border and as hills on one side of each plot, were inoculated with *P. triticina* race BBG/BP. Leaf rust severities, and host responses to infection were determined from weekly readings, and area under the disease progress curves (AUDPC) were calculated. Several lines were identified with significantly lower final leaf rust severity responses and AUDPC values than the most resistant parent in each cross. Our results show that enhanced levels of slow rusting can be generated by pyramiding diverse genes present in different parents. The trial is being repeated during the 2008-2009 season at Obregon to validate the results. In addition these lines are being used for transferring slow rusting resistance into high yielding, superior quality adapted backgrounds using the single-backcross approach.

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56. Stacking Leaf Rust Resistance Genes in Wheat Breeding Populations Using Telocentric Chromosomes

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Resistance to the wheat rusts is improved in level and durability when resistance genes are stacked. Selecting gene stacks in breeding populations by phenotype can be difficult or impossible and marker-assisted selection is expensive. Furthermore, when stacks are selected the effective size of the population is reduced thus limiting the available variability from which to select other characters. We propose using telocentric chromosomes to fix resistance gene stacks in breeding populations by selecting double monotelodisomic F₁ plants ($2n = 40 + t + t$) with the pair of resistance genes in the hemizygous condition. This method was demonstrated in two wheat populations, each with a different two-gene stack of leaf rust resistance genes. The presence of critical telocentric chromosomes in the populations rapidly drove stack frequencies toward fixation by a combination of selection for euploid pollen and zygotic selection for diploid and near-diploid (i.e. no ditelosomics) plants. Thus, telocentric chromosomes provide a tool to fix gene stacks in a population while maintaining the effective size of the population for selection on other criteria. One point of consideration is the relatively large size of the linkage blocks being fixed.

57. A Systemic Approach to Germplasm Development: a Simple Way to Reach a Complex Goal

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The fight against rusts relied heavily on major genes, but other genes also exist. Our own experience has been mostly with BYDV and FHB, both diseases having very complex genetics. Twenty five years of attempts to breed resistance based on major genes gave poor results. Then we undertook to seek simultaneous resistances to all diseases present in Eastern Canada. We thus breed against rusts, powdery mildew, BYDV and FHB. Using much more biodiversity and selecting intensively for resistance to all diseases should single out plants that resist nearly all diseases. Doing this, more than 99% of the germplasm was destroyed by diseases. Among 10,000 F₁ plants inoculated, one single cross combination gave the sought-after result. Within one year, we had introgressed in one genotype the FHB resistance of Sumai 3, very good BYDV and powdery mildew resistances, and rust resistance equal to that of the most resistant parent. Important lessons follow. The value of a gene source cannot be fully judged by its disease reaction because epistatic hidden genes can exist in any line. Making many crosses is the way to get the most out of the hidden genetics. A very severe, complex selection protocol can work. The method gave resistance to all Eastern rust races. BYDV tolerance correlated with yield and biomass potential. Applying a multiple-stress system to more rust species is worth a try. Good outcomes are expected in pyramiding slow rusting genes, and multiple genes form durable horizontal resistance. Multiple approaches constitute the best strategy address a disease that can ruin part of the world food basket.

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Theme 4:

Plant Protection and Seed Delivery

58. Initiatives and Progress Through Participatory Varietal Selection in Promoting Race Ug99 Resistant Wheat Lines on the Eastern Gangetic Plains

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The threat of stem rust epidemics caused by *Puccinia graminis* f. sp. *tritici* race Ug99 to the wheat crop on the northeastern Gangetic Plains is real. The warm and humid conditions experienced in the region are conducive to rapid disease development. Identification and breeding Ug99-resistant varieties are therefore major priorities for the region. Because of the underdeveloped seed industry and small farm sizes, various strategies are needed to disseminate resistant cultivars in a relatively short time before Ug99 reaches South Asia. Although the Indian wheat program, in collaboration with CIMMYT and KARI, has identified some existing resistant wheat varieties. The

areas they occupy must increase to about 5% of the total wheat area to ensure replacement of current popular varieties if necessary. In addition to national evaluation trials including advanced selections from all breeding programs, there are also farmers' participatory selection approaches in several districts in the eastern Gangetic Plains. Whereby new superior lines and newly released varieties are disseminated to farmers. The objective is to enhance genetic diversity and to provide more options to farmers. The inclusion of Ug99-resistant high yielding lines distributed during last three years (2006-2009) is enabling farmers and the region to prepare for future challenges. Some of the new lines included in this fast-track participatory approach have shown significant yield superiority over the highly popular variety HUW234, and better resistance or tolerance to other biotic and abiotic stresses that occur in the region. Moreover, the incomes of farmers, who choose to sell grain of their preferred varieties as seed, have also increased. Our results show that participatory variety selection of diverse promising lines and released varieties enables them to be disseminated to farmers in a way that enhances productivity and income simultaneously.

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