

**BGRI 2010 Technical Workshop  
Poster.Abstracts**

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# Borlaug Global Rust Initiative 2010 Technical Workshop Poster Abstracts

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## POSTER ABSTRACTS

### 1. Achievements of stem rust screening facilities in east Africa

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The east-Africa stem rust phenotyping screening facilities were established in 2005 under the auspices of Borlaug Global Rust Initiative (BGRI) in Kenya and Ethiopia to alleviate threat of Ug99 lineage on national and international wheat production, and the world's vulnerability to evolving stem rust races by evaluating germplasm for new sources of resistance, to incorporate them in breeding programs, and deploy them as durably resistant varieties. Since the establishment, the stem rust screening programs of Kenya and Ethiopia have screened more than 100,000 advance breeding lines, identified diverse sources of resistance including adult plant resistance based on minor genes, and initiated comprehensive shuttle breeding and seed multiplication program. The 2009 main season nursery accommodated more than 30,000 lines in Kenya and more than 10,000 lines in Ethiopia (the largest main-season nursery ever) from 23 countries (Afghanistan, Algeria, Argentina, Australia, Canada, Chile, China, Afghanistan, Ethiopia, India, Iran, Iraq, Kazakhstan, Kenya, Nepal, Pakistan, Paraguay, South Africa, Syria, Tunisia, USA, Uzbekistan, Yemen), CIMMYT, ICARDA and IAEA. The frequency of germplasm with acceptable level of stem rust resistance was less than 20 per cent for bread wheat and less than 10 per cent for durum wheat. From the resistant germplasm, an elite set of 300 lines was selected to further validate, characterize and determine the inheritance of resistance and/or for use as a source of resistance in crossing program or direct variety releases after national varietal trials. In addition, more than 25 promising lines with superior agronomic traits and resistance to the Ug99 lineage have been identified, and are under further evaluation for use in breeding programs world-wide.

### 2. Monsanto's Beachell-Borlaug International Scholars Program

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Monsanto's Beachell-Borlaug International Scholars Program honors two of the World's best known plant breeders who are widely credited for bringing the green revolution to rice and wheat production. The dramatic increase in rice and wheat production per unit area of land prevented starvation for billions of people. The MBBIS program is funded at \$2 million per year for 5 years for a total of \$10 million. The program provides complete support for PhD students in rice and wheat breeding. The MBBIS program was announced on Dr. Norman Borlaug's 95<sup>th</sup> birthday on March 25, 2009. The 1<sup>st</sup> round of application were evaluated by an internationally acclaimed panel of judges and 12 scholars were selected for support.

Second round of funding closed on February 1, 2010. Applications for years 3<sup>rd</sup>, 4<sup>th</sup>, and 5<sup>th</sup> rounds of funding should be submitted between November 1, 2010, 2011 and 2012 and February 1 in 2011, 2012 and 2013. Funds are encumbered for the duration of the PhD program. Scholars must complete part of their PhD program in Australia, Canada, Western Europe or the United States and part in another country of the World. Students work with their advising professor or scientist who then submits the application for the student. To learn more about how to apply, please visit [www.monsanto.com/mbbischolars](http://www.monsanto.com/mbbischolars).

### **3. Molecular tools to decrease work-life conflict in plant breeding**

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The extended travel related to phenotyping required by most plant breeding positions can lead to complications and deter individuals with personal responsibilities from entering the field. Technologies such as genomic selection (GS) alleviate work-life conflict by reducing the labor and time commitment of phenotyping. This allows greater job-flexibility since data analysis and GS model creation could potentially be done locally with flexible schedules whereas phenotyping often takes place in remote locations at specific times. This study will quantify the reduction in work related travel and increase in job flexibility that can result from using GS in a wheat breeding program. Also, we will provide examples of how molecular tools such as GS can reduce work-related travel and other work-life conflicts. Although difficult to measure, we propose that minimizing work-life conflicts will expand the labor pool in plant breeding. This expansion will likely increase gender parity in agricultural research and is especially needed in plant breeding.

### **4. Farmers' preference and informal seed dissemination of first Ug99 tolerant wheat variety in Bangladesh**

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Farmers' preference and informal seed dissemination was carried out through farmer participatory variety selection (PVS) during 2006-07 to 2008-09 by the Wheat Research Centre (WRC), Bangladesh Agricultural Research Institute (BARI), Dinajpur, Bangladesh in collaboration with CIMMYT. Four varieties including widely grown Shatabdi and four advance lines including Ug99 tolerant BAW 1064 were tested in Mother - baby approach in 8 villages in each of the years. Villages changed each year. Mother trials were researchers' designed but farmers' managed. However, baby trials were designed and managed by farmers themselves. Preference scores of 30 farmers for varieties were recorded two times viz., pre

and post-harvest stages. Farmers preferred BAW 1064 owing to its 10% yield superiority over best check Shatabdi, bolder white grains, higher grains spike-1, non-lodging behavior, earliness and resistance to diseases. This variety was found moderately resistant to Ug99 at Kenya. BAW 1064 was released as BARI Gom 26 (Hashi) recently in 2010. After three years of PVS work 19.4 tons seeds reached informally to 969 farmers of 24 PVS villages from only 252 kg source seed supplied for trials. In 2009-10, seed production of this variety is being done in 44 ha; 33.8 ha in 111 farmers' fields and 10.2 ha in research stations. Around 150 tons seed is expected to be produced. Hence, for selection and dissemination of CIMMYT developed Ug99 tolerant lines, farmer-participatory approach is being deployed.

### **5. Evaluation of the cost-effectiveness of fungicide application for control of fungal diseases of wheat in the Western Cape, South Africa**

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Wheat grain forms a major part of South Africa's food supply. However, rising input costs renders wheat production less sustainable. Yield losses can partly be ascribed to fungal diseases. Host plant resistance is generally not an alternative for chemical disease control as resistant cultivars are not always available. Therefore, control of fungal diseases relies on fungicide application. Field trials were conducted over three seasons (2007-2009) at two localities to determine the cost-effectiveness of fungicide application. One predominantly susceptible and one predominantly resistant cultivar were treated. Profitability of fungicide application was calculated. Results indicate that a single application of fungicide were mostly more profitable than double fungicide applications. It was not profitable to apply fungicides to the more resistant cultivar, while it was profitable to apply fungicides to the more susceptible cultivar. Overall a better quality grain was obtained when fungicides were applied.

### **6. Population structure of *Puccinia graminis* f.sp. *avenae* in oat fields in Sweden**

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Stem rust, caused by *Puccinia graminis*, is a serious disease of cereal crops and the incidence of oat stem rust has increased recently in Sweden. One possible explanation could be an increase in the occurrence of barberry (*Berberis* spp.), on which the sexual cycle of *P. graminis* can be completed. In this project, the population biology and epidemiology of *P. graminis* f. sp. *avenae* are investigated.

Multiple samples of *P. graminis* f. sp. *avenae* were collected from 11 oat fields during the summer of 2008 and 7 fields during 2009. DNA from one single pustule was extracted from each field sample and was used to screen Simple Sequence Repeat (SSR) markers developed for *P. graminis* f.sp. *tritici*. Some of the markers successfully produced amplicons indicating that they are useful for genotyping isolates of *P. graminis* f. sp. *avenae*. The results from this study indicate that the oat stem rust pathogen is reproducing sexually in Sweden.

#### **7. Race analysis of stem rust isolates collected from Pakistan in 2008-09**

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In 2001, stem rust infection was noted on mega-wheat cultivars grown in the coastal areas of Sindh in Pakistan (Khanzada, 2008). Periodic stem rust infections were observed from 2006 to 2009 on spring wheat crops in Sindh, which in 2008-2009 extended to the lower Punjab (Bahawalpur). This became an alarming scenario nationally, particularly in light of the reported spread of 'Ug99' (race TTKSK) to Iran and the high possibility as to whether it had entered Pakistan as well. Samples were collected during 2008-09 from crops in the Sindh and lower Punjab. Samples were analyzed in Pakistan, preserved urediniospores were sent to Australia (R. Park) for DNA fingerprinting for Ug99 and Canada (T. Fetch) for race confirmation. The combined analyses indicated the absence of Ug99 in the Pakistan stem rust samples. Race RRTT was identified in analyses at Murree in Pakistan. This was identical to RRTTF race identified in Canada but lacked the fifth nomenclature code, as the fifth subset of the North American differentials was not used in the Murree analyses. A high (susceptible/virulent) response on *Sr9e* in 'Vernstein' background was noted in the Murree analyses whereas 'K253/7\*LMPG-6' (another source of *Sr9e*) gave a low (resistant/avirulent) reaction in the Canadian analyses. The different reactions between these two *Sr9e* lines have been observed in the rust laboratories in USA (Y. Jin) and Canada (T. Fetch). Race RRTTF differs from TTKSK ('Ug99') in being virulent to *Sr36* and *SrTmp*, and in being avirulent to *Sr9e*, *Sr8a*, and *Sr31*. In addition, differential genotypes carrying the resistance genes *Sr22*, *Sr25*, *Sr26*, *Sr27*, *Sr32*, *Sr39* and *Sr40* were all resistant to RRTTF, indicating avirulence to these genes. The differential line carrying *Sr13* appeared susceptible to RRTTF (T. Fetch), indicating that this pathotype is virulent for this resistance gene. The presence of the race RRTT in Pakistan and the imminent threat of race TTKSK ('Ug99') has moved our national wheat breeding programs to consider adopting a dual screening procedure that first select germplasm resistant to RRTTF within Pakistan and then screen these selections for response to race TTKSK in Kenya. We see this as a means of ensuring resistance durability within Pakistan and in the region.

### **8. Occurrence of wheat rusts in Turkey during the 2009 growing season**

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The rusts are major diseases of wheat in Turkey and they can cause significant yield losses and quality 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 2009. Survey trips were conducted covering the South-East Marmara, Thrace, East Mediterranean, Southeast Anatolia, Central Anatolia, and Mid-Blacksea regions. Two hundred and twenty 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. Eighty four fields were infected with rusts. Of these, 65 were infected with yellow rust, 30 with leaf rust, and 10 with stem rust. In some fields, more than one rust was present. In 2009, especially Central Anatolia suffered from severe yellow rust epidemic. Leaf rust was most prevalent in South-East Marmara and Thrace region. Stem rust determined very limited location. Severities of yellow and leaf rust diseases were significant.

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### **9. Squeezing the bottleneck: A new paradigm for managing cereal rusts**

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Developing resistant cultivars has been the principal strategy for managing cereal rusts. However, one should question if cultivars with all important traits and sufficient resistance to rusts can be developed on a global basis to keep up with recent changes in pathogen populations. Populations of cereal rust fungi annually undergo tremendous reductions in size (i.e. bottlenecks) that reduce genetic variation and delay subsequent epidemics. Continuous cereal cropping or growing winter and spring cereals in the same region lessen this bottleneck effect, resulting in large population sizes, more genetic diversity, and severe epidemics.

Conversely, practices that enhance this bottleneck effect will result in smaller, less diverse populations causing less severe epidemics that are more likely to be managed by resistant cultivars. Wheat stem rust in the United States and Canada will be used as an example to demonstrate the potential for sustainable management of cereal rusts by enhancing the bottleneck effect.

#### **10. Surveillance and race analysis of stem rust in Kenya for the years 2008 and 2009**

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Limited but targeted stem rust race characterization was undertaken in Kenya in 2004 and 2005 which led to the detection of Ug99 present in Kenya and designation of Ug99 as race TTKS (based on North American stem rust race nomenclature system). Further surveillance in 2006 and 2007 detected variants of TTKS with virulence on *Sr24* (TTKST) and *Sr36* (TTTSK), respectively. Stem rust surveillance was undertaken at an extended level in 2008 and 2009 within predominant wheat growing regions of Kenya. Three hundred and sixty farms were surveyed from regional districts of Naivasha, Narok, Nakuru, Laikipia, Meru, Uasin-Gishu, Nandi, Elgeyo and Trans-Nzioa, during 2008 main season (May to September and December). The information from farmers indicated that more than 95% of these farms were sprayed with fungicides. Despite the use of fungicides, stem rust was detected in 67% of the surveyed farms. Stem rust ranged from trace amount -100% in severity with minimum infection in Naivasha district (40%) and maximum in Narok district (90%). Yellow rust was detected in 22% of the farms. Out of one hundred and twenty-six stem rust samples collected, 37 and 39 (a total of 76 ) samples were sent to Cereal Disease Laboratory (CDL) Minnesota, USA and Cereal Research Laboratory of Agriculture and Agri-Food Canada respectively, for race typing using the respective differentials used by these labs. From the 39 collections sent to Canada, 17 (43%) survived, of which majority were typed to TTKST (65%) followed by TTKSK (18%), PTKST (12%) and mixture of TTKST and TTKSK (5%). The CDL typed vast majority of pathotypes as TTKSK (84%) followed by TTKST and TTTSK (7% each). The combined results of two labs indicated that predominant frequency in Kenya in 2008 was TTKSK (51%) followed by TTKST (31%), PTKST (6%) and TTTSK (6%). The frequency of TTKST significantly increased in 2008 compared to 2007 which is not surprising, given that *Sr24* carrying wheat cultivar KS Mwamba is cultivated on large acreage in Kenya. In 2009, 262 farms were surveyed from regional districts of Narok, Laikipia, Nyandarua, Meru, Uasin-Gishu, Nandi, Elgeyo and Trans-Nzioa. The 2009 season experienced heavy drought in many areas. Nevertheless, stem rust was detected in 79% of the farms with disease severity ranging from trace to 100%. Yellow rust was detected in 15% of the farms. Stem rust infection ranged from 0 to 100% with minimum infection in Nyandarua (18%), Laikipia (42%) and maximum in Uasin-Gishu and Elgeyo (100% each). Out of seventy-four stem rust samples collected, 55 samples were sent to Canada for race typing. Only 20% of the samples survived, of which majority were typed to TTKST (50%), PTKST (34%) and PTKSK (16%).

The 2009 results did not depict real situation of predominance of pathogenic variability because of small sample size, however it provided fair indication that race TTKST is still the most prevalent. This information generated on the distribution of stem rust races, and the incidence of stem rust is important for anticipatory breeding and release of cultivars with effective sources of resistance in Kenya, and at same time mitigating global threat of stem rust by reducing intensity of stem rust inoculum in East Africa.

### **11. Races of *Puccinia graminis* f. sp. *tritici* identified from the 2009 Njoro stem rust nursery**

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In 2009, barley germplasm planted in the Njoro stem rust screening nursery (Njoro, Kenya) was severely infected with stem rust. Most notable was the susceptible response on line Q21861 (rpg4/Rpg5) that exhibited resistance to the TTKS (or Ug99) lineage in this nursery in previous years and in seedling tests with these races. We hypothesized that virulence on rpg4/Rpg5 might be present. We derived 17 single pustule isolates from collections made from barley and wheat lines in the Njoro nursery, including Q21861. Race-typing experiments using the North American stem rust differential set identified all isolates to be either TTKSK or TTKST. Q21861 remained resistant (producing infection types 0; to 1+) to these isolates in seedling tests at 18-20°C, comparable to the infection types produced by check isolates of the TTKS lineage. We concluded that virulence on Q21861 was not present in this nursery. The susceptible response observed on Q21861 in the nursery might be due to unique environmental conditions, as it is known that rpg4-mediated stem rust resistance in barley seedlings is effective at 21°C, but ineffective at 28°C. Isolates derived from susceptible pustules on triticale in the 2009 Njoro nursery were not virulent on Sr27 or SrSatu. Triticale plants observed in the field with susceptible pustules likely lacked Sr27 and SrSatu.

