



# Poster Abstracts

Edited by Robert McIntosh

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Borlaug Global Rust Initiative

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# Theme 1:

## Rust Surveillance and Genetics

### 1. Global distribution of aggressive wheat yellow rust strains

*S. Walter*<sup>1</sup>, *A. Fejer-Justesen*<sup>1</sup>, *C. de Vallavieille-Pope*<sup>2</sup> and *M. S. Hovmøller*<sup>1</sup>

Yellow (stripe) rust caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) is currently the most important disease of wheat worldwide and thus threatens global food security (Hovmøller et al. (2010) *Science* 329:369). Major wheat growing areas on five continents are facing repeatedly severe yellow rust epidemics since 2000, when two highly aggressive and high temperature-tolerant *Pst* strains appeared (Hovmøller et al. (2008) *Mol Ecol* 17:3818-3826). *Pst* readily spreads via wind dispersal or human transmission of urediniospores (Brown & Hovmøller (2002) *Science* 297:537-541; Hovmøller et al. (2009) *Plant Pathol* 51:24-32; Hovmøller et al. (2020)). Based on genomic data from high-throughput sequencing molecular markers for rapid detection of aggressive strains 1 and 2 of *Pst* were developed. Marker-assisted screening of *Pst* isolates revealed an alarming global situation. Since detection in 2000 aggressive strains spread globally and are now present on at least five wheat producing continents and especially frequent in Northern and East Africa, the Middle East, and Western and Central Asia. Hence, the likelihood and severity of wheat yellow rust epidemics may increase.

<sup>1</sup>Dept. of Integrated Pest Management, Faculty of Agricultural Sciences, Aarhus University, Forsøgsvej 1, DK-4200 Slagelse, Denmark; <sup>2</sup>UMR 1290 BIOGER CPP, INRA AgroParisTech, BP01, F-78850 Thiverval-Grignon, France. Email: [stephanie.walter@agrsci.dk](mailto:stephanie.walter@agrsci.dk)

### 2. Status of wheat diseases in Morocco during the 2009-10 growing season: Yellow rust is becoming a more dangerous disease

*A. Ramdani*<sup>1</sup>, *C. Nazari*<sup>2</sup>, *D. Hodson*<sup>3</sup>, *S. Lhaloui*<sup>1</sup>, *F. Abbad-Andaloussi*<sup>1</sup> and *N. Nsarellah*<sup>1</sup>

Leaf rust, Septoria leaf blotch and yellow rust are the most damaging diseases on wheat in Morocco. The objective of this survey was to assess the prevalence and severity of wheat diseases across Morocco. The survey was carried out during April-May when the growth stages ranged from anthesis to physiological maturity. Severities of the main diseases were recorded and necrotrophic foliar diseases were assessed as a complex named Septoria-Like-Diseases (SLD). A total of 53 and 19 bread and durum wheat fields, respectively, were inspected. The most prevalent diseases on both bread and durum wheats were SLD, leaf rust, yellow rust and to some extent, root rots. Stem rust was observed on some fields of durum. Overall, 91 and 79% of bread and durum wheat fields, respectively, were infected by SLD, and leaf rust was detected on 75 and 58%, respectively. Yellow rust was detected on 64 and 32%, respectively. The severities of SLD ranged from zero to 100%, and the coefficient of infection for leaf rust ranged from zero to 50 whereas that for yellow rust was zero to 80. The same trend was reported during previous surveys except for yellow rust, which was more prevalent than in previous seasons and was detected in almost all wheat growing areas. This fact is presumably due to changes in virulence patterns and hence the lost of effectiveness of *Yr* genes.

<sup>1</sup>Institut National de la Recherche Agronomique (INRA), Avenue de la Victoire, B.P. 415, Rabat, Morocco; <sup>2</sup>International Center for Agricultural Research in the Dry Area, P.O.Box 5466 Aleppo, Syria; <sup>3</sup>AGP Division, Food and Agriculture Organization of the United Nations, viale delle terme di Caracalla, 00153 Rome, Italy. Email: [ramdani.abdelhamid@gmail.com](mailto:ramdani.abdelhamid@gmail.com)

### 3. The reason behind the serious outbreaks of wheat yellow rust in Morocco: *Yr27* is no longer effective

A. Ramdani<sup>1</sup>, C. Nazari<sup>2</sup>, D. Hodson<sup>3</sup>, M. Nachit<sup>2</sup>, S. Lhaloui<sup>1</sup>, F. Abbad-Andaloussi<sup>1</sup>, N. Nsarellah<sup>1</sup>

Septoria leaf blotch, leaf rust and yellow rust are the most damaging diseases on wheat in Morocco. While leaf rust and Septoria were known from early times, yellow rust (*Puccinia striiformis*) appeared in the areas near the Atlas Mountains during the late 1980s. It recently spread to many other cereal-growing areas, probably because of changes in virulence patterns and hence lost effectiveness of *Yr* genes. In order to monitor virulence changes in the pathogen and to assess the effectiveness of yellow rust resistance genes, a set of bread wheat differential cultivars comprising the Avocet S near-isogenic lines and varieties/lines having known resistance genes was grown under field conditions and tested for rust responses at five locations and during five cropping seasons. Scoring occurred during grain filling. At most sites and locations coefficients of infection (CI) on susceptible lines exceeded 80. Lines possessing *Yr1*, *Yr5*, *Yr10*, *Yr15* and *YrSP* exhibited complete immunity. The line carrying *Yr27* exhibited a wide variation, CI ranged from 0 at Meknès in 2006-07 to 100 in 2008-09. At Marchouch and during 2009-2010, it was almost as susceptible as Morocco (the susceptible check) whilst at Annoceur, it exhibited a CI of 40 when Morocco was completely destroyed (CI = 90). Thus *Yr27* is no longer effective under Moroccan conditions.

<sup>1</sup>Institut National de la Recherche Agronomique (INRA), Avenue de la Victoire, B.P. 415, Rabat, Morocco; <sup>2</sup>International Center for Agricultural Research in the Dry Area, P.O.Box 5466 Aleppo, Syria; <sup>3</sup>AGP Division, Food and Agriculture Organization of the United Nations, viale delle terme di Caracalla, 00153 Rome, Italy. Email: ramdani.abdelhamid@gmail.com

### 4. Last decade (2000-2010) cereal pests situation in Algeria

N. Bouhaouchine Kehili<sup>1</sup> and A. Benbelkacem<sup>2</sup>

Since the year 2000, cereal production is facing several abiotic (drought, cold and salinity) and biotic (diseases and insects) constraints. During the best seasons, diseases and insects are widespread and are the most damaging in all cereal growing areas of Algeria. Annual surveys were undertaken to assess the prevalence, incidence and severity of cereal diseases across the northern part of the country in order to draw maps that are very useful tool to tailor breeding objectives. The survey permits also the collection of pathogen samples for determination of genetic diversity and virulence phenotyping. It is carried out from milk to physiological maturity stages. Data recorded were: host species, growth stage, visual assessment of grain yield, and incidences and severities of the main diseases from which prevalence was computed. Because of the similarity of the symptoms of septoria leaf blotch, septoria glume blotch and tan spot, we assessed the complex that we named "septoria-like-diseases" (SLD). A total of 122 to 216 fields were inspected during the different years. The surveys revealed that diseases or insects are variable from year to year and are related to the overall climatic conditions. The most prevailing diseases were BYDV, septoria like diseases, leaf rust and, to some extent, yellow rust, which was epidemic in the year 2003-2004 and reduced the cereal production to 80%. Powdery mildew, root rot and the smuts and bunt were less prevalent. Overall, 50 to 65% of wheat fields were infected by SLD and BYDV, while leaf rust was detected in 48% of the fields. Barley fields were infected by net blotch, leaf stripe and BYDV diseases by 70 to 80%; scald was also infecting around 35% of the fields in some relatively humid seasons. The most prevalent insects found every year were in order of importance, cereal leaf beetle, aphids and cephus. The surveys provided information on the potential threat of various pests and drove decision makers to consider seriously this problem.