### **12. Races of *Puccinia graminis* f. sp. *tritici* with Virulence on Sr13 and Sr9e in Durum Screening Nursery in Ethiopia**

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Durum wheat (*Triticum turgidum* ssp. *durum*) of North America generally has a higher frequency of resistance to race TTKSK (or Ug99) of *Puccinia graminis* f. sp. *tritici* than common wheat based on evaluations conducted in Njoro, Kenya. We postulated TTKSK resistance in durum is likely due to Sr13, a common gene in North American cultivars. However, when resistant selections were evaluated in Debre Zeit, Ethiopia, many became susceptible to stem rust. Thus, we hypothesized that stem rust races in Debre Zeit may possess a virulence combination that overcomes the TTKSK resistance. The objective of this

study was to identify and characterize races of *P. graminis* f. sp. *tritici* present in the Debre Zeit stem rust screening nursery in 2009. Forty-one samples of infected stems were collected from durum and common wheat. Thirty-eight single-pustule isolates were derived and race-typed based on the North American stem rust differentials. The isolates were further characterized on a set of “universal” resistant lines. Three races of *P. graminis* f. sp. *tritici* were identified from the 38 isolates: JRCQC, TRTTF, and TTKSK. Both JRCQC and TRTTF possess virulence combination on Sr13 and Sr9e, which may explain why the TTKSK-resistant durum in Kenya became susceptible in Debre Zeit. The virulence combination on Sr9e and Sr13 is of a particular concern because these two genes constitute major components of stem rust resistance in North American durum cultivars. In addition to virulence on Sr9e and Sr13, race TRTTF appears to be virulent to stem rust resistance conferred by the 1AL.1RS translocation in winter wheat in the United States. Fifty-two (5.2% of 996 entries) durum lines resistant in the field nursery in Debre Zeit were also resistant to races JRCQC, TRTTF, and TTKSK in seedling evaluations. These materials can serve as sources of stem rust resistance for wheat breeding programs. Genetics of JRCQC and TRTTF resistance in selected lines are being investigated.

### 13. Wheat rust diseases status in SNNPR

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SNNPR is one of the regions of the country, commercially wheat and barley grown. In this region wheat and barley occupy about 160,137 and 104,124 hectares with annual production of 6.5 and 2.0 million quintals, respectively. Three rust diseases- stem rust, leaf rust and stripe/Yellow rust are the most destructive and are responsible for reduction of wheat production.

A survey of the wheat rust was carried out in the SNNPR during 2008 to watch and monitor rust diseases status. The rust diseases survey was made in different major wheat grown zones of the region using survey format developed by BGRI. Roadside and extend to the farmer wheat fields were visited and data were collected from each 5-10km stops as per wheat fields available and representative sites as well. In all the surveyed areas of the region, the rust diseases were occurred with varying incidences and severities. The highest incidence (100%) of yellow rust was observed in KT (K/Gamela, Angacha) and Silte (A/Berer) zones at altitudes ranged from 2200-2570masl. Its highest severity of 45 and 50% was also observed at K/Gamela and Angacha districts, respectively. Similarly the high incidence (80%) and severity (30%) of leaf rust were recorded at Lemo area. Stem rust infection was very minimal during the survey seasons.



Wheat rust diseases observation in the nursery site



**Stem rust samples**



**Yellow rust attacks**



Relatively low attack of rust

#### **14. New virulence of *Puccinia striiformis* f.sp. *tritici* on wheat in Iraq**

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Yellow rust of wheat incited by *Puccinia striiformis* f. sp. *tritici* is the most widespread rust disease in the cooler and humid wheat growing areas. Distribution of the disease in Iraq was limited formerly in the northern parts particularly in the mountainous zones. It has been rarely seen in the central and southern areas. In 1988 the disease was observed for the first time in some wheat fields in the middle zones area. Later on the disease has rapidly spread on susceptible wheat cultivars in these areas and then moved to the wheat fields in the south.

Many outbreak of yellow rust were observed in all wheat growing areas in these regions particularly in the irrigated fields in the last decades. The most sever epidemic form was recorded in 1998 which has caused significant decline in the national grain production. This

was probably due to the evolution of new virulent rust pathotypes which have resulted in breakdown of resistance genes and resulted of widespread epidemics in these areas or due to the recently climatic condition changes. During 2009, severe outbreak of yellow rust disease

occurred in most Iraqi wheat growing areas during April and May. The middle region explored early and more sever epidemics than the northern and southern parts. Most of the released cultivars showed susceptible reaction to the pathogen. Disease severity reached up to 100 S at milky stage on Sham 6 in the middle, while the highest disease severity (75 S) was observed on Um Rabia at the same growth development stage in the north. Virulence

analysis of *Puccinia striiformis* f. sp. *tritici* population using the near isogenic lines developed by C.R. Willings, revealed from detection of virulence against the known yellow rust resistant genes Yr1, Yr5, Yr6, Yr8, Yr11, Yr15, Yr26, Yr Sk, Yr18 and Yr A at adult plant stage in the North.

### 15. Current status of wheat rusts in Ethiopia

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In the main crop growing season of 2009, a total of 880 wheat fields planted with improved and local cultivars and breeding lines were assessed for the intensity of the three rusts. The number of stem rust (*Puccinia graminis*) affected fields was zero in the north and high (41 - 62.2%) in central, south eastern and southern parts of the country. This disease was found on less than a quarter of the surveyed fields. The mean incidence and severity of stem rust for all zones didn't exceed 7%. Moderate levels of leaf (*P. recondita*) and yellow (*P. striiformis*) rust epidemics have been recorded in almost all regions and the mean prevalence of these rust diseases was 50% each. The mean incidences of leaf and yellow rust were in between 17 and 24%, while the severities were around 8%. Improved wheat, cultivars such as Kubsa, Galama and Dashen were infected by the three rusts. On these cultivars, stem rust incidences ranged from 1.1 to 16% and severities were below 6%. The incidences of leaf and yellow rust on these cultivars were up to 42% and the severities reached up to 29%. In this cropping season, the distribution of stem rust was low while it was moderate for leaf and yellow rust.

### 16. Virulence structure of the wheat stem rust in Georgia

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Stem rust caused by *Puccinia graminis* f.sp. *tritici* is one of the most destructive diseases of wheat world-wide. Stem rust has become increasingly important since appearing of new virulent race Ug99 in Uganda. The feature of race Ug99 is that it carries virulence to most of the resistance genes of wheat and to several European and Australian cultivars. According to our study this virulence has not yet been detected in Georgia population.

A field survey conducted during the 2006-2007 wheat growing season showed that stem rust occurred moderately in some regions. Incidence and severity of stem rust varied depending field location, environmental conditions and producing cultivars.

Samples of Stem Rust and leaf rust were collected from five agroecological zones from wheat varieties (Bezostaya 1, Bagrationi, Dolis Puri 35/4, Dika, Gumatly), barley, wild grass (*Agropyron repens* L) and alternative host *Berberis vulgaris* L.

The virulence of 21 single aecial and 136 uredial isolates were characterized on the set of international differential hosts including the host resistance genes. Genes Sr7, Sr8, Sr11,

Sr12, Sr13, Sr14, Sr22, Sr24, Sr25, Sr26, Sr27, Sr31, Sr32, Sr33, Sr35 were resistant to all of the isolates. Virulence on Sr6, Sr8a, Sr9b, Sr21 and Sr29 has been rare (0.7-2%). Nearly 5% and 7.2 of the isolates were virulent on Sr7a and Sr37, respectively. Virulence to genes Sr5, Sr7b, Sr9a, Sr9f, Sr10, Sr16, Sr17, Sr23, Sr30, Sr34 and Sr36 varied between 11.5-25.1%. High percent (50.3-97.8%) of isolates virulent to Sr1, Sr9g, and Sr15 was recorded.

32 pathotypes were described in Stem Rust population. Frequency of pathotypes was between 0.7-24.5%. Pathotype with virulence genes 1, 5, 9d, 9g, 18, 28 was common (24.5%). Pathotype 1, 5, 9d, 9g, 9e, 15,18,23,28 was distributed with frequency 14.4%. 4.3% of isolates had virulence formulae 1, 5, 9d, 9g, 15,18,23,28 and 1, 5, 7b, 9d, 9g, 9f, 18, 28. Frequencies of the rest pathotypes varied from 0.7% to 3.6%. Dominant pathotypes were less virulent; they consist of 6-8 virulence genes. Pathotypes with low frequency consisted of 12-16 virulence genes. High pathotype diversity was found in Akhaltsikhe region which is main source of stem rust infection.

## **17. Structure of populations *Puccinia Triticina* in various regions of Russia in 2006-2008**

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Leaf rust of wheat, caused by fungus *Puccinia triticina* Erikss., is one of the most widespread diseases in Russia, leading to grain yield losses.

In 2006-2008 the structure of populations *P. triticina* on territories of the main wheat growing country regions - Central, Central-Chernozem, North Caucasian, Middle Volga, Low Volga and West Siberian was studied.

Virulence of 390 monoisolates of *P. triticina* to 40 monogenic lines and cultivars with single genes of resistance Lr1, Lr2a, Lr2b, Lr2c, Lr3a, Lr3bg, Lr3ka, Lr9, Lr10, Lr11, Lr14a, Lr14b, Lr15, Lr16, Lr17, Lr18, Lr19, Lr20, Lr21, Lr23, Lr24, Lr25, Lr26, Lr27 + Lr31, Lr28, Lr29, Lr30, Lr32, Lr 33, Lr36, Lr38, Lr39, Lr40, Lr41, Lr42, Lr44, Lr45 Lr46, Lr47, LrB was studied.

Lines with genes Lr9, Lr24, Lr29, Lr38, Lr41, Lr42, Lr45 and Lr47 have shown absolute efficiency (they were resistant against all isolates).

Lines with genes Lr3a, Lr3bg, Lr11, Lr14a, Lr17, Lr18, Lr30, Lr 33, LrB have shown absolute inefficiency (they were susceptible to all isolates).

Lines with genes Lr1, Lr2b, Lr2c, Lr3ka, Lr10, Lr14b, Lr16, Lr20, Lr21, Lr25, Lr27+ Lr31, Lr32 had weak efficiency (they were susceptible to 51%-100% isolates).

Lines with genes Lr2a, Lr15, Lr23, Lr26, Lr28, Lr36, Lr39, Lr40, Lr44, Lr46 in various regions have shown different degree of efficiency. Virulent to Lr19 isolates were found out in all regions with frequency of occurrence from 22,6 % to 50 %.

Method developed by Long and Kolmer was used to identify *P. triticina* races. During three years 50 races concerning to 7 racial groups C- F- K- M- P- R- T- were identified.

Distinctions between regional populations *P. triticina* for different regions on frequency of occurrence of racial groups and separate pathogen races were established. Races of groups

C- F- K- and M- were found out more often in the European part of Russia than in the Asian part.

Races of groups P- and T - were identified throughout all studied territory: racial group P - 51,6%, T - 31 %.

In the central fungus population following races dominated FGKT(14 %) and PGTT (33 %); in Central-Chernozem – KHTT(13 %), PBKT (30 %), TCTT (33 %); in North Caucasian – FHHT (17 %), PHTT (45 %); in Middle Volga – THTR (44 %) and THHT(69 %); in Low Volga – PGKT (57%), PHKT (28 %); in West Siberian – KGTT (27 %), TGTT (27 %).

### **18. A panel of SNP-based real-time PCR probes for the rapid and accurate detection of Ug99**

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Timely response to the threat of the wheat stem rust (*Puccinia graminis* f.sp. *tritici*; Pgt) race TTKSK and its variants (the “Ug99” lineage) requires the availability of sensitive, fast and easily implemented diagnostic assays to accurately monitor movement of the pathogen by pathologists, breeders and diagnostic personnel. Existing molecular technologies such as DNA sequencing, SSR and AFLP marker assays are capable of discriminating between Ug99 and several races of Pgt, but none of these methods are suitable for rapid, high-throughput monitoring of Ug99, as they require either specialized equipment, a high level of user expertise, and/or require several days or weeks before results can be generated and analyzed. To overcome these limitations, we predicted that rapid and accurate identification of Ug99 could be routinely performed through real-time PCR technology, based on the detection of single nucleotide polymorphisms (SNPs) between Ug99 and other Pgt races. With the development of suitable SNP markers for use as DNA probes and optimized protocols, real-time PCR could provide a platform that could be implemented quickly and routinely in monitoring facilities, with only a minimum of user training, and would make use of equipment already available to most U.S. diagnostic and research laboratories.

Homozygous SNPs for use in the development of real-time PCR hydrolysis probes were identified by mapping Illumina sequence data from four members of the Ug99 lineage as well as three additional Pgt isolates against the assembled reference genome. The Ug99 strains of the fungus represent the four variants of the pathogen that have been identified from Africa, with each member possessing distinct virulence profiles based on their response to stem rust resistance genes Sr24, Sr31 and Sr36. Thirty-eight probes and primer sets were selectively designed from the resultant database of >1 million SNPs, with each probe containing at least two SNPs, and primer sequences containing between 0-5 SNPs. When used to screen a worldwide collection of Pgt isolates, the probes were individually not capable of uniquely discriminating between Ug99 and other races of the fungus. However, when a suite of probes was used in combination, a fingerprint distinct for Ug99 was obtained in a repeatable manner. Our data show that once optimized, rapid and accurate SNP-based real-time PCR

detection of Ug99 will be an important component in the identification and monitoring of this pathogen.

### **19. Functionality of the wheat stripe rust resistance gene *Yr10* using VIGS**

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Wheat stripe rust, caused by *Puccinia striiformis* Westend. f. sp. *tritici*, is a destructive disease of wheat worldwide. The *Yr10* gene encodes a cytoplasmic CC-NB-LRR protein containing a nucleotide-binding site (NBS) and leucine-rich repeats (LRR) and 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 role of *Yr10* in the resistance response in Moro wheat. Systemic silencing was observed after infection with BSMV constructs carrying different *Yr10* domain fragments such as kinase 3a and proximal and distal region of LRR. Wheat infection by *P. striiformis* following transfection with vectors was examined at morphological, cytological and transcriptional levels. A susceptible response consisting of pustule formation and symptoms of compatible reactions were observed in leaves of resistant Moro transfected with *Yr10* domains after inoculation with avirulent strain SRC-84. Silencing efficiencies varied slightly for the different vector constructs targeting different domains of *Yr10* with the highest levels of silencing observed with distal LRR repeats construct. A corresponding decrease in *Yr10* transcript level was observed using qRT-PCR following VIGS treatment with the different constructs from 2-14 days following rust inoculation while no major changes were observed in *Yr10* transcript abundance in the non-transfected controls. Silencing of stripe rust resistance by three independent gene constructs using the VIGS protocol confirms that the identified sequence is the *Yr10* gene conferring resistance to stripe rust in Moro.