<sup>1</sup>ITGC, Algiers; <sup>2</sup>NARS, Algeria. Emails: kehilinadia@yahoo.fr; benbelkacem@mail.com

## 5. Races of *Puccinia graminis* f. sp. *tritici* in Ethiopia and Kenya

P. D. Olivera<sup>1</sup>, M. Rouse<sup>1,2</sup>, A. Badebo<sup>3</sup>, B. Abeyo<sup>4</sup>, G. Woldeab<sup>5</sup>, R. Wanyera<sup>6</sup>, and Y. Jin<sup>1,2</sup>

The objective of this study was to identify and characterize races of *P. graminis* f. sp. *tritici* present in Ethiopia and Kenya in 2010. In Ethiopia, 39 samples of infected stems were collected from wheat cultivars and breeding lines at five EIAR research centers and substations (Debre Zeit, Kulumsa, Melkassa, Holetta, and Denbi), and demonstration plots at four farmer fields. Forty single-pustule isolates were derived and race-typed based on the North American stem rust differentials. Two races of *P. graminis* f. sp. *tritici* (*Pgt*) were identified: TTKSK and JRCQC. TTKSK was the predominant race as it appeared in 38 isolates, all collected from bread wheat. The two isolates classified as race JRCQC were collected from durum wheat at the Debre Zeit stem rust screening nursery. The same race was identified in 2009 from Debre Zeit. JRCQC possesses virulence to both *Sr9e* and *Sr13*, two genes that constitute major components of the stem rust resistance in North American durum cultivars. In Kenya 24 collections of *Pgt* were made from 6 locations throughout Kenya including the Plant Breeding Station at Njoro. A total of 48 single pustule isolates derived from these 24 collections were race-typed. A total of 47 of the 48 isolates were identified as TTKST, a variant of TTKSK with additional virulence to *Sr24*. Only one isolate was identified as TTKSK. These data indicate that TTKST has largely displaced TTKSK throughout Kenya.

<sup>1</sup> Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108, USA; <sup>2</sup> USDA-ARS, Cereal Disease Laboratory, St. Paul, MN 55108, USA; <sup>3</sup> Ethiopian Institute for Agricultural Research (EIAR), Debre Zeit, Ethiopia; <sup>4</sup> International Maize and Wheat Improvement Center (CIMMYT), Addis Ababa, Ethiopia; <sup>5</sup> Ethiopian Institute for Agricultural Research (EIAR), Ambo, Ethiopia; <sup>6</sup> Kenyan Agricultural Research Institute (KARI), Njoro, Kenya.  
Email: [oliv0132@umn.edu](mailto:oliv0132@umn.edu)

## 6. Races of *Puccinia graminis* f. sp. *tritici* detected on wheat in South Africa during 2010

T. G. Terefe<sup>1</sup>, Z. A. Pretorius<sup>2</sup>

Stem rust caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*) is an important disease of bread wheat in South Africa. The sustainable management of stem rust resistance as the most important control strategy requires a continuous monitoring of the *Pgt* population. A survey was conducted in 2010 to determine the frequency and distribution of stem rust races in South Africa. Samples of infected wheat and triticale were collected from farmers' fields and trap nurseries at 24 localities. Races were identified based on their avirulence/virulence on the North American standard differential set, supplemented with additional tester lines. TTKSF (78% of all isolates) and BPGSC+*Sr27,Kw,Satu* (15%) were isolated most frequently. Other races detected at low frequencies (<5%) were TTKSP, BPGSC+*Sr27*, BPGSC+*Sr27,Kw* and PTKST. TTKSF has been the predominant race in South Africa during the last ten years. PTKST, one of the races in the Ug99 lineage, was detected at one locality in the Free State. Resistance genes *Sr13*, *14*, *22*, *25*, *26*, *29*, *32*, *33*, *35*, *36*, *37*, *39*, *42*, *43* and *Tmp* are effective against current *Pgt* races in South Africa.

<sup>1</sup>Agricultural Research Council-Small Grain Institute, Private Bag X29, Bethlehem 9700, South Africa; <sup>2</sup>Department of Plant Sciences, P.O. Box 339, University of the Free State, Bloemfontein 9300, South Africa. Email: [terefet@arc.agric.za](mailto:terefet@arc.agric.za)

## 7. The expression of *Sr21* to South African Ug99 and related races

Z. A. Pretorius and T. G. Negussie<sup>1</sup>

Three races of *Puccinia graminis* f. sp. *tritici* within the Ug99 lineage occur in South Africa. These races are TTKSF (detected in 2000), TTKSP (2007) and PTKST (2009). According to their descriptions on the North American differential set, the races differ for virulence to *Sr21* (line CS\_T\_mono\_deriv), *Sr24* (LCAgSr24) and *Sr31* (Sr31/6\*LMPG). All three races are avirulent on Einkorn, but only PTKST produces a low reaction on CS\_T\_mono\_deriv. Since this reaction is in the intermediate infection type range, it is possible that expression of the gene is influenced by environment. The objective of this study was to determine whether temperature affects the response of *Sr21* in seedlings, leading to inconsistencies in allocating race codes. In addition, adult plants with *Sr21* and control lines were inoculated to examine severity of infection and response types on stems and flag leaves. Tests conducted at 25°C and 16°C showed that PTKST produced intermediate seedling infection types (2 range) on CS\_T\_mono\_deriv at both temperatures, whereas infection types in the upper 3 range were produced by TTKSF and TTKSP. Einkorn was clearly resistant in all race x temperature treatments. In adult plant tests in a greenhouse, TTKSF and TTKSP produced high stem severities (60-70S) and flag leaf infection types on CS\_T\_mono\_deriv. The response to PTKST was 30-40MS on stems and 1+ to 2+ on flag leaves. This study confirmed that the three Ug99 races were correctly characterized in terms of expression of the CS\_T\_mono\_deriv differential line.