### **20. Effectiveness of DNA markers associated with yellow rust resistance for diverse wheat (*Triticum aestivum* L.) Germplasm**

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Tolerance to yellow rust caused by *P. striiformis* f. sp. *tritici* is one of the most important objectives of wheat breeding programs in all wheat (*Triticum aestivum* L.) growing regions of the world. In the present study, Bulk Segregant Analysis (BSA) was used to identify molecular markers associated with yellow rust disease resistance in wheat. The BSA was performed on DNA pools from the selected yellow rust tolerant and susceptible F<sub>2</sub>

individuals derived from crosses between yellow rust resistant and susceptible wheat genotypes and five DNA markers (two SSRs, two EST-SSRs and one AFLP) associated with yellow rust resistance were identified. 108 wheat genotypes differing in yellow rust resistance were screened with these markers and 60% - 85% of the wheat genotypes, known to be yellow rust resistant, had these markers, further suggesting that the presence of these markers correlates with yellow rust resistance in diverse wheat germplasm.

### **21. Genetic map of stem rust resistant gene *Sr35* in *T. monococcum***

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With the TTKS family of races virulent on most genes currently providing protection against stem rust worldwide, identifying, mapping, and deploying resistance genes effective against these races has become critical. We present here a genetic map of *Sr35*. Both parents of our diploid mapping population (DV92/G3116, 142 SSD lines) are resistant to TTKSK, but the population segregates for resistance to TRTTF (Yemen) and RKQQC (US). Race analysis suggests that G3116 carries *Sr21* and DV92 both *Sr21* and *Sr35*. Resistance to TRTTF and RKQQC was mapped to a 6 cM interval on chromosome 3A<sup>m</sup>L between markers *BF483299* and *CJ656351*. This interval corresponds to a 178-kb region in *Brachypodium* which contains only 16 annotated genes and exhibits a small inversion (including 2 genes) and a putative insertion (2 genes) relative to rice and sorghum. This map contains closely-linked markers to *Sr35* and provides the initial step for this gene's positional cloning.

### **22. Genetic maps of stem rust resistance gene *Sr13* in tetraploid wheat**

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The new stem rust race Ug99 is virulent on many wheat resistance genes, making the identification and mapping of resistance genes effective against Ug99 crucial to the development of resistant varieties. We present here genetic maps of *Sr13* developed from three tetraploid wheat (*T. turgidum* ssp. *durum*) mapping populations. In the first population (Kofa/UC1113, 93 SSD lines), resistance to Ug99 was mapped to a 20 cM interval on the long arm of chromosome 6A, flanked by markers *Xgwm617* and *Xdupw167*. In the other two populations (Mindum/Medora, 97 F<sub>2</sub> lines; Mindum/Sceptre, 80 F<sub>2</sub> lines), resistance was mapped to a similar region. Based on its chromosome location, this resistance gene is most likely *Sr13*. These maps will facilitate the development of tightly-linked markers to *Sr13* as well as provide the foundation for its high-density mapping and eventual position cloning.

### **23. Efficient incorporation of adult plant resistance to stem rust in adapted germplasm using genomic selection**

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A new breeding methodology, Genomic Selection (GS), will facilitate rapid incorporation of adult plant resistance (APR) to stem rust into high-yielding, adapted cultivars while reducing the need for phenotyping. The GS process consists of model training and selection. We are using a training population of 200 CIMMYT lines and 2 recombinant inbred line (RIL) populations segregating for APR. Phenotypic data collected in three locations over two years will be combined with genotypic data to train the GS model. Once the model is trained, we will use the models in a recurrent selection scheme to evaluate gain from selection. Individual lines will be selected in early generations based only on Genomic Estimated Breeding Values (GEBVs). This breeding scheme will be the first empirical study of GS in plants and is expected to yield elite lines with high levels of resistance to multiple races of stem rust. Eventually, GS models will also be developed for APR for leaf rust, and yellow rust resistance.

### **24. Validation of 86 molecular markers and identification of 56 genes, alleles and QTLs in Chinese wheat cultivars**

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In order to improve the wheat breeding efficiency through marker assisted selection (MAS), the validation of 86 molecular markers previously reported was analyzed, including powdery mildew resistance (12), rust resistance (26), fusarium head blight resistance (5), sharp eyespot resistance (3), barley yellow dwarf disease resistance (1), response to vernalization (6), response to photoperiod (2), plant height (7) and grain quality (24). Moreover, the distribution of 76 markers associated with 56 different genes, alleles and QTLs in a total of 75 Chinese wheat cultivars collected from ten wheat growing provinces was identified. The results indicated that 9 markers were non-specific and unsuitable for genotype identification, 31 markers were moderately specific and worthy of further genetic study, and 46 markers were highly specific and very suitable for MAS. 11 genes, such as *Yr5*, *Yr10*, *Yr15*, *Lr34*, *Lr35*, *Wx-4A* and *Wx-7D*, were not found in the 75 wheat cultivars; the distribution ratio of 23 genes was lower than 10%, including *Pm21*, *Pm4a*, *Pm4b*, *Pm13*, *Pm24*, *YrCH42*, *Yr26*, *SC-W37U*, *Bx14*, *Vrn-B1* and *Ppd-D1b*. The usefulness of current information in wheat breeding is discussed.

### **25. Haplotype and association analyses of stem rust resistance in current wheat breeding germplasm**

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Stem rust is one of the most destructive diseases of wheat worldwide. The recent emergence of wheat stem rust race TTKS (Ug99) and related strains threaten global wheat production because they overcome widely used genes that had been effective for many years. To identify loci conferring adult plant resistance to stem rust in wheat, we employed haplotyping and association analyses of 237 current wheat breeding lines from the International Maize and Wheat Improvement Center (CIMMYT) and the International Center for Agricultural Research in the Dry Areas (ICARDA). Wheat germplasm was haplotyped for stem rust resistance genes *Sr2*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr36*, *Sr40* and 1A.1R using linked microsatellite or simple sequence repeat (SSR) and sequence tagged site (STS) markers. Haplotype analysis indicated that 83 out of 115 current spring and winter wheat breeding lines from the International Maize and Wheat Improvement Center (CIMMYT) likely carry *Sr2*. Among those, five out of 94 CIMMYT spring lines tested had both *Sr2* and *Sr25* haplotypes. Five out of 22 Agriculture Research Service (ARS) lines likely have *Sr2* and a few have *Sr24*, *Sr36* and 1A.1R. Two out of 43 Chinese accessions have *Sr2*. No line was found to have *Sr26* or *Sr40* haplotypes in this panel of accessions. For association analysis, wheat breeding lines were genotyped with 1103 polymorphic DArT markers using the Diversity Array Technology and phenotyped for adult plant resistance (0-100% severity scoring) in Njoro, Kenya in 2008 and 2009. A mixed linear model with population structure controlled by the kinship matrix (K) and principal components was used for detecting marker-trait associations by the TASSEL program. DArT markers significantly associated with race TTKS resistance included two on chromosome 1B and 3B that appear to be linked to known *Sr* genes. Four DArT markers were significantly associated with *Sr2* and one with *Sr25*. The rest 2 were located on different chromosomes where no *Sr* genes have been previously identified. If successfully validated, these markers will be useful for breeding new wheat varieties with adult plant stem rust resistance to Ug99 and related races.

## **26. Characterisation of cellular and molecular defense responses of wheat to *Magnaporthe* species reveals a post penetration resistance role for the gene *WIR1***

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Blast disease has emerged as a serious field disease affecting wheat production. The causal agent of wheat blast, *Magnaporthe oryzae*, infects cultivated crops, while *M. grisea* is adapted to infect wild grasses. Durable disease resistance of crops against fungal pathogens may be achieved through non-host resistance. Cellular defence responses and transcriptional changes of wheat cv. Renan, infected with adapted and non-adapted isolates of *Magnaporthe* spp., were investigated. Appositions formed beneath attempted penetration sites prevented colonization by the non-adapted isolate, but were breached by adapted isolates. Microarray analysis identified transcripts induced in response to both adapted and non-adapted isolates. Virus induced gene silencing of one of these genes (*WIR1*) increased cell-to-cell spread of *M. oryzae* hyphae, but not penetration efficiency. This study characterizes the development of *Magnaporthe* spp. on wheat, and provides insight into the function of *WIR1*, a potential basal resistance gene important against a broad range of pathogens.

**27. QTL Analysis in an Intraspecific Recombinant Inbred Population of Durum Wheat (*Triticum turgidum* L. var. *durum*) to Recent Eastern African Isolate of Stem Rust, *Puccinia graminis* f. sp. *tritici*, Ug99**

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A Recombinant Inbred Lines (RILs) from the cross ‘Sebatel’/’Kriestal’ was made to identify molecular markers linked to the stem rust resistance QTLs that provides resistance against many devastating races, including TTKSK (or Ug99), in durum wheat. Ninety-Five RILs were tested at Debre Zeit (Ethiopia) and in addition artificially inoculated with a stem rust isolate including Ug99. Infection type and severity were evaluated and the data showed that there is the existence of major resistance genes. Based on this gene mapping using SSRs markers was initiated in IPK and some SSRs showed polymorphism.

**28. Mapping of two linked TTKSK stem rust resistance genes on chromosome arm 2BL in hexaploid wheat**

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Race TTKSK (Ug99) of *Puccinia graminis* f. sp. *tritici*, the causal fungus of stem rust, threatens global wheat production because of its virulence to many stem rust resistance genes in current wheat cultivars. Identification and mapping of resistance to TTKSK will facilitate breeding resistant cultivars. We describe the genetics and mapping of resistance in two hexaploid wheat lines: SD 1691 and Gabo 56. SD 1691 is a South Dakota breeding line from the 1940’s that exhibits field resistance to stem rust in Kenya (trace to 10% MR-MS infection). Seedling resistance in SD1691 is inherited as a single dominant gene. Allelism and race-specificity tests indicate the stem rust resistance gene in SD1691 is Sr28. Though monogenic lines with Sr28 do not confer a high level of field resistance to TTKSK, seedling and adult-plant screening of SD1691/LMPG-6 progeny suggest that the adult-plant resistance exhibited by SD 1691 is conferred by Sr28. We mapped Sr28 to chromosome 2BL using DArT and SSR markers, the closest SSR marker being wmc332. Gabo 56 is a CIMMYT cultivar released in 1956 that displays resistance to stem rust in Kenya (30-40% R-MR infection). Resistance in Gabo 56 was inherited as a single dominant gene we refer to as SrGabo56. This resistance locus was mapped to chromosome 2BL using DArT and SSR markers, the closest SSR marker being gwm47. In order to test for linkage between Sr28 and SrGabo56, we examined 418 F<sub>2</sub> progeny of a cross between the two resistant parents. Four F<sub>2</sub> plants were found to be susceptible indicating linkage. The genetic distance between the

two genes using Kosambi's function was estimated to be 20.7 cM. We are currently increasing seed of progeny that possess both Sr28 and SrGabo56 in coupling that may facilitate the pyramiding of these genes in breeding populations. Pyramiding multiple genes for resistance to stem rust may result in more durable resistance.

### **29. Development of Thatcher near-isogenic lines for recently discovered leaf rust resistance genes**

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The Thatcher near-isogenic line series, developed by the late Dr. Peter Dyck, has been used extensively on a world-wide basis. Thatcher is a universal leaf rust susceptible cultivar in which introduced resistance genes are generally expressed very well. Dr. Dyck developed the Thatcher near-isogenic series by crossing lines or cultivars with a unique leaf rust resistance gene, selecting resistant progeny, then backcrossing to Thatcher. The process was repeated typically to five backcrosses. Thatcher near-isogenic lines were created for most of the characterized leaf rust resistance genes, but many of the recently discovered genes have not been incorporated into the Thatcher series. A program has been initiated to incorporate recently discovered genes into the Thatcher genetic background. Genes initially targeted include: Lr27 & Lr31, Lr39, Lr42, Lr46, Lr47, Lr48, Lr49, Lr50, Lr51, Lr53, Lr54, Lr55, Lr56, Lr57, Lr58, Lr59, Lr61, Lr62, Lr66, and derivatives of Lr19 and Lr26. Many of these genes were supplied by collaborators at other institutions. Once these lines are developed, they will be useful for numerous applications such as pathogen virulence analysis, host/parasite interaction studies and comparative studies with other resistance genes.

### **30. Exploring new rust resistance sources in wheat by mutagenesis**

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Genetic suppressors of rust resistance are known to exist in the wheat genome. These suppressors have been shown to repress the effects of some rust resistance genes that were transferred to bread wheat from its wild, diploid relatives. We have identified three EMS mutants from the spring wheat cultivar 'Alpowa' that inactivated different suppressors of wheat rust resistance. Mutants MNsAI-180 and MNsAI-220 have dominant mutations with enhanced resistance to races of leaf, stripe, and stem rusts (including Ug99) that are virulent to the wild type Alpowa. Genetic analysis indicates that the mutations are located at different loci. Mutant MNsAI-271 has a dominant mutation and enhanced resistance only to leaf rust. All three above-mentioned mutants have lesion mimic only on the old leaves but have similar

growth characteristics as wild type Alpowa, and could prove useful in breeding rust resistance cultivars including resistance to Ug99.

### **31. QTL mapping of stem rust resistance in wheat**

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To identify and validate molecular markers closely linked with major and minor resistance genes effective against Ug99, a double haploid mapping population (Diamondbird/Janz) has been phenotyped for adult-plant resistance to stem rust. Seven trials have been conducted in three countries (Kenya, Australia and India), using pathotypes predominant in each location. The mapping population was screened against Ug99+*Sr24* at Njoro, Kenya, in 2008 and 2009. DArT markers were used to construct an initial linkage map consisting of 382 markers spanning 1737 cM. Preliminary QTL analysis indicated the involvement of chromosomes 1A, 2A, 2B, 3A, 3B, 3D, 4B, 6B, 7A, 7B and 7D in controlling stem rust resistance in the Diamondbird/Janz population. These chromosomes are being enriched for marker coverage using SSR markers to improve localisation of QTL position. SSR markers are being genotyped using Multiplex-Ready Technology. Results from QTL analysis of the multi-environment trials will be presented.

### **32. Association mapping for resistance to Ug99 and the Ethiopian stem rust races in durum wheat**

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A panel of 187 durum cultivars suitable for association mapping studies (Molecular Breeding, 2010, DOI: 10.1007/s11032-009-9353-0) were profiled with 186 SSRs and were investigated in Ethiopia under artificial inoculation with Ug99 (TTKSK) and a mixture of races that overcome a number of *Sr* genes both at seedling and adult stages. Eight genotypes (4.2%) had Disease Severity Scores (DSS<sub>max</sub>) < 10% and 16 genotypes (8.6%) exhibited DSS<sub>max</sub> averaging 10-20%. Two chromosomal regions were significantly associated with

stem rust resistance: one on the long arm of chromosome 1B near *Sr14* and one on chromosomes 2B near *Sr28* and *Sr9*. Significant associations were also detected in other regions not known to harbor stem rust resistance genes. These results confirm that durum wheat resistance to the Ethiopian races of stem rust and to Ug99 is likely oligogenic and that there is potential to identify previously uncharacterized resistance genes of minor effect.

### **33. Accessing leaf rust resistance genes in wheat breeding**

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Leaf rust, caused by *Puccinia triticina* Eriks., is a broadly distributed, yield limiting disease of wheat (*Triticum aestivum* L.) that is controllable through deployment of effective leaf rust resistance (Lr) genes in cultivars. Five effective Lr genes all from the primary gene pool were previously discovered at our institute; these are *Lr21*, *Lr22a*, *Lr32*, *Lr52* and *Lr60*. Out of these five, only *Lr21* has so far attained any significant rate of deployment in farmers' fields: the other four genes have been largely bypassed by ongoing breeding. Appropriate germplasm and selection tools will facilitate the use of known Lr genes that are underutilized or undeployed. Here we evaluate all five genes in terms of their applicability to plant breeding. Included are a validated single gene source, genetic location, expression and effectiveness of resistance, frequency of virulence (if any) and the closeness, cross-applicability and the ease of use of markers.

### **34. Breeding strategies to cope with new stem rust challenges for sustainable wheat production**

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Stem rust (*Puccinia graminis* f. sp. *triticii*) problem re-emerged after appearance of race Ug99 from Uganda. The race spread from regions to continents and stem rust become serious threat to wheat cultivation in North Africa, Middle East and South West Asia. Susceptibility of reportedly resistant Sr genes (Sr<sub>2</sub>, Sr<sub>24</sub>, Sr<sub>25</sub>, Sr<sub>27</sub>, Sr<sub>28</sub>, Sr<sub>29</sub>, Sr<sub>32</sub>, Sr<sub>34</sub>, Sr<sub>35</sub>, Sr<sub>36</sub>, Sr<sub>37</sub>, Sr<sub>38</sub>, Sr<sub>39</sub> and Sr<sub>40</sub>) and CIMMYT advance lines Chonte #1, Quaiu #1 and Munal #1 under natural epiphytotic conditions of Pakistan suggest, either presence of some race(s) other than Ug99 or more aggressive behaviors of Ug99 under agro-climatic conditions prevailing in Pakistan. Under this grave stem rust situation, different combinations of major and minor genes in following cross combinations (1) F<sub>6</sub> (TJ-83 x SD-4085/3) x Inqilab-91, (2) F<sub>6</sub> (TJ-83 x SUNCO) x TD-1 and (3) F<sub>6</sub> (VASCO x TJ-83) x Inqilab-91 were found effective. Susceptibility, effectiveness of different gene(s) at various ecological niches and their introgression in different combinations in well adopted genotypes to medicate the rust ravages will be discussed.

### **35. Cumulative resistance to Ug99 stem rust variants in wheat cultivar AC Cadillac**

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The Canadian cultivar AC Cadillac is resistant to Ug99 and variant derivatives. The objective of this study was to determine the inheritance of resistance from Cadillac. From the cross AC Cadillac/Carberry, 282 doubled haploid progeny lines and control cultivars were evaluated for stem rust reaction near Njoro, Kenya in 2009. The absence of completely susceptible progeny relative to susceptible control lines indicated at least one unidentified partial resistance gene is common between AC Cadillac and Carberry. Both parents have the *csLV34* marker molecular variant commonly linked to the *Lr34* resistance allele. The presence of *Lr34* could partially explain the absence of completely susceptible progeny. The skewed continuous distribution, with a preponderance of resistant progeny, indicated multiple genes segregating with additive effects. A significant association of resistance with *Xgwm533* confirmed AC Cadillac possesses *Sr2* and association of resistance with *Xcfd49* provided evidence for the presence of the *SrCad* resistance allele.

### **36. New wheat rust resistance genes derived from species of *Aegilops*, *Triticum Erebuni* and Amphidiploid 4**

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At the Plant Breeding and Genetics Institute an introgression of Pm, Lr, Bt, Ut, Stb and Fhb-genes from *Aegilops cylindrica*; Pm, Sr, Bt-genes from *Aegilops variabilis*; Pm, Lr, Sr, Bt-genes from *Triticum erebuni*, and Lr, Sr, Bt - genes from Amphidiploid 4 (*Triticum dicoccoides* x *Triticum tauschii*) into winter bread wheat by interspecific hybridization has been carried out. A couple of those dominant genes are new and not identical to known ones. On the basis of those genes after 4-6 backcrosses lines and varieties of winter bread wheat have been developed which possess integrated resistance to powdery mildew, fusariosis, septoriosis and some species of rust and smut.

### **37. *Puccinia triticina* independent effects of specific Lr genes**

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As parasite specific were defined Lr genes effective towards reaction type decrease or latency period prolongation. According to results of adult near isogenic Lr lines leaf (ratio between two leafs below fleg one lengths) and stem (ratio between sum of the two last internodia and

stem lengths) growth ratios in field rust nursery they were of the next plant parts low decreaseable.

More recent study was performed in greenhouse using not infected seedlings after two weeks from frequently sowing, growth at controlled air temperature around 20°C. Growth ratio (GR) was the sum of first leaf and stem length divided with second leaf one. In comparison to Thatchers with (GR=1,40) and without Lr 22b (1,20) the genes transferred in one of them, Lr 1, Lr 2a (1,45), Lr 16, Lr 19 and Lr 24 (1,25) were near the same effective. The activity of specific Lr genes without influence of parasite ones was evident. Beside not infected and infected seedlings (four days after sowing by spore trashing) the large difference was of Thatcher with Lr 22b (+0,20) and Lr 16 (+0,15) while of Thatcher without Lr22b was (+0,10). Low reaction type to applied race 2 of other investigated genes was linked to such differences below 0,05.

Beside of effect on *Puccinia triticina* reduction, specific Lr genes could be used for slowing the next plant parts growth, related equalizing visible plant parts growth and especially lower leaf green area prolongation.

### **38. Difficulties and advancements in the introgression of resistance to wheat stem rust race TTKSK from Sharon goatgrass into wheat**

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In a previous report a scheme was presented for a fast introgression of a chromosome segment carrying resistance to stem rust race TTKSK from Sharon goatgrass into wheat. The genetic procedure that was used was based on the production of a haploid hybrid between wheat and Sharon goatgrass which is also a *ph* mutant. Plants of this genotype were highly sterile and failed to produce viable seeds when pollinated by wheat. Instead, two alternative procedures are exercised. In the first one the chromosomes of the haploid hybrid were doubled to produce an octoploid BBAADDS<sup>sh</sup>S<sup>sh</sup> *ph/ph* genotype. Plants of this genotype are crossed with a durum (BBAA) *ph* mutant to produce an offspring which is homozygous for A and B genomes and hemizygous for S<sup>sh</sup> and D genomes. Homoeologous pairing is expected to occur preferably between chromosomes of S and D genomes. Similarly, the octoploid is crossed with an amphiploid AADD and in this case preferential homoeologous pairing between chromosomes of the S<sup>sh</sup> and B genomes are expected. In the second alternative procedure hybrids between a durum wheat *ph* mutant and Sharon goatgrass were produced and their chromosomes were doubled to yield a BBAAS<sup>sh</sup>S<sup>sh</sup> *ph/ph* genotype. Plants of this genotype will be crossed with a bread wheat *ph* mutant to yield offspring with BBAADS<sup>sh</sup> *ph/ph* genotype in which preferential homoeologous pairing between D and S<sup>sh</sup> chromosomes during meiosis are expected. Plants with such induced homoeologous recombination from both procedures will be pollinated by an "anti gametocidal mutant" capable of counteracting gametocidal effect from Sharon goatgrass. A series of backcrosses to a wheat cultivar accompanied by selection for TTKSK resistance will follow to recover the wheat genetic background of resistant progenies.

### 39. Identification of sources of seedling and adult-plant resistance to wheat rusts in primitive and wild *Triticum* species

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The persistence of problem of wheat yellow rust (caused by *Puccinia striiformis* West. f.sp. *tritici*) in many parts of the world including CWANA is closely associated with the continuous shift in pathogenic variability resulting in appearance of new virulent races. One of the major causes of this phenomenon could be due to the fact that in many breeding programs, improvement for resistance to yellow rust has been founded on narrowed genetic base of resistance using few race specific resistance genes such as *Yr9*, *Yr17*, and *Yr27*. It is not easy to find new sources of resistance to yellow rust in advanced wheat genotypes because of saturated utilization of available common wheats in breeding programs. Identification of new sources of resistance to yellow rust in primitive and wild relatives of wheat and utilization of such resistances, particularly when adult-plant resistance, are expected to broaden the genetic basis of resistance and hence its durability. ICARDA's genetic resource section (GRS) retains a large collection of wild relatives of wheat collected from a wide range of geographical areas. In the present study 500 accessions of primitive and wild relatives of wheat belonging to 18 species were screened for resistance to wheat yellow rust and stem rust at Tal Hadya. Yellow rust adult-plant screening was conducted against the most prevailing mixed races of yellow rust carrying virulence for the major *Yr*-genes and stem rust adult-plant screening was carried out under plastic house condition. Artificial inoculation was applied at tillering, heading and flag-leaf stages using fresh spores mixed with talcum powder. Adult-plant responses were recorded for the major infection types (Roelfs et al., 1992) and diseases severity was scored using Modified Cobb's scale (Peterson, 1945). In case of yellow rust field scoring was repeated three times at 10 days intervals. Area Under Disease Progress Curve (AUDPC) was calculated for the three scorings and then adjusted to relative AUDPC (rAUDPC%) in accordance to the reaction of susceptible cultivar Morocco. According to rAUDPC% of yellow rust and coefficient of infection (CI) of stem rust reaction and final disease reactions to *Yr* and *Sr* on flag leaf, it was found that *Triticum aestivum* subsp. *spelta*, *T. aestivum* subsp. *sphaerococcum*, *T. karamyshevii*, *T. timopheevii* subsp. *timopheevii*, *T. monococcum* subsp. *monococcum*, *T. turgidum* subsp. *polanicum*, *T. turgidum* subsp. *carthlicum*, *T. turgidum* subsp. *turanicum*, *T. turgidum* subsp. *dicoccon*, *T. turgidum* subsp. *turgidum*, *T. aestivum* subsp. *macha*, *T. aestivum* subsp. *compactum*, *T. fungicidum*, *T. kiharae* showed varied level of resistance to yellow rust. Among the species *T. timopheevii*, *T. spelta*, *T. monococcum*, *T. turgidum* subsp. *polanicum*, *T. turgidum* subsp. *carthlicum*, *T. turgidum* subsp. *dicoccon*, and *T. turgidum* subsp. *turgidum* showed more than 80% resistance. Stem rust reaction of the same accessions indicated that among the species resistant to yellow rust, except for *T. aestivum* subsp. *sphaerococcum*, *T. karamyshevii*, and *T. turgidum* subsp. *turanicum*, the other species showed varied level of resistance to stem rust. *Triticum monococcum*, *T. timopheevii*, *T. turgidum* subsp. *dicoccon*, and *T. turgidum* subsp. *carthlicum* showed high level of resistance to stem and yellow rusts. *Triticum ispahanicum*, *T. jakubzineri*, *T. vavilovii*, and *T. zhukovskiyi* were susceptible to both rusts. Seedling assessment to *Yr*, *Sr*, and *Lr* and adult-plant screening of these accessions to *Lr* are underway. Further to this study and using molecular markers, it will be possible to find new sources of resistance in this collection.

#### **40. Mining a collection of wheat landraces for resistance to new races of *Puccinia graminis* f. sp. *tritici***

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In an effort to identify new sources of stem rust resistance, spring wheat landrace accessions from the USDA-ARS National Small Grains Collection (NSGC) are being screened against the new races (TTKSK, TTKST, and TTTSK) as seedling stage at the USDA Cereal Disease Laboratory and as adult plants in the field at KARI in Njoro, Kenya. Overall, there was a tendency for a higher proportion of accessions with some resistance originating from Ethiopia (7.2%) and Iran (4.6%) and from some countries in Southern Europe (7.5%) compared to accessions from South America (1.1%) and Western Asia (2.4%). Of those screened, 77 accessions (4.3%) showed moderate to high levels of resistance in multiple tests. Since many landrace accessions are heterogeneous, single plant selections have been derived from resistant accessions and are being re-tested for resistance. Resistant selections are being used in bi-parental crosses to establish the inheritance of the resistance.

#### **41. Identification of sources of seedling resistance to wheat stem rust race Ug99 in Iranian wheat genotypes**

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Stem (black) rust caused by *Puccinia graminis* f.sp. *tritici* was one of the most important endemic diseases of wheat in Iran. Although occasional infection of stem rust has been observed in local susceptible cultivars in very small areas, the risk of stem rust has been significantly decreased to negligible level by the use of resistant cultivars since 1976. The deadly stem rust race TTKSK (commonly known as Ug99) was first detected in Uganda and spread to Kenya, Ethiopia, Sudan, and Yemen detected in west of Iran in 2007. Most of the wheat cultivars grown in north, south and western wheat belt in Iran are vulnerable to Ug99. Use of resistant cultivars is considered by Iranian national wheat breeding program as the most important control strategy in combating wheat rust epidemics. Objective of present study was to evaluate seedling responses of 100 Iranian wheat germplasms against two stem rust races which were mainly were different on virulence for *Sr31* and *Sr36* genes. Ug99 with avirulence/virulence formula

*Sr5, Sr22, Sr24, Sr26+9g, Sr27, SrGt/Sr6, Sr7a, Sr7b, Sr8a, Sr8b, Sr9a, Sr9b, Sr9d, Sr9e, Sr9f, Sr9g, Sr10, Sr11, Sr12, Sr13, Sr14, Sr15, Sr16, Sr17, Sr19, Sr20, Sr21, Sr23, Sr25, Sr28, Sr29, Sr30, Sr31, Sr32, Sr33, Sr34, Sr35, Sr36, Sr37, SrTT3+Sr10, SrDp2, SrPl, SrWld, SrH* and a local

race with avirulence on plant with *Sr31* and *Sr36* were used. Seedling plants were grown under 20°C and 16 hours light (20,000 Lux) regime. Nine-days old seedlings were inoculated with fresh urediniospores of each races using dusting procedure. Inoculated seedlings were placed in a dew chamber for 16 hours at 18°C and dark followed by 4 hours 5000 lux flourecent light. Seedling were then moved to a greenhouse with 22-24°C and supplementary light. Seedling infection types were recorded 14 days after inoculation following 0-4 scale (McIntosh *et al.*, 1995). Seedling data indicated that the among wheat cultivars, six Bahar, Arya, Sivand, Parsi, Yavarous and Karkhah were resistant to avirulent and virulent race for *Sr31* gene. Thirteen elite lines N-83-3, D-79-15, S-83-4, M-85-16, WS-86-8, WS-86-11, WS-86-12, WS-86-14, C-84D-5517, C-85D-13, DH-7, MKH3 and MKH4 were also resistant to both Ug99 and local race. Use of new sources of resistance to Ug99 would accelerate development of resistance cultivars. Further study is required to investigate adult-plant resistance of selected seedling resistant genotypes to Ug99 race.