<sup>1</sup>Department of Plant Sciences, University of the Free State, Bloemfontein 9300, South Africa. Email: pretorza@ufs.ac.za

## 8. Wheat Rusts Status in Iraq

M. Al-Hamdany<sup>1</sup>

Remarkable shifting in virulence pattern of *Puccinia triticina* was observed in pathogen population in Baghdad Region. In contrary to 1997- 1998 season, the pathogen overcame *Lr22*, *Lr 24*, and unknown Lr genes carried on K 4500.2 B<sub>jy</sub> (M10). Meantime, both *Lr15* and *Lr 17* were still effective. The new avirulent/virulent formula for *P. triticina* in Baghdad region could be Lr 15,17/1,2a,2b,2c,3,9,10,11,12,13,14a,14b,18,19,20,22,24,30,B,Exch.1+, and C. However, many unknown resistant genes carried on the following wheat genotypes; (Tob D Man X Db/Adl) Sx (M1), ktn M12 Up 30 301/D Man 7C X Adl (M3), Pasula S (M4), Maya S Mon S (M5), Chiroca-Amahnae (M8), HD 2205-A1d S (M11) and Clement-Mo 73 X Torim 73 (M12) were highly effective. Most Iraqi wheat cultivars showed moderate susceptible to susceptible reactions to *P.triticina*. For wheat yellow rust, artificial inoculation on Near Isogonics' Lines of Avocet, revealed that virulence of *P.striiformis* overcame Yr6, 7, 9, 11, 18, A, and Sk. Data of disease response on lines carried these Yr genes ranged from 25 MS to 100 S. Lines carrying Yr1, Yr5, Yr8, Yr10, Yr12, Yr15, Yr17, and YrSp showed resistant reaction which reflected the effectiveness of these genes. Host reaction of many Iraqi wheat cultivars with *P.graminis* were investigated during late epiphytotic form at milky stage in Baghdad region. Early mature cultivars were completely disease escaped, while, the late mature cultivars showed rust symptoms. Cultivars such as Sali, Adnanyia, Saber beg, Hamrah, Tamoze 3, IPA 99, Iez, Babil, and the genotype IR722 showed susceptible reactions, while al-Qaied, Noor, IPA 95 and Race R-24 could be considered having moderate-susceptible to susceptible reactions. Data of disease severity on these cultivars ranged from 10 to 20% at that time. This level of disease severity could be increased if there is an extra time for vegetative growth. Although, Hashimia cultivar is very late mature cultivar, resistant reaction was observed on the plants. The first symptom of black stem rust however was observed on IR722. The genotype IR722 is always used as spreader for leaf and yellow rust diseases in our experiments.

<sup>1</sup>Lynn, MA, USA. Email: ma\_alhamdany@yahoo.com

## 9. Detection of Yr27 virulence in *Puccinia striiformis* f.sp. *tritici* populations

E. M. Al-Maaroo<sup>1</sup>, K. Nazari<sup>2</sup>, A. H. Naser<sup>3</sup>, A. M. Razak<sup>3</sup>, S. S. Ali<sup>3</sup>, S. A. Fatteh<sup>3</sup>, N. J. Rasheed<sup>3</sup>, R. S. Nae<sup>3</sup> and K. K. TufEEK<sup>3</sup>

Outbreaks of yellow rust have been observed in most of wheat growing areas in Iraq. The most important one caused a significant decline in national grain production in 1998. This was due to virulence for Yr9, which was present in most cultivars as a single major gene. During 2010, a severe epidemic of yellow rust occurred in most wheat growing areas in Kurdistan. The epidemic was very severe and was detected in the early stages of wheat development in irrigated fields in the Iraqi-Turkish-Syrian Triangle. About 10,000 hectares of wheat were at risk. Disease severities reached 80MSS at the heading stage on Tamuz 2, followed by 85S and 100S on Maxipak and Azadi, respectively at the heading to milky stages. The highest severity and infection type in Sulaimania was recorded on SaberBeg(75HS) at the stem elongation stage in Bakrajo, whereas disease incidence reached up to 80% in the field at the same stage, followed by 80S on Sham 6 in both Tanjaro and HalabjaTaza with 90% and 80% incidence in each location, respectively. Severe disease epidemics were also recorded in Erbil and Garmian. Pathogenicity analyses revealed virulence against known resistant genes Yr2, Yr6, Yr7, Yr9, Yr18, YrA, Yr21, Yr25, Yr27, Yr28, Yr29 and Yr31 at the adult plant stage. Breakdowns of resistant genes Yr27 and Yr25 were further confirmed at seedling stage.

<sup>1</sup>Plant Pathology Department, College of Agriculture, University of Sulaimani, Sulaimania, Iraq; <sup>2</sup>International Center for Agriculture Research in the Dry Areas (ICARDA), Tel Hadya, Syria; <sup>3</sup>Plant Protection Department, Agriculture Research Directorates, Ministry of Agriculture, Kurdistan Region, Iraq.  
Email: ealmaarooof@yahoo.com

## 10. Role of date of sowing and meteorological parameters on stripe rust of wheat under Punjab conditions (India)

M. M Jindal<sup>1</sup>, L. K. Dhaliwal<sup>2</sup> and I. Sharma<sup>1</sup>

Stripe rust is a major disease problem under the North-Western Plain Zone of India, which is the major wheat producing area in the country. The disease requires cooler temperatures for infection and spread, and there is also a monoculture of wheat variety PBW 343 in the region. The high degree of pathogenic variability in rust pathogen have made development and breeding of rust resistant wheat throughout the world much more difficult. Keeping this in view, the present study was planned to study the effect of different dates of sowing and relative contribution of different meteorological parameters for spread of stripe rust on different commercially released genotypes of wheat during seasons of 2007-08 and 2008-09. The stripe rust severity was recorded at 10 day intervals as per standard rating scale. The high temperature, high relative humidity and rainfall contributed to stripe rust's incidence under field conditions. The sudden rise in temperature during February was favourable for stripe rust development. During 2007-08, the maximum disease was observed (20.5 S) under 25th October sowing and minimum (14.9 S) under 21st November sowing. But during 2008-09, the 21st November sowing recorded the maximum disease (16.1 S) and minimum (14.4 S) under 30th October sowing. This all happened due to prevailing different environmental conditions during the crop season .

<sup>1</sup>Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana (Punjab), India; <sup>2</sup>Department of Agricultural Meteorology, Punjab Agricultural University, Ludhiana (Punjab), India. Email: madhujindal@gmail.com; madhumeeta@pau.edu

## 11. Wheat Rusts in Bangladesh

*K. Mustarin, P. K. Malaker, M. M. A. Reza and M. A. Hakim<sup>1</sup>*

Leaf rust is the second most important wheat disease in Bangladesh after *Bipolaris* leaf blight. Leaf rust is usually observed in mid February and its severity increases between mid and late March. Among the other rusts, stem rust was last observed in the mid 1980s, and the yellow rust occurs occasionally with low to moderate severities. This disease is restricted to the north-western districts, where relatively cooler climates prevail during the winter months. So far none of the rusts has reached an epidemic level, but there is no guarantee that damaging epidemics will not occur in the future, particularly if a new virulent race develops or is introduced. Among our common wheat varieties only Prodig is susceptible to leaf rust at research stations, following inoculation of border rows, but in farmers' field this variety is showing sporadic infection with low to moderate severity. Yellow rust was last observed in 2008 at Wheat Research Centre, Dinajpur and Jamalpur. Wheat materials from Bangladesh are being regularly sent to KARI, Kenya, for testing with race Ug99. BARI Gom-26 showed moderate resistance. Ug99-resistant materials have been included in multi-location yield trials and multiplied for future use. The resistant lines are included in hybridization programs in order to develop increased genetic diversity of rust resistance.