#### **42. Stem rust (*Puccinia graminis* f. sp. *tritici*) resistance genes in Ethiopian wheat cultivars and breeding lines**

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Wheat cultivars in Ethiopia are released for production without information on race specific genes against stem rust. Hence, genes responsible for resistance in commercial wheat cultivars are not known. 60 bread and durum wheat genotypes (39 commercial cultivars and 21 breeding lines) were tested for gene postulation. Stem rust infection types produced on the wheat genotypes by ten *P. graminis* f. sp. *tritici* races were compared with infection types produced on 40 near isogenic lines carrying single stem rust resistance genes. A total of 11 stem rust resistance genes were postulated to be present either singly or in combination in the durum and bread wheat cultivars and breeding lines. Except *Sr30*, the other postulated genes were susceptible to most of the prevalent *P. graminis* f. sp. *tritici* races in Ethiopia. Since *Sr30* is also ineffective against Ug99, a gene management strategy that incorporates a combination of genes (gene pyramiding) that provide sufficient protection should be devised to achieve a durable control of stem rust. In addition, the significance of *Sr27*, *Sr29* and *Sr37* has to be investigated for Ethiopian agriculture.

#### **43. Screening of wheat germplasm collections for multiple disease resistance in Algeria**

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There are many biotic constraints to wheat production in Algeria. Stripe rust (*Puccinia striiformis*) and leaf rust (*Puccinia recondita*), *Septoria tritici* leaf blotch, Tan spot (*helminthosporium tritici repentis*) and are among the most prevalent diseases that occur

every year mostly all over the Northern part of the country. Yellow (stripe) rust appeared as epidemic in 2004 and is present every year sporadically in most humid areas where leaf rust is always prevalent. Septoria and Tan spot are mostly present in the sub littoral inlands or interior plains. In the high plateaus, Barley Yellow Dwarf Virus disease (BYDV) is present each year with different levels of severity. A search for multiple disease resistances have been undertaken in the new National Wheat improvement Program conducted in collaboration with ICARDA since 2005. A collection of 150 durum wheat and 100 genotypes of bread wheat was tested under natural conditions in two hot spots for most diseases (Oued Smar and Elkhroub representing favorable and semi arid sites where the prevalent diseases are normally expressed each year under field conditions) for the three last seasons (2006-2009). The different lines present in this collections were screened to widen the genetic base for wheat crop improvement.

As a result we could identify wheat lines that carry simultaneously adult plant resistance (APR) to leaf rust, yellow rust, Septoria leaf blotch and Tan spot in the favorable site and tan spot, septoria leaf blotch and BYDV in the semi arid site. Severities and reaction types for the rusts and pycnidial coverage for leaf blight diseases were scored.

Globally a moderate frequency of multiple resistance entries was observed and selected (43% of durum wheat lines and only 28% of the bread wheat). This is serving now the germplasm enhancement program of Algeria. Powdery mildew, Fusarium head blight, Root rot and smut appeared also in both sites but with a low frequency levels.

#### **44. Accelerating the adoption of Ug99 resistant wheat cultivars in Nepal\***

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Wheat is a priority cereal in Nepal for securing food security. It is cultivated in about 0.7 million hectares with an annual production of 1.5 million tones. Wheat diseases such as leaf and yellow rusts and helminthosporium leaf blight (HLB) are the major constraints in wheat production. Stem rust race Ug99 has further threatened wheat crop as almost all commercial cultivars currently in use have been found susceptible to this pathogen.

Identification and delivery of high yielding, disease resistant cultivars to the poverty-stricken farmers living in the rural and remote areas of Nepal are the biggest challenges faced by breeders, extension workers and seed delivery system in the country.

National Wheat Research Program in close collaboration with BGRI/CIMMYT has identified Ug99 resistant genotypes such as Francolin, Picaflor, Pauraque, Damphe, and BL 3063. These genotypes along with other new recent selections are being evaluated into different parts of the country in a participatory mode. Participatory variety selection (PVS) offers opportunity to identify and deploy farmer preferred crop varieties among farming communities. It ensures that the cultivar selected is preferred and rapidly adopted by the farmers. Large quantity of pre-release seeds of Ug99 resistant genotypes is being produced through private seed companies to cover at least 15 to 20 % wheat area of the country by the end of 2011.

Participatory variety selection activities are being conducted in 73 locations; informal research and development (IRD) seed kits have been distributed in 50 farm families along with community based seed production. To create awareness regarding Ug99 threat among wheat growers, different Medias such as TV, FM radios, farmers' fairs, posters, and leaflets are currently in use.

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#### **45. Molecular genetic assessment of wheat rust in the Western Cape province of South Africa**

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Microsatellite markers were used to differentiate Leaf (*Puccinia triticina*) and Yellow rust (*Puccinia striiformis* f. sp. *tritici*) pathotypes and a combination of microsatellite and Amplified Fragment Length Polymorphisms (AFLP) markers were used to differentiate Stem rust (*Puccinia graminis* f. sp. *tritici*) pathotypes. Following marker development 99 field isolates were collected from 12 sites in the Western Cape during 2008 and 2009. Four different Leaf rust pathotypes were identifiable with the most prevalent UVPgt13 and UVPgt10. The most prevalent Stem rust pathotypes were UVPgt50, UVPgt52, UVPgt54 and UVPgt57. Only 6E16A- was identifiable in the Yellow rust isolates. Leaf and Stem rust were widely distributed, while Yellow rust was confined to four sites in the central South Cape, due to climatic conditions. The low levels of diversity observed in the field isolates is probably due to the lack of a host for sexual reproduction, relative small sample size and selective pressure created by artificial control methods.

#### **46. Molecular detection and resistance evaluation to Chinese stripe rust among 59 cultivars from the Northwest of America**

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The 59 wheat cultivars from Northwest America were infected by mixed races (prevalent Chinese stripe rust races CY31, CY32 and CY33) to evaluate their resistance at seedling and adult stage. The molecular markers tightly linked to *Yr10*, *Yr15*, *Yr18* and *Yr39*, which still show resistance to prevalent stripe rust worldwide, were chosen to detect above-mentioned *Yr* genes among the 59 tested cultivars. Of 59 American cultivars, 33 cultivars show resistance to stripe rust in adult stage, and 5 cultivars are all stage-resistance. Based on the molecular detection, none of the 59 tested cultivars carries *Yr10*. There are 12 cultivars with *Yr15*, 33 cultivars with *Yr18* and 29 cultivars with *Yr39*, showing that most of the tested American wheat cultivars carry *Yr18* or *Yr39* and are useful for Chinese wheat stripe rust resistance breeding.

#### **47. Resistance to leaf rust in a collection of durum wheat varieties grown in Southern Spain**

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Leaf rust is an important disease on wheat caused by the fungus *Puccinia triticina*. It affects to both bread and durum wheat, but in the last years is causing troubles on the latter, especially since a new virulent race spreaded in 2001.

Different types of durum wheat varieties have been screened for resistance to leaf rust: 29 durum wheat cultivars commercially grown in Southern Spain (Andalusia), ten Spanish durum wheat landraces selected for their resistance, 15 durum wheat cultivars, from an 'Agrovegetal-CIMMYT' agreement, and 6 novel lines from CIMMYT, with well characterized resistance ('Jupare', *Lr27+31*; 'Storlom', *Lr3*; 'Camayo', *Lr3*; 'Somateria', *Lr14a*; 'Llareta', *Lr14a*; and 'Guayacán', *Lr61*).

All this material was characterized for their resistance level against the Andalusian races in seedling stage and field screening of severity was performed as well. Since the resistance sources of the Spanish cultivars are not clear, crosses were made between them and the novel CIMMYT lines of known origin, and with susceptible genotypes to characterize the genetics of the resistance. These lines were also inoculated with several Spanish isolates of leaf rust in order to postulate their resistance sources.

#### **48. Increasing genetic diversity of wheat to minimize yellow rust on Himalayan region of Nepal**

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In the past 10 years, resource poor wheat farmers in the hilly region of Himalayas in Nepal have experienced substantial losses due to high yellow rust (*Puccinia striiformis* f.sp. *tritici*) epidemics on the widely grown cultivars Sonalika and Nepal 297. The spread of available yellow rust resistant wheat cultivar has not happened due to unawareness and poor seed system. Participatory varietal selection was adopted to accelerate the replacement of old varieties with new resistant ones. Pre-release rust resistant wheat lines WK1182, WK1444, BL3235, BL3503, and BL3046 were evaluated across 10 districts in 2009 year. In 2010 BL2818, NL1073, NL1050, NL1053, NL1067 with resistance to yellow rust and Ug99 were tested. The farmers especially woman selected BL3235 and BL3503 for earliness. A set of activities has been undertaken to promote WK1204, BL3235, BL3503 and Pasang lahamu through up-scaled seed dissemination, thus improving genetic diversity for rust resistance at farmer's field level

#### **49. Resistance to rusts in Bangladeshi wheat**

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Among the three rust diseases of wheat, leaf rust caused by *Puccinia triticina* Eriks., is most important in Bangladesh. The disease usually appears in mid February with increasing severity between mid and late March. Stem rust caused by *P. graminis* Pers. f. sp. *tritici* Eriks. & Henn., was a historical disease and observed last during mid 80s, while the yellow rust caused by *P. striiformis* West. f. sp. *tritici* Eriks. & Henn., occurs occasionally with low to moderate severity. The rusts are controlled mainly through the use of genetic resistance. The rust resistance genes present in the released varieties and advanced breeding lines of wheat were postulated in DWR-India and CIMMYT-Mexico using selected pathotypes of different virulence groups. Based on seedling infection type matrices, six leaf rust resistance genes viz. *Lr1*, *Lr3*, *Lr10*, *Lr13*, *Lr23* and *Lr26*; seven stem rust resistance genes viz. *Sr2*, *Sr5*, *Sr7b*, *Sr8b*, *Sr9b*, *Sr11* and *Sr31*; and two yellow rust resistance patterns *Yr2KS* and *Yr9* were characterized in the test lines and varieties. The most frequently occurring resistance genes were *Lr13*, *Lr26*, *Sr5*, *Sr31* and *Yr9*. Some unidentified factors for resistance were also observed in most of the varieties and lines tested. An adult plant slow rusting resistance gene designated as *Lr34*, was also identified in some breeding lines and varieties based on the observation of clear leaf tip necrosis under field condition. So far none of the rusts has occurred in an epidemic form in Bangladesh, but there is no guarantee that it will not appear on a large scale and inflict severe damage in future, particularly if a new virulent race is developed or introduced. Considering the possible risk of migration of the devastating Ug99 race of stem rust into the Indo-Pak subcontinent, the Bangladeshi wheat lines and cultivars are also being sent to KARI in Kenya for testing their resistance against this race. A few of these lines were found resistant, and these lines along with some other resistant lines from CIMMYT have been included in multi-location yield trials, and seeds of the selected promising lines are being multiplied for future use towards mitigation of the menace if appears. The resistant lines have also been included in the hybridization scheme to develop genetic diversity of rust resistance.

#### **50. Enhancement of wheat stem rust resistant germplasm in Kenya**

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Wheat breeding program at the Kenya Agricultural Research Institute (KARI) was fortified considerably with support from CIMMYT and BGRI after notable increase in stem rust incidence and severity throughout wheat growing regions of Kenya. This was attributed to the wheat stem rust (*Puccinia graminis*) race TTKS (commonly known as Ug99) carrying virulence for many resistant genes/gene combinations carried by the Kenyan varieties cultivated on large acreage. In fact, all Kenyan commercial varieties are susceptible or partially susceptible to race Ug99, leaving no choice for farmers. In order to enhance and diversify stem rust resistance germplasm in the country, three lines selected from CIMMYT-

Kenya shuttle breeding were promoted to National Performance trials (NPT) and tested at seven diverse agro-ecological sites (Njoro, Eldoret, Naivasha, Narok, Rongai, Kitale and Lanet) distributed over predominant wheat growing areas of Kenya. The trials were conducted under the guidelines of Kenya Plant Health Inspectorate Service (KEPHIS) who is the authorized body for national variety testing and release. All three lines outperformed the check varieties at majority of sites in terms of yield and resistance. In addition, these lines were early maturing and produced high quality grains. Line R115 (Babax/LR42//Babax\*2/3/Tukuru) outperformed the best check by over 27%; and in average, it out-performed the mean of the checks by 81%. The second NPT confirmed and validated the outperforming results of these lines. After clearance from national variety release committee, all three lines have been recommended and released as varieties for commercial production in Kenya. In addition, in 2009, advance yield trials were performed at three locations (Njoro, Eldoret and Timau) on 30 advance CIMMYT elite lines selected at KARI Njoro station on the basis of resistance to Ug99 lineage and plant type. Four lines were selected based on confirmation of partial resistance, high yield and red grain. Red grain is preferred in Kenya by farmers because of its better tolerance to sprouting given that the Kenyan wheat is grown in rain-fed environment with unpredictable rains at maturity. These lines will be entered for NPT and Distinctiveness, Uniformity and Stability (DSU) tests in 2010. The development and release of new replacement varieties resistant to Ug99 will contribute to the protection of Kenyan wheat production and food security, and at the same time will protect global wheat production by reducing stem rust inoculum levels in Kenya and hence curbing the migration of Ug99 along the predicted migratory path.

### **51. Wheat rust in Ukraine and wheat varieties resistance to it**

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In Ukraine leaf rust (*Puccinia recondita* Rob. ex. Desm. f. sp. tritici), yellow (*Puccinia striiformis*) and stem (*Puccinia graminis* f. sp. tritici) rusts can be found everywhere. For the last 10 years on susceptible wheat varieties epiphytotics of leaf rust occurred in 2000, 2001, 2004 and 2006, yellow rust - in 2001, 2005, 2006, 2007, but at the same time epiphytotics of stem rust did not occur. There are over 50 races in the population of leaf rust, and among them races with virulence genes pp9, pp19, pp42, ppAc, ppAd4 are very rare and they are not highly aggressive to the carriers of genes Lr9, Lr19, Lr42, LrAc, LrTe and LrAd4. In the population of *Puccinia striiformis* the races OEO, 6EO, 6E16 prevail and also others can be found. In the population the races with virulence genes pp3c, pp5, pp9, pp10, pp15 and pp17 are not available, the races with genes pp2, pp3a, pp3b, pp4a, pp4b are very rare, and they are not aggressive to carriers of genes Yr2, Yr3a, Yr3b, Yr4a and Yr4b. In the population of stem rust 10 races occur, and the races 34, 11, 21, 15, 40 are prevailing. In the population there are no races with virulence genes pp13, pp31, ppTe, ppAv, ppAd4; races with genes pp24, pp25, pp26, pp27, pp36 are very rare, and they are not highly aggressive to carriers of genes Sr24, Sr25, Sr26, Sr27 and Sr3b. The gene LrAc derives from *Aegilops cylindrica*, LrTe and SrTe - from *Triticum erebuni*, LrAd4 and SrAd4 - from Amphidiploid 4 (*Triticum dicoccoides* x *Triticum tauschii*), SrAv - from *Aegilops variabilis*. All these genes were introgressed into winter bread wheat by a geneticist of the Plant Breeding and Genetics Institute. They are new and not identical to known ones.