<sup>1</sup>Wheat Research Centre, BARI, Nashipur, Dinajpur-5200, Bangladesh.  
E-mail: rimubari@yahoo.com

## 12. Occurrence of wheat rusts in Turkey during the 2010 growing season

*Z. Mert<sup>1</sup>, L. Çetin<sup>1</sup>, K. Akan<sup>1</sup>, L. Demir<sup>2</sup>, A. Tülek<sup>3</sup>, H. Ay<sup>4</sup>, S. Tekdal<sup>5</sup>, C. Şermet<sup>6</sup>, A. Yorgancılar<sup>7</sup>, R. Ünsal<sup>8</sup>, B. Ercan<sup>9</sup>, Ü. Küçüközdemir<sup>10</sup>, A. İlkhani<sup>11</sup> and A. H. Paksoy<sup>12</sup>*

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 2010. Survey trips were conducted covering the South-East Marmara, Thrace, Mediterranean, Southeast Anatolia, East Anatolia, Central Anatolia, Aegean and Mid-Black Sea regions. Three hundred and ten 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. Two hundred and twenty fields were infected with rusts. Of these, 142 were infected with yellow rust, 65 with leaf rust, and 45 with stem rust. In some fields more than one rust was present. In 2010 Southeast Anatolia, Central Anatolia, Aegean, East Anatolia and the Mid-Black Sea regions suffered severe yellow rust epidemics. Leaf rust was most prevalent in Southeast Marmara, Thrace and Southeast Anatolia region. Stem rust occurred at very few locations. Severities of yellow and leaf rust diseases were significant.

<sup>1</sup>Central Research Institute for Field Crops, P.O.B. 226, Ulus, Ankara, Turkey; <sup>2</sup>Sakarya Agricultural Research Institute, P.O.B. 325, Adapazarı, Turkey; <sup>3</sup>Thrace Agricultural Research Institute, P.O.B. 72, Edirne, Turkey; <sup>4</sup>Cukurova Agriculture Research Institute, P.O. B. 300, Adana, Turkey; <sup>5</sup>South East Anatolia Agriculture Research Institute, P.O.B. 72, Diyarbakır, Turkey; <sup>6</sup>Black Sea Agricultural Research Institute, P.O.B. 39, Samsun, Turkey; <sup>7</sup>Anatolian Agricultural Research Institute, P.O. B. 17, Eskisehir, Turkey; <sup>8</sup>Aegean Agriculture Research Institute, P.O.B. 9, Menemen, İzmir, Turkey; <sup>9</sup>Bahri Dagdas International Agricultural Research Institute, Konya, Turkey; <sup>10</sup>Eastern Anatolia Agricultural Research Institute, Erzurum, Turkey; <sup>11</sup>GAP Soil - Water Resources and Agricultural Research Institute P.O.B. 75, Sanliurfa, Turkey; <sup>12</sup>Kahramanmaraş Agricultural Research Institute, Kahramanmaraş, Turkey. E-mail: mert\_zaffer@yahoo.com

### 13. Virulence of the wheat stem rust pathogen in the Volga region of Russia

E. S. Skolotneva and S. N. Lekomtseva<sup>1</sup>

Stem rust occurs regularly on wheat in the Volga region, but damaging epidemics are rare. Virulence surveys of *Puccinia graminis* f. sp. *tritici* were conducted there in 1965-1974 and in 1998-2006 using international differential sets of 12 and 16 genotypes, respectively.

*Surveys during 1965-1974:* Over this period virulences for *Sr5*, *Sr7b*, *Sr9g* and *Sr36* were common. But in some years avirulence for *Sr36* was as high as 60% and was 100% for *Sr5*. During 1969 to 1973 virulence for *Sr17* ranged from 30 to 100%. Virulences for *Sr21*, *Sr9e*, *Sr11*, *Sr6*, *Sr8a*, and *Sr30* were low or absent. The combination of *Sr11* and *Sr6* was highly effective in conferring resistance.

*Surveys in 1998-2006:* Virulences for *Sr5*, *Sr9e*, *Sr7b*, *Sr6*, *Sr8a*, *Sr9g*, *Sr36*, and *Sr9a* were common. In 2002, for example, 83% of population consisted of isolates avirulent to both *Sr21* and *Sr30*, but isolates virulent to both genes were identified in the following year, and by 2005, reached 100%. Concurrently, there were low frequencies of virulence to *Sr9b* and *Sr17*. Virulence for *Sr11* was absent.

It was evident that *Sr21*, *Sr9e*, *Sr6*, *Sr8a* and *Sr30* were no longer effective. *Sr9b* and *Sr11* were therefore only recommended for use in the Volga region.

<sup>1</sup>Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia.  
Email: sk-ska@yandex.ru

### 14. Distribution of wheat rusts and effectiveness of resistance genes in the Russian North Caucasus region

G. V. Volkova, L. K. Anpilogova, E. V. Sinyak and Y. V. Shumilov<sup>1</sup>

The Russian North Caucasus winter wheat region is affected by numerous plant pathogens, including the three rusts. Under severe epidemic conditions yield losses to any single rust can reach 50-70%. In 2008-2010 surveys of commercial and breeding wheat fields at the post-flowering stages stripe rust at 5-10% mean severity was detected in all zones. However, in some cultivars severities reached 30% (cvs. Donskaya 50, Continent) and even 80-90% (cvs. Donskaya Lira, Zimtra, Pallada). Stem rust was regularly found at low levels in the Stavropol region. Leaf rust was detected everywhere with 5-30% severities. In some cultivars (Krasnodarskaya 99, Batko and others) disease levels reached 80-90%. Seedling tests with local isolates of the three pathogens showed that the following genes were effective: *Yr5*, *24*, *26* and *Sp*; *Sr8a*, *9e*, *11*, *13*, *20*, *21*, *24*, *25*, *26*, *27*, *30*, *31*, *32*, *33*, *35*, *37* and *Wld*; *Lr9*, *19*, *24*, *29*, *41*, *42*, *43+24*, *45*, *47* and *52(W)*. Under field conditions the most effective resistance genes included *Yr5* and *Sp*; *Sr5*, *9e*, *11*, *13*, *25*, *31*, *35* and *Wld*; *Lr9*, *19*, *24*, *25*, *41*, *43+24* and *47*.

<sup>1</sup>All-Russian Research Institute of Biological Plant Protection, Krasnodar, Russia.  
Email: volkova1@mail.kubtelecom.ru

## 15. Virulence phenotypes and molecular genotypes in collections of *Puccinia triticina* from Italy

**P. Mantovani<sup>1</sup>, M. Maccaferri<sup>2</sup>, R. Tuberosa<sup>2</sup> and J.A. Kolmer<sup>3</sup>**

Leaf rust caused by *Puccinia triticina* Eriks. is a common disease of cultivated wheat, with distinct races affecting durum and common wheat. To find new sources of leaf rust resistance in durum or common wheat, genetic analyses should be conducted with isolates specialized to the host species under investigation. In this study, we determined the host specialization of 24 *Puccinia triticina* isolates collected in Italy in order to properly utilize them in genetic analysis of leaf rust resistance in wheat. Single uredinial isolates were derived and characterized for virulence to seedlings of 22 common wheat Thatcher isolines, and for molecular genotypes at 15 simple sequence repeat (SSR) loci. The isolates were then compared with a set of previously characterized *P. triticina* isolates from either durum or common wheat in order to determine their host specialization. Clustering based on virulence phenotypes and SSR genotypes grouped the Italian *P. triticina* isolates into three groups: i) isolates with virulence phenotypes and SSR genotypes similar to isolates collected from durum wheat, ii) isolates closely related to those from common wheat, and iii) "unique isolates" with virulence similar to those from common wheat, but with distinct SSR genotypes compared to the reference isolates from both durum and common wheat. The isolates were subsequently grouped based on the known or assumed host of origin, virulence phenotype, and SSR genotypes. Measures of  $F_{ST}$  and  $R_{ST}$  for SSR genotypes, and  $\Phi_{ST}$  for virulence phenotype were significant, confirming differentiation between all three groups.

<sup>1</sup>Società Produttori Sementi S.p.A., via Macero 1, 40050, Argelato (BO), Italy; <sup>2</sup>Department of Agroenvironmental Sciences and Technology, Viale Fanin 44, 40127, Bologna, Italy; <sup>3</sup>Cereal Disease Laboratory, ARS-USDA, 1551 Lindig Avenue, St. Paul, MN 55108, USA. **Email: p.mantovani@prosementi.com**

## 16. Virulence of *Puccinia triticina* on wheat in Poland from 1998 to 2009

**A. Pietrusińska<sup>1</sup>, A. Strzembicka<sup>2</sup> and G. Czajowski<sup>2</sup>**

Leaf rust, caused by *Puccinia triticina* is the most prevalent wheat disease in many regions of the world, including Poland. This disease can cause serious epidemics in Poland. A total 2,519 leaf rust samples was collected from wheat in Poland from 1998 to 2009. Isolates from them were tested for virulence on seedlings of a set of near-isogenic Thatcher NILs with resistance genes. There were high virulence frequencies ranging from 67 to 100% for most of the *Lr* genes (e.g. *Lr3*, *Lr10*; *Lr11*, *Lr12*, *Lr13*, *Lr14a*, *Lr14b*, *Lr21*, *Lr22*, *Lr30*, *Lr32*, and *Lr33*). The frequencies of virulence to lines with *Lr1*, *Lr2a*, *Lr2b*, *Lr2c*, *Lr20*, *Lr23*, and *Lr38* were low. No virulence was found to resistance genes *Lr9*, *Lr19*, *Lr23*, *Lr24*, *Lr25*, and *LrW*, and these resistance genes were the most effective in wheat from 1998 to 2007. Based on the results obtained during 2008/09, only *Lr19* was effective against all isolates. Moreover, at the turn of the year 2006/07 9 isolates (Pt Zorro 2, Pt Zorro 1, Pt 705, Pt RPA-1, Pt 5601, Pt 1002, Pt 2902, Pt 1202, Pt 1602) were tested for virulence on a set of 241 wheat varieties from different countries and 42 sources of resistance with known *Lr* genes. Ten cultivars (Beeugar, Bristol, Koch, Križinka, Landrel, Lexus, Mandub, Merkur, Patret, Tulsa) and 5 *Lr* gene lines (*Lr9*, *Lr19*, *Lr24*, *Lr28*, *Lr29*) were resistant in all tests.

<sup>1</sup>Department of Plant Breeding and Genetics, Plant Breeding and Acclimatization Institute, National Research Institute, Radzików, 05-870 Błonie, Poland; <sup>2</sup>Plant Breeding and Acclimatization Institute, Cereal Department, 30-423 Cracow, Poland. **Email: a.pietrusinska@ihar.edu.pl; a.strzembicka@ihar.edu.pl; g.czajowski@ihar.edu.pl**

## 17. Genetic variability in collections of *Puccinia graminis* f. sp. *avenae* and *P. graminis* f. sp. *tritici* from Sweden, Ethiopia and Tajikistan

A. Berlin<sup>1</sup>, G. Woldeab<sup>2</sup>, M. Rahmatov<sup>3</sup>, H. Muminjanov<sup>3</sup>, A. Djurle<sup>1</sup>, B. Samils<sup>1</sup> and J. Yuen<sup>1</sup>

Stem rust, caused by *Puccinia graminis*, is a serious disease of cereal crops, and in the past, this pathogen has caused severe epidemics worldwide. The *formae specialis* infecting oats, *P. graminis* f. sp. *avenae*, is not as well studied as the one infecting wheat, *P. graminis* f. sp. *tritici*. In this study, we compare both *formaes specialis* within and between Sweden, Ethiopia and Tajikistan. Multiple samples of *P. graminis* collected from oats (herein referred to as *P. graminis* f. sp. *avenae*) and wheat or rye (*P. graminis* f. sp. *tritici*) were collected at different locations in the respective countries. Samples from Sweden were collected during the summers of 2009 and 2010, samples from Ethiopia were collected in November 2009, and samples from Tajikistan were collected in May and June 2010. DNA was extracted from single uredinia on infected straw tissue. The DNA samples were screened with Simple Sequence Repeat (SSR) markers developed for *P. graminis* f. sp. *tritici*. Population differentiation was estimated using F-statistics, and the computer software 'Structure' was used to investigate population structure by Bayesian analysis. Each combination of *formae specialis* and country clustered into separate groups in the analysis with 'Structure'. The F-statistics indicate that the isolates from oats were more closely related to each other than to the isolates from wheat and rye. The genetic variation within each country and *formae specialis* is large, suggesting the occurrence of sexual reproduction.

<sup>1</sup>Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Box 7026, SE-750 07 Uppsala, Sweden; <sup>2</sup>Plant Protection Research Centre, P.O. Box 37, Ambo, Ethiopia; <sup>3</sup>Tajik Agrarian University, 146 Rudaki Ave., Dushanbe 734017, Tajikistan. **Email: Anna.Berlin@slu.se**

## 18. Recent wheat disease changes in Brazil

A. Barcellos and C. Turra<sup>1</sup>

The diseases of wheat (*Triticum aestivum* L.) in Brazil, viz. blast, leaf rust and stripe rust, have changed in relative occurrence over recent years. During growing season 2003/2004 wheat blast, first detected in 1985, was reported to cause high levels of infection in some populations around latitude 23°S. It was sporadic until 2009 when it caused significant damage to Brazilian wheat production. The disease was serious in a radius of 250 km, and also reached Central Brazil. Large yield losses occurred even at altitudes close to 1,000 m, where blast had not caused damage previously. It reached 24°S and reduced grain yields from 7,000 kg/ha (in the previous year) to 1,000 kg/ha, even when fungicides were applied. Leaf rust was also atypical in the 2009 growing season. The disease cycle was not concluded because telia developed much earlier than usual. The lack of leaf rust control by fungicides traditionally effective against leaf rust resulted in amended recommendations. While a check race maintained its sensitivity to triazoles, three new races had reduced sensitivity. These results were confirmed under field conditions. We confirmed the efficacy of control using strobilurins, and proposed that triazoles should not be used alone on cultivars susceptible to races with reduced triazole sensitivity. This recommendation is still valid. Although stripe rust is only an occasional disease, it was more widespread than usual in southern Brazil in 2010. From a single focal point, the disease incidence increased to a low-to-intermediate level. Low inoculum pressure was reasonably widespread in commercial cultivars.