## 52. Effective yellow rust resistance genes in wheat under Moroccan conditions

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In order to monitor yellow (stripe) rust (*Puccinia striiformis*) virulence changes in time and space and to assess the effectiveness of yellow (stripe) rust resistance genes, a set of wheat (*Triticum aestivum*) differential cultivars comprising Avocet near isogenic lines and varieties/lines having known resistance genes was grown under field conditions and tested for rust resistance at five contrasting locations (Meknès, Douyet, Annoceur, Allal Tazi and Marchouch) during four cropping seasons (from 2005-06 to 2008-09). Planting date was towards the end of November in plots of two 0.5 m rows 30 cm apart. Yellow rust disease was scored during grain filling using modified Cobb scale coupled with reaction types to determine the coefficients of infection (CI). During the four years and at all locations, the CI for yellow rust on susceptible lines/cultivars exceeded 80% except at Annoceur and Meknes in 2007-08 where the CI did not exceed 60 and 30 respectively. In 2007-08 cropping season, yellow rust was almost absent at Allal Tazi except some pustules on some lines and at Marchouch the most susceptible lines exhibited a CI of 15. The coefficients of infection for yellow rust ranged from 0 to 100, 0 to 30, 0 to 90 and 0 to 100 at Meknes during 2008-09, 07-08, 06-07 and 05-06 cropping seasons respectively. During 2007-08, the maximum value of CI at Douyet, Annoceur, Meknes, Marchouch and Allal Tazi was 80, 60, 30, 15 and 0.5 respectively. Lines possessing *Yr1*, *Yr5*, *Yr15* and *YrSP* exhibited complete immunity towards yellow rust across years and locations. Line possessing *Yr10* was immune except in 2005-06 where the CI was 5 and reached 60 at Marchouch and Douyet respectively. Line possessing *Yr17* was also immune except at Meknes in 2005-06 and 2008-09, at Annoceur in 2008-09 and at Marchouch in 2005-06 where the CI was 50, 10, 20 and 0.5 respectively. Line carrying *Yr 27* exhibited a high variation with regard to its reaction to yellow rust. Its CI ranged from 0 at Meknes in 2006-07 to 100 in 2008-09.

## 53. Stripe rust resistance status in Indian popular cultivars of wheat

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Wheat rusts pose a constant threat to sustainable wheat production and thus global food security. Stripe rust or yellow rust (*Puccinia striiformis* Westend f. sp. *tritici*) of wheat (*Triticum aestivum* L., *T. durum*), is an important disease of wheat globally including India, especially in areas with cool and wet environmental conditions. Stripe rust is very important in North Western Plain Zone (NWPZ) as well as Northern Hill Zone (NHZ) and poses a potential threat to the main wheat belt of India, if cool and humid weather persists from December to March. Sometimes, disease inflicts yield losses in other cooler parts of the country also. Cultivation of resistant varieties is the most effective, eco-friendly and economically viable method of managing wheat rusts. Stripe rust appeared in severe form in parts of Haryana, Punjab and plains of western Uttar Pradesh and Jammu and Kashmir during

2008-09 crop season as Indian ruling variety, PBW 343 has become vulnerable to stripe rust new pathotype, 78S84. In present study, 49 popular cultivars of wheat grown in different agroclimatic zones of India were evaluated at multilocations during 2006-07 to 2008-09 crop seasons under artificially inoculated conditions. Stripe rust epidemic was initiated by inoculating 3-week-old plants of spreader rows with urediniospore-water-tween 20 suspension having equal proportions of predominant four stripe rust pathotypes (67S8, 47S102, 46S103, 70S69, 46S119, 78S84), collected from the actively sporulating plants of susceptible varieties maintained in isolation in poly house. Hypodermic syringes and sprays were both used to inoculate the spreader rows to ensure timely establishment of stripe rust in the field. High humidity was maintained for rust development. The infection types (TR, R, TMS, MS, TS and S) were recorded combining the disease severity and average coefficient of infection (ACI) of multilocal data. ACI was less than 15.00 on 12 varieties, HPW 251, VL 616, VL 804, VL 829, DBW 16, DBW 17, DBW 14, HD 4672, HI 8498, HW 2004, NIAW 34 and NIDW 295 during 2006-07 to 2008-09. Among these, DBW 17 and DBW 16 have been recently released for North Western Plain Zone for timely and late sown conditions, respectively. Varieties, HPW 251, VL 616, VL 804, VL 829 which have shown good resistance for stripe rust are commercially grown in Northern Hill Zone.

#### **54. Molecular detection and resistance evaluation to Chinese stripe rust among 59 cultivars from the Northwest of America**

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The 59 wheat cultivars from Northwest America were infected by mixed races (prevalent Chinese stripe rust races CY31, CY32 and CY33) to evaluate their resistance at seedling and adult stage. The molecular markers tightly linked to *Yr10*, *Yr15*, *Yr18* and *Yr39*, which still show resistance to prevalent stripe rust worldwide, were chosen to detect above-mentioned *Yr* genes among the 59 tested cultivars. Of 59 American cultivars, 33 cultivars show resistance to stripe rust in adult stage, and 5 cultivars are all stage-resistance. Based on the molecular detection, none of the 59 tested cultivars carries *Yr10*. There are 12 cultivars with *Yr15*, 33 cultivars with *Yr18* and 29 cultivars with *Yr39*, showing that most of the tested American wheat cultivars carry *Yr18* or *Yr39* and are useful for Chinese wheat stripe rust resistance breeding.

#### **55. Resistance to leaf rust in a collection of durum wheat varieties grown in Southern Spain**

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Leaf rust is an important disease on wheat caused by the fungus *Puccinia triticina*. It affects to both bread and durum wheat, but in the last years is causing troubles on the latter, especially since a new virulent race spreaded in 2001.

Different types of durum wheat varieties have been screened for resistance to leaf rust: 29 durum wheat cultivars commercially grown in Southern Spain (Andalusia), ten Spanish

durum wheat landraces selected for their resistance, 15 durum wheat cultivars, from an 'Agrovegetal-CIMMYT' agreement, and 6 novel lines from CIMMYT, with well characterized resistance ('Jupare', *Lr27+31*; 'Storlom', *Lr3*; 'Camayo', *Lr3*; 'Somateria', *Lr14a*; 'Llaretà', *Lr14a*; and 'Guayacán', *Lr61*).

All this material was characterized for their resistance level against the Andalusian races in seedling stage and field screening of severity was performed as well.

Since the resistance sources of the Spanish cultivars are not clear, crosses were made between them and the novel CIMMYT lines of known origin, and with susceptible genotypes to characterize the genetics of the resistance. These lines were also inoculated with several Spanish isolates of leaf rust in order to postulate their resistance sources.

### **56. Addressing old challenges to a sustainable durum wheat production in Tunisia while preparing to face new threats: Development and deployment of cultivars with combined resistance to *Septoria tritici* blotch, leaf rust and stem rust Ug 99+**

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While durum wheat represents only 8-10% of the total wheat area worldwide, its relative importance around the Mediterranean basin is much higher, superior to 50% in several countries. For decades in Tunisia, durum has represented 85% of the 0.9-1.2 million hectares sown to wheat each year. It is grown under a wide range of weather and management conditions, some being highly conducive to the development of *Septoria tritici* blotch (STB) induced by *Septoria tritici* and, to a lesser extent to attacks of leaf rust. Widely grown (more than 90% of the total area) cultivars such as Karim, Razzak and Khiair are highly susceptible to both diseases. Yield losses, of up to 60%, have been reported in favorable years due to STB. Genetic resistance to the Tunisian strains of this pathogen has been, and remains, the primary focus of the Tunisian National Breeding Program at INRAT. However, concerns were recently raised as to the threat posed by stem rust race Ug99 and variants should their predicted advance path changes direction westward and starts threatening North Africa. As new resistant cultivars were released to farmers in Tunisia and new sources of resistance to *Septoria* were identified by INRAT at the Béja experiment station, these were evaluated for their reaction to stem rust race Ug99 and its newer variants (in Kenya and Ethiopia) as part of an on-going collaborative testing effort with CIMMYT. Results indicate that 2 of the 3 *Septoria* resistant cultivars recently released in Tunisia, namely MAALI and SELIM, show promisingly low stem rust infection both at the Njoro-Kenya (traces) and Debre Zeit-Ethiopia (10-15 MS/S) sites. In addition, these two cultivars are resistant to the prevailing leaf rust races in Tunisia and exhibited excellent levels of resistance to the Mexican races of the same pathogen, including to the latest virulence (BBG/BP) which appeared in 2008. The other previously released cultivar, namely NASR 99, has excellent resistance to *Septoria* but does not provide a good enough genetic protection against either rusts. These preliminary results have allowed the Tunisian National Program to target its seed multiplication efforts toward the deployment of MAALI and more recently SELIM in order to provide effective protection against the current main production-limiting factor, SLB, and at the same time against the

potentially devastating threat of stem rust. MAALI is already commercially deployed in farmers' fields (around 2000 hectares sown in 2009-10 cropping cycle) while SELIM is under accelerated seed multiplication. Both have been used extensively in a collaborative crossing/selection program with CIMMYT and advanced segregating populations are being selected in parallel between Tunisia (for Septoria) and Mexico (fast advance and leaf rust resistance) to produce more advanced lines combining resistance to Septoria tritici blotch, leaf rust and stem rust.

### **57. Improving wheat stripe rust resistance in Central Asia and the Caucasus: Present status and future outlook**

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Wheat is the most important cereal in Central Asia (Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan and Uzbekistan) and the Caucasus (Armenia, Azerbaijan and Georgia). Stripe rust, caused by the fungal pathogen *Puccinia striiformis* f.sp. *tritici* is considered the most important disease of wheat in Central Asia and the Caucasus (CAC). Though stripe rust has been present in the region for long time causing sporadic problem, it has become a serious perennial constraint to wheat production in the past 10 years. It is reflected through the occurrence of four epidemics of stripe rust in one or other parts of the CAC region since 1999, the most recent happening in 2009. A number of major wheat varieties occupying substantial area are either susceptible to stripe rust or possess low level of resistance. During 2009 epidemics, 22 of the 24 varieties recommended for cultivation in Uzbekistan and most of the varieties in southern Kazakhstan showed high severity of stripe rust. The leading commercial varieties showing susceptibility to stripe rust in the region are 'Bezostaya-1' in Armenia, 'Azmatli-95' 'Nurlu-99' and 'Azeri' in Azerbaijan, 'Bezostaya-1' and 'Pobeda-50' in Georgia, 'Oktyabrina' in Kazakhstan, and 'Kroshka' and 'Pamyat' in Uzbekistan. Cultivation of these susceptible varieties could result in considerable economic losses due to stripe rust, which is alleviated through the use of fungicides. Stripe resistant varieties are not widely grown because of either some deficiency in them or unavailability of their seed. Information on stripe rust pathogen in terms of prevalent races and epidemiology is scarce and not clearly understood. There is poor understanding of effective stripe rust resistance genes in the region, and little is known about the resistance genes present in the commercial varieties and advanced breeding lines. The deployment of resistant varieties is further complicated by change in virulence of pathogen population in different parts of the CAC. Despite above bottlenecks in understanding of pathogen races and effective resistance genes to stripe rust, progress are being reported on developing stripe rust resistant varieties in the CAC region. Many improved wheat germplasm received in the region through international nurseries or other exchange programs have shown good level of resistance to stripe rust. A few of them have been released, while a number of them are either under testing in advanced varietal trials or being used in crossing program. Reports show that there is an increasing trend in percent of stripe rust resistant lines being introduced in the region through

international wheat nurseries. Even during the recent stripe rust outbreak in several parts of CAC in 2009, many lines tested in the nurseries provided by International Winter Wheat Improvement Program (IWWIP) showed high level of resistance to stripe rust. For example, 55% of the 166 winter wheat lines from IWWIP tested in Uzbekistan in the epidemic zone of 2009 showed high levels of resistance to stripe rust. Similar results have been found in other countries. A number of these stripe rust resistant lines are also resistant to leaf rust and powdery mildew, and possess high yield potential and acceptable agronomic traits. Besides, there are a few of yellow rust resistant varieties ('Zamin-1', 'Saidaziz' and 'Esaul' in Uzbekistan; 'Bitarap' in Turkmenistan; 'Alex', 'Norman' and 'Orman' in Tajikistan and 'Tungysh', 'Mereke-70', and 'Yrum' in Kazakhstan) currently occupying limited area in the region, which are expected to expand over larger area in future. These results demonstrate that there is an increase in number of stripe rust resistant improved wheat germplasm being introduced into CAC region through internal co-operation. Apart from introduction of stripe rust resistant germplasm, International co-operation in the region through ICARDA, CIMMYT, BGRI and advanced laboratories in Australia, Denmark, and the U.S.A is helping national wheat programs in the CAC region in understanding of the epidemiology and pathogen race. A great deal of effort is being placed on training of young researchers on different aspects of wheat rusts. There are a couple of centers of excellence in the region that could help strengthen regional capacity on wheat stripe rust research with some support through international collaboration. Regional and international conferences on wheat stripe rust allow wheat researchers from the CAC region in sharing their research results and strengthening cooperation. Based on above outlined ongoing activities through international cooperation and efforts by the different national research institutions in the CAC, there is promising prospect of improving wheat stripe rust in the region.

#### **58. Researches of cereals resistant to rust in Kazakhstan**

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In Kazakhstan, as well as the great cereals production region of the world, the most widespread are stem, leaf and yellow rust. From 1990 to 1999 in North Kazakhstan the late appearance and low and moderate level of *Puccinia graminis tritici* 6 times was observed at spring wheat (Koishibayev et al., 1999). In 2006 and 2007 in Kostanay and North-Kazakh oblasts moderate and high level of stem rust was observed at spring wheat varieties. Distribution of disease varied from 20% to 40%, but in some locations it was reached 90-100%. But level of infection did not exceed 25% (Rsaliev, Koishibayev, 2008).

In the late 1990s and early 2000s wheat yellow rust were show as the major factor that adversely affects wheat yield and quality and caused considerable economic damage in the South and South East of the country. In 1999-2000 severe development of *Puccinia striiformis* was observed in highlands of the Almaty region, South-Kazakh and Zhambyl regions. For example, yield losses reached 20-40 % (Morgounov et al., 2004). In the period between 2001 and 2007 in North Kazakhstan 4 times (2002, 2003, 2005 and 2007) epidemic developments of *Puccinia recondita tritici* occurred. The pustules of yellow rust were recorded also on barley up to 60-80% and wild relatives of wheat (*Elimus*, *Aegilops*

*cylindrica*) up to 80-100% (Koishibayev et al., 2003; Yahyaoui, 2003; Koishibayev, 2008). In 2009 in the main wheat producing regions yield losses reached 30-50%.

In 2002 leaf rust had severe development in South and South-east of Kazakhstan. Commercial varieties infected up to 20%, collection accessions in demonstrative plots was damaged up to 20-100% (Koishibayev, 2003). Earlier it was shown that on a background leaf rust of wheat, weight of 1000 grains decreased twice. A nature of grain below, than in the control, on 128g, grain vitreousness - on 14,0 %, protein content - on 3,0 %, on 0,4 and 0,7 % the maintenance forage protein and fodder units.

As is known, appeared in Uganda new virulent race of stem rust Ug99 is found out in many countries of Africa, Middle East and Asia. Occurrence of new race near to Kazakhstan, in Iran, causes activation of research of stability and tolerant sources. In this connection the priority directions of breeding cereals on resistant to vitopatogens are: selection on tolerance, with adaptability to biotic factors of environment, creation of varieties with field nonspecific stability using effective Sr-, Lr-, Yr-genes, association nonspecific and race specific stability; developing of "mosaic" distribution of varieties with different stability in crop production system.

Main sources of breeding material are local germplasm collection, genetic resources from CIMMYT, ICARDA, Russian and Ukrainian breeding centers etc. The list of institutes involved in national wheat breeding programme is: Kazakh Research Institute of Farming and Plant Growing, Scientific-Production Center of Grain Growing by A.Barayev, Karaganda Research Institute of Farming and Breeding, Pavlodar Research Institute of Agriculture, Kazakh Research Institute of Plant Protection and Quarantine, Actobe and Krasnovodopad Agricultural Experimental Stations of the Ministry of Agriculture of Kazakhstan, Scientific-Research Institute of Biological Safety Problems and Institute of Plant Biology and Biotechnology of National Center of Biotechnology of the Ministry of Education and Science of Kazakhstan.

In 2009 the nurseries of wheat isogenies lines for studying biotype structure of populations of rust activators are generated in southern, east, western and northern Kazakhstan. There are conducted: the analysis of the hydrometeorological information of season, accounts of phenology of growth and development winter and spring wheat; phytosanitary monitoring and diagnostics of display, distribution and development of brown and stem rust; an integrated assessment of phytosanitary status of cereals; the degree of tolerance of genotypes and commercial cultivars of wheat were estimated; the samples of rust types from various varieties of winter and spring wheat, barley, rye and triticale, cereals wild relatives and intermediate owners were collected; the structural analysis and samples on stability to types of rusts were established and complex tolerance forms were transferred to breeders; the training for farmers on knowledge transfer were organized.

Disputes and herbarium of the damaged plants are collected, the collections and expositions are made. Population researches of *Puccinia. recondita* and *P.graminis* are proceed in Scientific-Research Institute of Biological Safety Problems. Analyses of results show that in 2009 the picture of occurrence of wheat rust types in cereals production regions of Kazakhstan was the next: leaf rust were occurred in all study regions, but the frequency was weak. Stem rust was found only in north Kazakhstan with moderate frequency.

The investigation will be continued in the next years. The researchers are supported on the World Bank project «Phytosanitary monitoring of stem and brown rust of wheat in connection with occurrence of new aggressive races».

### **59. Resistance to stem rust race TTKSK in *Aegilops tauschii* accessions from the Vavilov Collection**

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Race TTKSK and its variants threaten wheat production worldwide. New sources of diverse resistance alleles are needed to provide broad-spectrum resistance for wheat. The wild progenitors of cultivated wheat are known to be rich sources of disease resistance. To identify new sources of resistance, 46 accessions of *Aegilops tauschii* from the Vavilov Collection were inoculated with race TTKSK at the seedling stage and assessed for their reaction. Fourteen (30.4%) of the accessions exhibited resistant infection types of 0, 1, or 2. These accessions originated from the countries of Azerbaijan (with 4 accessions), Armenia and Iran (both with 3 accessions), Turkmenistan (2 accessions), and Russia (Dagestan) and Tajikistan (both with 1 accession). Additional tests are being made on this germplasm with other stem rust races to postulate the identity of the resistance genes. These sources may be useful in developing broad-spectrum resistance in wheat against stem rust, including race TTKSK.

### **60. International collaboration on wheat improvement in Kyrgyzstan**

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Wheat is a major crop in Kyrgyzstan occupying approximately 500,000 ha, which is 75-80% of all cereal crops. The average wheat yield in Kyrgyzstan is between 2.5 and 2.7 t/ha. In the last 50 years, more than 40 wheat varieties have developed, some of which could produce yield upto 8-10 t/ha under high input irrigated management. At present, the Kyrgyz wheat varieties occupy about 50% of winter, facultative and spring sown wheat areas. These are ‘Intensivnaya’, ‘Adyr’, ‘Tilek’, ‘Bermet’, ‘Kairak’, ‘Asyl’, ‘Kyal’, ‘Dank’, ‘Araket’ and ‘Kasiet’. However, not all farmers have possibilities of growing improved varieties and use improved management technologies for lacks of herbicides, fertilizers, irrigation and other inputs. Therefore, development of improved varieties that could produce high yield, and possess resistance to biotic and abiotic factors for different agro-climatic zones Kyrgyzstan is

a major challenge to wheat breeding efforts. To achieve this goal, purposeful collaborative work was initiated in 1996 by Kyrgyz Agricultural Cooperative 'MIS', CIMMYT-Turkey and CIMMYT-CAC. Since 2004, this work has been further supported by ICARDA and SIDA across the diverse agro-climatic zones of the country with elevation ranging from 500 to 2000 masl. The wheat improvement efforts have focused on developing improved varieties with yield potential of 9 to 10 t/ha, possessing resistance to diseases and high end-use quality. Annual crop losses caused by rust diseases (*Puccinia striiformis* f. sp. *tritici* and *P. triticina*) in Kyrgyzstan are 10-30%. In 2001, an epiphytotic of yellow rust was recorded in Kyrgyzstan with crop losses estimated between 70 and 90%. A few hundred resistance lines were selected, that went through breeding program for adaptation to ecological conditions, and yield trials were conducted for selection of the most promising lines. The advanced lines from yield trials were sent to Kenya for testing their reaction to stem rust. These lines are being further evaluated in three ecological zones of Kyrgyzstan: Issyk-Kul, Naryn and Chu regions. Besides these yield trials, germplasm received in the international nurseries from CIMMYT and ICARDA are regularly tested and promising lines are advanced to advanced yield trials. These international collaborations have resulted in development of new wheat and triticale varieties – 'Azibrosh', 'Almira', 'Jamin', 'Zubkov', 'Zagadka', 'Aichurek', 'Keremet', 'Merim-MIS', 'Cholpon', 'Alesha' and 'Missim'. Also, a number of promising lines and varieties resulting from the International and National programs in Kyrgyzstan are being further evaluated in competitive varietal yield trials. These include 'Petr', 'Hans', 'Suleiman', 'Maksat' and Farhad. Simultaneously, preliminary seed production of promising varieties is being carrying out.

#### **61. Effect of crop season on stem rust epidemics and identification of resistant bread wheat genotypes to current stem rust population in Ethiopia**

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In Ethiopia, wheat grows in two seasons, March to July and August to December. Hundred five to 205 obsolete/commercial and advanced bread wheat genotypes, and 220 other advanced genotypes were planted in two-rows of 1m x 0.4m plot either in one or both seasons and evaluated from 1996 to 2004 and 2008, respectively. In 2009, forty seven stem rust resistant genotypes selected from preliminary evaluation in 2008 were re-evaluated at Agarfa, Ethiopia and Njoro, Kenya in two-rows of 1m x 0.4m plot using either artificial inoculation of Ug99 variants or natural stem rust epidemics enhanced by susceptible variety as spreader rows. This work was done with the objectives to characterize stem rust epidemics variation by seasons and to identify stem rust resistant genotypes. Stem rust epidemics varied by seasons, with low severity between March to July and high severity between August and December. More number of wheat genotypes was found infected in the latter season. However, susceptible and resistant bread wheat cultivars predominantly and invariably escaped stem rust infection in the March to July crop season. Thus, this season can be exploited as one of the method of stem rust management options. Out of genotypes evaluated over years to stem rust in August-December, K6295-4A is the most resistant variety in Ethiopia. Among genotypes evaluated in Ethiopia and Kenya in 2009, ETBW5538,

ETBW5540, ETBW5542, ETBW5545, ETBW5559, ETBW5576 ETBW5579 and ETBW5584 were found to be as resistant as the best standard check cultivar, K6295-4A.

## **62. Ukrainian and Russian common wheat varieties carrying the stem rust resistance gene Sr1RSAmigo conferring resistance to Ug99**

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Till the end of the 20th century the rye stem resistance gene Sr31 located on the 1BL/1RS translocation, the most widespread alien translocation among commercial varieties (Rabinovich 1998), was effective to all known stem rust races. However, with the appearance of the race Ug99 (TTKSK) with virulence to Sr31 (Pretorius 2000) in Uganda, later in Kenia and with the threat of its further spread, the situation dramatically changed. Among the genes conferring resistance to the stem rust race TTKSK is Sr1AR, located on the rye 1AL/1RS translocation from Amigo (Jin 2006), which is also designated Sr1RSAmigo (Olson et al. 2010). The 1AL/1RS translocation is the second wide-spread alien translocation among the commercial varieties. In most varieties it derives from the variety Amigo developed in the USA in 1976. The fragment the rye chromosome 1R in Amigo derives from the Argentinean rye Insave through the octoploid triticales Gaucho (Sebesta and Wood 1978).

In connection with the threat of spread of the stem rust race Ug99, of importance is identification of wheat material with effective stem rust resistance genes, in particular, identification of varieties with the rye 1AL/1RS translocation. The objective of our investigation was identification of the 1AL/1RS translocation among Ukrainian and Russian common wheat varieties using storage proteins as genetic markers. The secalin block Gli-A1w (GLD 1A17) is a convenient biochemical marker for the 1AL/1RS translocation and, thus, this Sr gene.

The material of investigation included 226 winter common wheat varieties of Ukrainian and Russian breeding and 24 Ukrainian spring common wheat varieties. Acid polyacrylamide gel electrophoresis of gliadins from 10–20 single seeds of each variety was performed by the procedure of Kozub and Sozinov (2000).

The allele Gli-A1w, which is a marker for the 1AL/1RS translocation, was identified in eight winter common wheat varieties of Ukrainian breeding (Expromt, Kolumbia, Zolotokolosa, Smuglyanka, Vesnyanka, Monolog, Rastavitsa, Knyaginya Olga) and in one spring variety (Etyud). Among the Russian varieties analyzed, the rye 1AL/1RS translocation was identified in the winter variety Bogdanka.

These varieties carrying the stem rust resistance gene Sr1RSAmigo can be considered as the most promising varieties for cultivation in the case of appearance of Ug99 as well as can be used as initial material for developing resistant varieties using marker-assisted selection.

### **63. New genotype of wheat resistant against biotic and abiotic stresses under rice – wheat cropping system of eastern Gangetic plains of India**

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North Eastern Plain Zone of India, Characterized by warm humid climate, falls under Mega Environment 5 E. In this zone, wheat is grown in 9 million hectare with the average productivity of 2.8 ton/ha. Among various diseases, spot blotch caused by *Bipolaris sorokiniana* is considered number one, followed by brown rust. Average loss due to Spot blotch is estimated to be 15 %. Brown rust causes severe damage to the crop when low temperature prolongs up to March. A farmer's appraisal under participatory varietal selection revealed that medium height, early maturity, spot blotch and terminal heat resistance should be main traits of wheat cultivars for this region.

Spot blotch pathogen *Bipolaris sorokiniana* constitutes heterogeneous population with varying aggressiveness. Most of the earlier cultivars adopted by the farmers of eastern Gangetic plains of India became susceptible to spot blotch with losses occurring up to >50% in susceptible cultivars, if it rained after anthesis. Heterokaryotic nature of the pathogen and parasexual recombination played important role in the evolution of aggressive isolates. Parasexual mechanism operates when two hyphae are vegetative compatible. Out of 1200 samples drawn between black and white present at a radial distance of 5 cm, only 3 new brown colonies were recovered. When the same experiment was conducted under laboratory conditions, frequency increased to 0.005%. No brown population was recovered when black and white were present at a distance of 10 and 15 cm. This process appears to throw variation in pathogen population and allows further selection on resistant genotypes. The dominance of new pathogen population is realized by higher susceptibility after 8 to 10 years after their release. Aggressive populations survive year after year within the infected seed and on undecomposed plant debris. New population was found to carry nuclei from both the parents. Lesion development by aggressive isolate was significantly faster as compared to the parental. Melanin content in new isolates was reduced to 25 to 50 % in cell wall in comparison to parental black type. Higher melanin content in the cell wall blocks the flow of extracellular enzymes that play important role in the pathogenesis.

New CIMMYT genotypes tested under farmers participatory varietal selection (PVS) revealed their superiority over the most popular genotype HUW 234 of the zone. The new lines selected by farmers possess significantly higher yield and resistance to spot blotch. Many of these lines are Ug99 resistant. These genotypes also performed well under zero tillage and surface seeding. Some of these lines are Francolin (WAXWING\*2/VIVITSI), Sarpat (KIRITATI/2\*WBL1), Picaflor#1 (KIRITATI//SERI/RAYON), Pauraque#1 (WAXWING\*2/4/SNI/TRAP#1/3/ KAUZ\*2/TRAP//KAUZ) and Agrim

(KIRITATI//HUW234+LR34/PRINIA). Most of these new lines display leaf tip necrosis, an indication of *Lr34* or *Lr46*. The superior yield under late sown conditions also indicates presence of terminal heat tolerance in these lines.

#### **64. Introgression of rusts resistance, grain quality and water use efficiency traits in bread wheat through integration of marker-assisted selection and doubled haploid breeding**

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In bread wheat, several traits of agronomic interest have been tagged with markers. Several such markers can be readily used for marker-assisted selection that could increase the genetic gain, efficiency and effectiveness of a specific breeding strategy. In this paper report integration of molecular markers and doubled haploid technique in conventional backcross breeding program aimed at improving rusts resistance, water use efficiency, and grain protein content. Molecular markers were used to screen a BC<sub>1</sub>F<sub>1</sub> population produced from a cross between the recurrent parent 'Tilila' (a well adapted variety to Moroccan condition with 1RS translocation) and the donor parent 'Yakora Rojo-GPC' (with high grain protein content and yellow rust resistance) for the presence of high grain protein content (GPC)/Yr genes. The anthers of selected BC<sub>1</sub>F<sub>1</sub> plants were used for developing haploid plants. These haploids were screened for presence of 1RS, GPC and Yr genes and selected, and the selected plants were diplotized using colchicine. Similar approach has been adapted to incorporate stem rust race Ug99 resistance using 'Aguilal' as recurrent parent. The results with respect to genetic improvement for the rust resistance and water use efficiency were discussed. In summary, the integration of marker-assisted selection for specific target genes, particularly at the early stages of a breeding program, is likely to substantially increase genetic improvement in bread wheat.