<sup>1</sup>OR Melhoramento de Sementes, Av Rui Barbosa 1300, 99050-120, Passo Fundo, RS, Brazil. **Email: amarilis@orsementes.com.br**

## 19. Emerging virulences to race-specific resistance genes in Mexican *Puccinia striiformis* populations

J. Huerta-Espino<sup>1</sup>, M. F. Rodriguez-Garcia<sup>1</sup>, S. A. Herrera-Foessel<sup>2</sup>, and R. P. Singh<sup>2</sup>

Yellow rust, caused by fungus *Puccinia striiformis* f. sp. *tritici*, is an important disease of wheat in the irrigated Bajío and northwestern Mexico, and in the High Plateau of Central Mexico during the summer rainfed season. Race 14E14 virulent to yellow rust differentials carrying resistance genes *Yr2*, 6, 7, and 27 was the most common race before 1995. In 1996, several isolates virulent on the *Yr9* differential were identified among collections from central Mexico and isolate MEX 96.11, virulent to the *Yr2*, 3, 6, 7, 9, and 27 differentials was the most prevalent. Several additional race-specific resistance genes are now defeated by new races, including an unknown resistance gene in "Pollmer" triticale. Virulences to *Yr1* and *Yr8* were detected from 2003 onwards. The *Yr1* and *Yr8* virulent races did not cause losses to the wheat crop other than increased levels of head infection in some cultivars. In 2007 virulence to differentials possessing *Yr17* was detected. During 2008, wheat varieties "Pastor" and "Rebeca F2000", which were highly resistant previously, showed 40 to 50% rust severities in farmers' fields. Isolates tested on the *Yr31* differential confirmed virulence to *Yr31* present in Pastor and its derivatives. Disease data recorded during 2010 in the field on yellow rust trap nurseries that included the Avocet isolines and other varieties, and greenhouse seedling tests, confirmed the existence of virulence for *Yr1*, 2, 3, 6, 7, 8, 9, 17, 27, and 31 in different *Pst* isolates.

<sup>1</sup>Campo Experimental Valle de México INIFAP, Apdo. Postal 10, 56230 Chapingo, Edo. de México, México; <sup>2</sup>International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 México DF, México.  
Email: [j.huerta@cgiar.org](mailto:j.huerta@cgiar.org)

## 20. Reactions of western Canadian wheat and triticale varieties to stripe rust

H. Randhawa, B.J. Puchalski, R. Graf, A. Goyal, T. Despins, D.A. Gaudet<sup>1</sup>

Stripe rust (*Puccinia striiformis*) is an important pathogen of wheat in western Canada. Infections generally are the result of urediniospores blown in from the Pacific Northwest U.S.A. during the spring and early summer. One hundred and four spring wheat and triticale varieties and ten winter wheat cultivars were evaluated in nurseries at Lethbridge and Creston B.C. Infection levels in all nurseries were high. Resistance occurred in all tested varieties in the triticale, amber durum, extra strong and soft white spring classes. Within the red Canada Prairie Spring (CPS) class, newer varieties were resistant but many of the older varieties were susceptible. Among the white CPS wheats, Vista is resistant whereas Snowwhite 475 and Snowwhite 476 are susceptible. Among the hard white wheats, only Karma was resistant whereas Snowstar and Snowbird were susceptible. Fifty-nine percent of the hard red spring wheats (HRS) were resistant; much of the resistance was attributed to the presence of the *Yr17* and *Yr18* resistance genes. Susceptible HRS varieties that are extensively seeded in western Canada include Barrie, Superb, BW881 and BW415. Sixty percent of the varieties belonging to the Hard Red Winter class were resistant. Effectiveness of the *Yr10* gene in Radiant has been lost due to the apparent occurrence of a new race. The lines were tested for the presence of markers for *Lr34/Yr18*, *Yr17*, *Yr36*, and *Yr10* genes.

<sup>1</sup>AAFC Lethbridge Research Center, Box 3000 Lethbridge AB. T1J 4B1.  
Email: [Harpinder.Randhawa@agr.gc.ca](mailto:Harpinder.Randhawa@agr.gc.ca)

## 21. Races and virulences of *Puccinia striiformis* in the United States in 2010

A. M. Wan<sup>1</sup> and X. M. Chen<sup>1,2</sup>

In 2010, 412 samples (336 from wheat, 30 from barley, 2 from rye, 8 from triticale, and 16 from grasses) obtained from 24 states were tested for virulence and race identification. Based on reactions on 20 Yr gene lines, 60 races of *Puccinia striiformis* f. sp. *tritici* (PST) were identified. The most frequent and widely distributed race was virulent to Yr2, Yr6, Yr7, Yr8, Yr9, Yr17, Yr26, Yr27, Yr43, Yr44, YrTr1, and YrExp2. The race with the broadest virulence spectrum was virulent to 15 genes (Yr2, Yr6, Yr7, Yr8, Yr9, Yr10, Yr17, Yr24, Yr26, Yr27, Yr32, Yr43, Yr44, YrTr1, and YrExp2) detected in western U.S.A. The frequencies of the virulences were in the order of Yr6 (94%), Yr2 (93%), Yr9 (91%), Yr7 (89%), Yr44 (89%), YrExp2 (89%), Yr8 (87%), Yr27 (79%), Yr43 (77%), Yr26 (76%), Yr17 (71%), YrTr1 (63%), Yr1 (36%), YrTye (36%), Yr10 (7%), Yr32 (7%), Yr24 (6%), and YrSP (4%). Virulences to Yr5 and Yr15 were not detected. Of 22 races detected using the old differentials, PST-141, PST-142, PST-143, and PST-144 were new and the five most predominant races were in the order PST-100, PST-139, PST-102, PST-127, and PST-98. Seven *P. striiformis* f. sp. *hordei* races (PSH-33, PSH-46, PSH-48, PSH-51, PSH-52, PSH-54, and PSH-81) were detected from barley and grass samples from California, North Dakota, Oregon, Utah, and Washington with PSH-33 the most predominant. These results should be useful for breeding cultivars with effective resistance to stripe rust.

<sup>1</sup>Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430, USA; <sup>2</sup>USDA-ARS, Wheat Genetics, Quality, Physiology, and Disease Research Unit, Pullman, WA, 99164-6430, USA. Email: xianming@wsu.edu

## 22. Potential summer and winter survival regions of the stripe rust pathogen in the United States

D. Sharma-Poudyal<sup>1</sup> and X. M. Chen<sup>1,2</sup>

Stripe rust, caused by *Puccinia striiformis* (*Ps*), is one of the most important diseases of wheat and barley. Epidemics are more frequent in regions where *Ps* can over-summer and over-winter. Regions for potential summer and winter survival of *Ps* were determined in the US using long-term means of temperature, relative humidity, rainfall, dew point and snow depth. A survival index (SI) ranging from 0 (the most unfavorable) to 10 (the most favorable) was developed. *Ps* can over-summer (SI $\geq$ 5) in most of the regions north of latitude 40°N and cannot (SI=0) or can marginally survive (SI=1-4) in most of the regions south of 40°N. *Ps* can over-summer in the highlands of AZ, CO, NC, NM, NV, TN, UT, VA and WV in the Rocky or Appalachian Mountains. Winter survival (SI $\geq$ 5) occurs in most of the regions south of 40°N and the Pacific coast, including AL, AR, AZ, CA, FL, GA, ID, LA, MS, NM, NV, OR, SC, TX and WA. *Ps* cannot over-winter in most of the regions north of 40°N and east of the Rocky Mountains (CO, CT, IA, ME, MN, MT, NE, NH, NY, SD, VT, WI and WY). Winter survival of *Ps* is marginal in DE, IL, IN, KS, KY, MA, MD, MI, MO, NC, NJ, NM, NY, OH, OK, PA, RI, TN, UT and VA. *Ps* can over-summer and over-winter in AZ, CA, ID, NC, NM, OR, PA, VA, WA and WV. These regions may provide primary inoculum for stripe rust epidemics.

<sup>1</sup>Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430, USA; <sup>2</sup>USDA-ARS, Wheat Genetics, Quality, Physiology, and Disease Research Unit, Pullman, WA 99164-6430, USA. Email: xianming@wsu.edu

## 23. Role of barberies in stem rust epidemics and race diversity in Washington and Idaho U.S.A., 2007-2009

T. D. Murray<sup>1</sup>, X. Chen<sup>2</sup>, D. Roberts<sup>3</sup> and Y. Jin<sup>4</sup>

Stem rust of wheat and barley is a chronic disease in eastern Washington and northern Idaho that typically does not cause significant damage because the dry and cool environment is sub-optimal for disease development. Nevertheless, epidemics occur in localized fields and cause significant damage in some years. Despite extensive efforts in Washington from 1944-1981, barberry was not completely eradicated and has made a comeback in some areas. In 2007, two fields of spring barley with severe stem rust were identified in Stevens and Whitman Counties, WA with over 60% yield losses. Samples were collected from these fields and analyzed at the USDA-ARS Cereal Disease Lab in St. Paul, MN. Fourteen races of *Puccinia graminis* f. sp. *tritici* were identified from the collections. Stem rust samples collected from wheat and barley in 2008 and 2009 from other areas of eastern WA and northern ID led to the identification of 11 and 22 races, respectively. Stem rust epidemics in this region are likely the result of inoculum from barberies and not urediniospores from other regions. Because of these outbreaks, we conducted surveys to locate barberies based on anecdotal reports and Barberry Eradication Program records. Barberry bushes were found in over 20 locations in Whitman and Stevens Counties, WA, and Latah County, ID. Consequently, a PNW Barberry Working Group was formed with state and federal personnel from Idaho, Montana, Oregon and Washington to investigate reports of stem rust and barberies and to educate the wheat and barley industries about this forgotten disease.

<sup>1</sup>Dept. of Plant Pathology, Washington State University, Pullman, WA 99164-6430, U.S.A.; <sup>2</sup>USDA-ARS, Wheat Genetics, Quality, Physiology and Disease Unit, Pullman, WA 99164-6420, U.S.A.; <sup>3</sup>Washington State University Extension, Spokane, WA 99202-4799, U.S.A.; <sup>4</sup>USDA-ARS, Cereal Disease Laboratory, University of Minnesota, St. Paul, MN 55108, U.S.A.  
Email: tim\_murray@cahnrs.wsu.edu

## 24. Barberry is more important as an alternate host for stem rust than for stripe rust in the U.S. Pacific Northwest

M. N. Wang<sup>1</sup>, A. Wan<sup>1</sup>, X. M. Chen<sup>1,2</sup> and C. K. Evans<sup>2</sup>

Barberry (*Berberis* spp.) plants are important in the life cycle of the stem rust pathogen (*Puccinia graminis* f. sp. *tritici*, *Pgt*) in many regions of the world, including the Pacific Northwest (PNW), and have been recently reported as alternate hosts for the stripe rust pathogen (*P. striiformis* f. sp. *tritici*, *Pst*). In 2010, we collected aecial samples from *B. vulgaris* plants at five locations. Pathogenicity testing was conducted by inoculating susceptible wheat cultivars Nugaines and Lemhi, incubating them at 20-25°C or at 10°C for 24 h, and growing them at 10-32°C or 8-20°C, respectively. Only *Pgt* was recovered from the samples in May. *Pst* was recovered from the samples in June and July but at lower rates of inoculated leaves (7%, 3%) than those of *Pgt* (12%, 5%), respectively, with more *Pgt* uredinia and fewer *Pst* uredinia on each infected leaf. Most *Pst* isolates were PST-127 and PST-139, predominant races in the region. Only *Pgt* was identified from 393 of 31 bulked and 426 single-aecial DNA samples in PCR tests with ITS and gene-specific primers. Germination of fresh *Pst* teliospores was 12% and the rate increased after one month (53%), two months (79%) and three months (78%) in laboratory conditions. In contrast, the germination rate of *Pst* teliospores collected from the field in December, January and February was 12%, 3% and 1%, respectively, with increased numbers of degraded teliospores, whereas *Pgt* teliospores remained intact and non-germinated until February. The results showed that barberry is not as important as an alternate host for *Pst* as for *Pgt* under PNW conditions.

<sup>1</sup>Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430, USA; <sup>2</sup>USDA-ARS, Wheat Genetics, Quality, Physiology, and Disease Research Unit, Pullman, WA 99164-6430, USA. Email: xianming@wsu.edu

## 25. Identification of *Berberis* spp. as alternate hosts of *Puccinia striiformis* f. sp. *tritici* in China

J. Zhao<sup>1</sup>, H. C. Zhang<sup>2</sup>, J. N. Yao<sup>1</sup>, X. M. Chen and Z. S. Kang<sup>1</sup>

Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is an important disease on wheat in China because of high virulence diversity. Since the discovery of the sexual stage of *P. striiformis* on *Berberis* spp., especially *B. chinensis*, our interests focused on identifying *Berberis* species as alternate hosts of the pathogen in China, the largest stripe rust epidemic area in the world. In 2010 some *Berberis* plants producing aecia were found around wheat fields in three provinces where the occurrence of wheat stripe rust is common. Aecial samples collected from rust-infected *Berberis* spp. were used for PCR amplification with a *Puccinia*-specific primer set. A unique band produced by aecial pustules of three *B. spp.* was the same as that produced by telial samples of *Pst*. Alignment of DNA sequence data showed that the tested aecial samples shared approximately 95% identity with the *Pst* sequence on the NCBI website. Inoculations using germinating teliospores of *Pst* resulted in a few pycnia and aecia on leaves of five *Berberis* species.