#### **65. The perspectives of agricultural conservation techniques for cereals production in semi-arid areas in Algeria**

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Algeria faces challenges of natural resources degradation in the most remote semi arid regions of the country. Water scarcity combined with frequent droughts aggravates the situation. Yields of rainfed crops, especially wheat, are low and highly variable. This situation can be improved through the introduction of new technologies for sustainable yield increase and conservation of natural resources.

The actual research-development program aims at promoting conservation agriculture system with no tillage being its key element. It will compare conventional tillage with minimum and zero tillage applied in durum wheat under highly variable semi-arid climatic conditions in the Tiaret, Setif, Khroub and Saida regions of Algeria. The use of minimum and zero tillage increases water availability for crops, improves soil fertility, reduces soil erosion, thus contributing to substantial increase in wheat yield. In addition, production costs will be reduced leading to increased incomes of the small farmers in the Tiaret region.

The major expected outputs of the program will be conservation agriculture practices adopted in semi-arid regions of Algeria. To achieve this, a long-term rotation experiment on comparing different treatments will be established at the ITGC experimental stations, for cereals, forage, legumes and oil crops.

Demonstration trials are duplicated in selected farmers' fields and used for demonstration and training of farmers and extensions agents.

The immediate beneficiaries of the program would be farmers producing cereals in semi-arid regions of Algeria, small-scale machinery manufacturers and national scientists. Future generations of farm families in the dryland areas of Algeria would benefit from increased soil fertility as a result of the reversion of soil degradation and improved cropping systems.

#### **66. Involvement of (1→3,1→4)-β-glucanase in compatible Russian wheat aphid-wheat interactions and the impact on durable resistance.**

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Russian wheat aphid (RWA), *Diuraphis noxia* (Kurdjumov), is an important insect pest of wheat (*Triticum aestivum* L.). Identifying broad-spectrum resistance, effective against all RWA biotypes, would provide a more durable solution to RWA. In a transcript profiling study, several genes were identified as being up-regulated in the susceptible cultivar, "Gamtoos-S" (*GS*), or down-regulated in the near-isogenic resistant line, "Gamtoos-R" (*GR*; carrying *Dn7*). Virus-induced gene silencing (VIGS) was used to test whether (1,3-1,4)-β-glucanase, identified in the microarray study, is involved in the susceptible reaction of *GS*. RWA2, the most virulent biotype to date, was used to estimate aphid fecundity and assess symptom development. Silenced plants showed significantly lower aphid fecundity compared to *GS* and similar fecundity to *GR*. Chlorosis for the silenced treatment was not significantly different from *GR*. (1,3-1,4)-β-glucanase is involved in expression of susceptibility and identification of a knockout mutant for this gene could provide broad-spectrum resistance to RWA.

**67. Genetic enhancement for yield, heat tolerance and rust resistance using synthetic hexaploids in wheat**

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Ninety synthetic hexaploids developed by CIMMYT were evaluated for three years for biotic, abiotic stresses and yield component traits under field and controlled environmental conditions. The experiments were conducted in RBD with three replications during rabi season from 2006-09. Elite varieties were included as checks. A majority of the synthetics out performed the checks for tillers/m<sup>2</sup>, ear length and better grain size as compared to checks. Syn 31, 33 & 38 were good for tillering and spike length. The genotypic performance under heat stress and non-stress conditions was evaluated using heat tolerance and susceptibility index. Syn 11, 18, 34, 52 and 71 were found to have heat tolerance as well as higher grain weight under both conditions. Ten synthetics were resistant to both rusts and leaf blight and nine were resistant to Yellow & Brown rusts. Six synthetics including Syn 11 & 34 were resistant to both rusts as well as heat tolerant. These synthetics have been used in extensive crossing programme to transfer these desirable traits into elite varieties.

**68. Breeding free-threshable, dwarf emmer wheat (*Triticum dicoccum* (Schrank.) Schulb.) genotypes through mutagenesis**

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Emmer wheat (*Triticum dicoccum* (Schrank.) Schulb.) is a very important form of wheat species endowed with high protein, heat tolerance and appreciable resistance to rust disease. High satiety value and low glycemic index made this wheat suitable for diabetic subjects. However, it is hard to thresh due to fragile rachis and tough glumes and resistance to leaf blight disease is not available. Hence, mutagenesis and shuttle breeding approaches are thought of as viable breeding strategies to transgress gene/s for free threshability and leaf blight resistance from *Triticum durum*. Two durum lines with resistance to Helminthosporium leaf blight (HLB) viz., HD-4502 and DWR-1006 and two semi dwarf dicoccum lines DDK-1001 and DDK-1025 which are susceptible to HLB but good in quality traits were crossed in all combinations during rabi 2006-07 at Wheat Improvement Project, MARS, UAS, Dharwad and F1 seeds were generated. Mutagenic treatments of F1s of all four crosses and four parental (2 durum and 2 dicoccum) lines were given (gamma irradiation and EMS treatments). Gamma irradiation was done at BARC at 150 Gy, 200 Gy, 250 Gy and EMS treatment was done at UAS, Dharwad at 0.2%, 0.3% and 0.4%. Using off season nursery facility at IARI, Regional Research Station, Wellington (Nilgiris), Tamil Nadu during summer (2007), M1 generations were advanced to M2 generation at Wheat Improvement Project, MARS, UAS, Dharwad during Rabi 2007-08. q Locus is around 4kb. Primers have been synthesized for isolation of 4 kb fragments. Nested primers have also been synthesized to isolate approx. 1 kb fragments. M<sub>2</sub> generation was advanced to M<sub>3</sub> generation at Wellington during 2008. M<sub>3</sub> generation was advanced to M<sub>4</sub> during rabi 2008-09. Among 2750 mutant lines, which are in M<sub>3</sub> generation, 140 lines were free threshable. In general, 52.86% of 140 lines were

free threshable when physically irradiated with gamma rays where as only 47.14% with EMS. Free threshability was observed more in 150 Gy and 200 Gy compared to 250 Gy. Parents had more free threshable lines with 55 % where as crosses had 45% free-threshable lines. Among parents out of 77, DDK 1001 had 63 free threshable lines compared to DDK 1025 which had 14. With in 140 free threshable lines 54 lines are resistance to leaf blight. 75.9% of 54 lines are from gamma irradiated lines. When compared between parents and crosses, crosses were given more leaf blight resistance lines with 61.1%. DDK 1025 X HD 4502 has given more number of free threshable lines with disease resistance. No negative effect on quality parameters like protein, starch, wet gluten and sedimentation value due to mutagenesis was observed among lines selected. From these lines, most promising shall be recommended for the North Karnataka districts, as present cultivars are non free threshable and susceptible to leaf blight which are major constraints in *Triticum dicoccum*. Beside free-threshability, in the analysis of variance, significant differences among the mutants were observed for yield, 1000-grain weight, and starch. This indicates large genetic variability for these characters hence are amenable to selection. Analyzing all results obtained from the M4 mutants, by the criteria of mean + SD for yield, 402 plants were selected which are also having more than mean value for 1000-garin weight were planted at UAS, Dharwad for further study. Presence of variability among free-threshable mutants assures of getting good combination of characters for both yield and quality.

#### **69. Resistance to race TTKSK of *Puccinia graminis* f. sp. *tritici* in Triticale (X *Triticosecale*)**

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Triticale (X *Triticosecale*), a hybrid between wheat (*Triticum aestivum*) and rye (*Secale cereale*), is an excellent source of resistance to wheat stem rust, but it has not been characterized for resistance to race TTKSK and its variants. A collection of 567 triticale accessions from 21 countries was evaluated for resistance to race TTKSK and other races at the seedling stage. A high frequency (73.5%) of accessions was resistant to race TTKSK with low infection types ranging from 0; to 2. TTKSK-resistant selections (358 accessions) were evaluated for their reaction to three South African BPGSC races with virulence, individually or in several combinations, to *SrSatu*, *Sr27*, and *SrKw* that are known to be present in triticales. Resistant genes *SrSatu*, *Sr27*, and *SrKw* were postulated to be present in 140 accessions and likely contributed to TTKSK resistance. The remaining 216 resistant accessions may possess combinations of known genes that could not be detected with these races or previously uncharacterized genes. These accessions were further evaluated for resistance to TRTTF, TTTTF, TPMKC, RKQQC, RCRSC, QTHJC, QCCSM, and MCCFC. Resistance remained effective across the entire set of races in all but seven accessions, suggesting that their stem rust resistance may be useful against a broad spectrum of races. Resistant selections are being further characterized by testing at the adult plant stage in field nurseries. Genetics of TTKSK resistance in several accessions, selected on a basis of diverse geographic origin and different infection types, is being investigated.

**70. Resistance to TTKSK in emmer wheat (*Triticum turgidum* ssp. *dicoccum*)**

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Emmer wheat (*T. turgidum* ssp. *dicoccum*) is known to be a source of resistance to stem rust (caused by *Puccinia graminis* f. sp. *tritici*). In attempts to identify stem rust resistance genes effective against race TTKSK (or Ug99) at the seedling stage, we evaluated 338 accessions of emmer wheat with race TTKSK and other races with broad virulence. A high frequency (31.4%) of accessions were resistant to TTKSK with low infection types ranging from 2= to 2+. Preliminary studies were conducted to determine the inheritance of TTKSK resistance in several accessions at the seedling stage. Results from evaluating F<sub>2</sub> populations derived from resistant × susceptible crosses revealed that resistance was conferred by single genes. Twenty-five accessions, selected for TTKSK resistance based on seedling tests, were evaluated for stem rust resistance in a field screening nursery at the Ethiopian Institute for Agricultural Research (Debre Zeit, Ethiopia). Eleven accessions exhibited resistant to moderately resistant responses to stem rust at the adult plant stage. These materials can serve as sources of stem rust resistance for wheat breeding programs. Since emmer wheat shares the same genome as durum wheat and is in cultivated form, resistance genes could be easily transferred to durum wheat by conventional breeding approaches.

**71. Association mapping of rust resistance in pre-green revolution wheat accessions**

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Association mapping detects correlations between genotypes and phenotypes in a sample of individuals based on the linkage disequilibrium and can be used to uncover new genetic variation among germplasm collections. Two hundred and five landraces collected by the English botanist A. Watkins in the 1920s were screened for rust response variation under field conditions during three crop seasons. An integrated map of 350 polymorphic DArT markers was developed. Association mapping identified the involvement of several genomic regions in controlling resistance to three rust diseases. Seven, eight and nine genomic regions, respectively, appeared to carry yet uncharacterized leaf rust, stripe rust and stem rust resistance. Three dimensional analyses indicated genetic association of leaf rust and stripe rust resistance in some accessions, whereas no such association was observed between stem rust resistance and resistance to either of the other two rust diseases. A new stripe rust resistance locus, *Yr47*, has been named.

## **72. Integrating Molecular Markers and Cytological Techniques for Genetic Mapping of Adult Plant Resistance Gene(s)**

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Biotic stresses particularly rust diseases in wheat inflict heavy losses in epiphytotic situations. Even though chemical control options are always there but genetic resistance is the most favoured ecofriendly and efficient approach. Hypersensitive seedling resistance genes have been frequently utilized to get clean plants because of their immune reactions. But such kind of resistance leads to boom and bust cycle, thereby allowing pathogen to overcome the resistance. Another, hitherto less utilized approach, is putting in durable resistance, normally non hypersensitive type of resistance. It is visualized that putting in several of these resistance genes together in a genotype will culminate into a near immune reaction. India has been routinely engaged in identifying lines possessing adult plant resistance of durable nature through its coordinated programme. Therefore an urgent need is to genetically characterize these genes for subsequent incorporation in high yielding background for durable resistance.

Genetic characterization using valuable cytogenetic stocks are of immense importance. Amongst them, use of nullisomics and monosomics to locate genes on specific chromosome are of prime importance. The chromosomal location of a gene can be determined by crossing a series of nullisomic lines against a line that is homozygous recessive for that trait. Similarly, monosomic lines are crossed with a line that is homozygous recessive for that trait to do physical mapping. With the advent of PCR techniques, it is now easier to go for initial screening of large number of progenies for capturing these monosomics (through the use of RT-PCR) and nullisomics and thus narrowing down to a smaller population size for cytological analysis where confirmation can be done at metaphase and anaphase.

Attempts were made to cross C306 variety having APR gene for leaf rust resistance with set of nulli-tetrasomic lines. In the meantime, for rapid identification of monosomic lines, quantitative RT-PCR was used taking samples from monosomics and its background genotype (Chinese spring). It was observed that numbers of cycles taken by the monosomic samples to reach to the threshold crossing point was attained later in monosomics as compared to Chinese spring. When the samples from these lines fixed at the inflorescence stage were cytologically analyzed, they showed 20 bivalents and one univalent at metaphase whereas anaphase stage had two poles with 20 and 21 chromosomes each, respectively. Therefore, PCR based marker technique in conjunction with cytological approach has been found advantageous in ascertaining the chromosomal location.

## **73. Three-way ordination of rust GWAS using 25 years of data from one of the CIMMYT global wheat breeding programs**

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High-throughput molecular markers when combined with phenotype data that are routinely collected as part of breeding programs allows cost efficient genome-wide association studies (GWAS) in many agricultural crops. A GWAS was conducted using data from 25 cycles of the CIMMYT Elite Spring Wheat Yield Trials for 20 traits. The concept of trait-associated marker (TAM) was introduced to deal with the problem caused by co-linearity of non-independent markers. A TAM block was defined as a block of closely linked markers in linkage disequilibrium that showed significant association ( $p < 0.0001$ ) for at least one trait. Many TAM blocks for the three rusts (stem, leaf and stripe rust) were identified from analyses of all trials (ALL) and for data from two mega-environments (ME1, ME2) separately. There were thirty-nine common TAM blocks across the three datasets. A three-way ordination of the line  $\times$  TAM block identified in ALL, ME1 and ME2 dataset  $\times$  rust trait array showed that the TAM block patterns for stem and stripe rust across lines were independent of each other. The pattern for the common TAM blocks was (with one exception) the same across the three datasets. The results of the three-way ordination presented here provide information about which TAM block combinations were favorable for particular combinations of traits in particular environment for individual lines.

#### **74. Identification and characterization of wild tetraploids wheat for durable stem rust resistance**

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Stem rust caused by *Puccinia graminis* f. sp. *Tritici* is a major disease of bread wheat controlled from mid 20<sup>th</sup> century using genetic resistance. Recently a new stem rust race TTKS designated Ug99 with virulence to widely deployed resistant genes was reported. We therefore started the search to identify new sources of resistance. Two hundred and sixty accessions selected based on field resistance against stem rust population under field conditions in Tel Hadya, were evaluated using virulent Syrian race of stem rust. About 40 and 60% of the accessions showed resistance and susceptibility respectively to stem rust at seedling stage. Similarly 37% possessed resistance at seedling stage against the prevalent stem rust isolates in Ethiopia including Ug99. Characterization with molecular markers indicated that 41% do not possess DNA haplotypes linked with effective Ug99 resistant genes. These wild tetraploids could provide new sources of durable stem rust resistance for wheat improvement.