<sup>1</sup>College of Plant Protection and Shaanxi Key Laboratory of Molecular Biology for Agriculture, Northwest A&F University, Yangling, Shaanxi 712100, China; <sup>2</sup>College of Life Sciences, Northwest A&F University, Yangling, Shaanxi 712100, China; <sup>3</sup>US Department of Agriculture -Agricultural Research Service and Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430, U.S.A. **Email: kangzs@nwsuaf.edu.cn**

## 26. Stem rust epidemic modeling: adapting ryegrass models to wheat

W. F. Pfender and J. F. Hernandez Nopsa

Epidemiological models are useful to predict the establishment and movement of a plant pathogen into new areas, and to develop decision tools for disease management in situations where genetic resistance is not available or stable. Over the past decade, we have constructed models for epidemic development of ryegrass stem rust (RSR) (caused by *Puccinia graminis* subsp. *graminicola*). We produced algorithms to quantify conduciveness of weather to stem rust infection (Pfender (2003) *Phytopathology* 93:467-477), latent period duration (Pfender (2001) *Phytopathology* 91:111-116), interaction of host development with pathogen activity (Pfender (2004) *Phytopathology* 94:308-316), and pre- and post-infection activity of two major classes of fungicides (Pfender (2009) *Phytopathology* 99:696-703). These components were combined in a simulation model that is currently used as a decision aid for stem rust management in Oregon ryegrass seed fields. A model for overwinter survival is in development. Recently we initiated a research project to adapt RSR epidemic models to wheat stem rust (WSR), because we expect such models to be useful in mitigating the effects of the Ug99 lineage. In initial research, we are developing algorithms for infection risk based on air temperature and leaf wetness duration. We expect this model to help scientists and producers in assessing the risk of disease outbreaks, and in making informed decisions for disease management.

USDA-ARS Forage Seed and Cereal Research Laboratory, 3450 SW Campus Way, Corvallis, OR 97331, USA. **Email: bill.pfender@ars.usda.gov**

## 27. Modeling leaf rust of wheat in response to combined effects of temperature and wetness duration

*P. Gautam, K. D. Bondalapati and J. M. Stein*

Leaf rust of wheat, caused by *Puccinia triticina*, can cause yield losses exceeding 50% depending upon the resistance level and growth stage at which infection occurs as modified by prevailing environmental conditions. Annual losses in the US wheat industry due to leaf rust are estimated to be greater than stem rust or stripe rust due to its more frequent and widespread occurrence. A greenhouse experiment was conducted to determine the impact of temperature and wetness duration on infection by *P. triticina*. Six cultivars; each three of spring and winter wheat, were evaluated. Plants were inoculated at the two-leaf stage with a bulk culture of *P. triticina* collected from wheat plots in South Dakota during 2010. Inoculated plants were then maintained in a growth chamber at 100% relative humidity under varying temperature (5-35°C) and duration (0-24 hr) combinations. Plants were then incubated in a greenhouse to allow for symptom development. Responses were determined by calculating percent symptomatic leaf area and number of uredinia per leaf sampled on the 13<sup>th</sup> day after inoculation. A Weibull function was used to model the infection in response to temperature and moisture duration. In general, winter wheat cultivars had higher leaf infection compared to spring wheat and the optimal temperature for infection was ~20°C. No symptoms developed when the wetness duration was less than four hours, at any temperature, and when the temperature was greater than 27.5°C. Field validation of the model for predicting leaf rust in wheat is in progress.

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Department of Plant Science, South Dakota State University, Brookings, SD 57007, U.S.A. **Email:** [Jeff.Stein@sdstate.edu](mailto:Jeff.Stein@sdstate.edu)

## 28. Wheat leaf rust (*Puccinia triticina* Eriks) genome sequencing and comparative resources for rust fungi

*C. Cuomo<sup>1</sup>, J. Fellers<sup>2</sup>, G. Bakkeren<sup>3</sup> and L. Szabo<sup>4</sup>*

Wheat leaf rust, *Puccinia triticina* Eriks, is an obligate biotrophic fungus that causes significant yield and quality losses each year. Unlike other wheat rusts, the leaf rust alternate host is not present in North America and the fungus propagates by asexual urediniospores. Race 1 BBBB is the most avirulent race and was chosen for sequencing and assembly. The complete genome was sequenced to 16X coverage using Roche 454 technology and assembled into a preliminary contig length of 126.6 Mb in 24,423 scaffolds. Four cDNA libraries made from fresh urediniospores, germinated urediniospores, infected leaf tissue, and isolated haustoria were also sequenced to develop gene call models and a preliminary computer annotation identified 11,638 genes. Race 1 and three other races were sequenced with Illumina Solexa and aligned back to the Race 1 assembly for SNP analysis. Race 9 and Race 161 are parents of a mapping population created by Peter Dyck in the 1960s. Race TNRJ was collected in Kansas and was the most virulent race available at the time of the project. BBBB, Race 9, Race 161, and TNRJ had 233,223, 265,611, 310,819, and 270,595 total SNPs, respectively. Future sequencing will evaluate different races from different lineages to examine fluctuations in the genome associated with adaptation.

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<sup>1</sup> Broad Institute of MIT and Harvard, Cambridge, MA, U.S.A.; <sup>2</sup> USDA-ARS HWWGRU, Manhattan, KS, U.S.A.; <sup>3</sup> Agriculture & Agri-Food Canada, Summerland, BC, Canada; <sup>4</sup> USDA-ARS, Cereal Disease Laboratory, University of Minnesota, St Paul, MN, U.S.A. **Email:** [jpf@pseru.ksu.edu](mailto:jpf@pseru.ksu.edu)

## 29. Functional genomic approaches for the wheat leaf rust fungus

G. Bakkeren<sup>1</sup>, X. Song<sup>1</sup>, V. Panwar<sup>1</sup>, R. Linning<sup>1</sup>, D. Joly<sup>1</sup>, X. Wang<sup>2</sup>, C. Rampitsch<sup>2</sup>, B. McCallum<sup>2</sup>, J. Fellers<sup>3</sup> and B. Saville<sup>4</sup>

The expansion of genomic resources for cereal rust fungi and their comparison has released a torrent of new ideas. Utilizing this information provides new approaches to assist pathologists and agriculture in general. The sequencing of gene transcripts during infection and the analysis of proteins from haustoria has yielded candidate virulence factors among which could be defense-triggering avirulence genes. Genome-wide computational analyses, including genetic mapping and transcript analyses by RNA sequencing of many fungal isolates, will predict many more candidates. We have made progress on converting this knowledge to beneficial outcomes by initiating development of functional assays such as leaf infiltration using *Agrobacterium* and *Pseudomonas* species for delivery of cloned fungal effectors. This will allow the screening of wheat germplasm for novel sources of resistance genes to be used for targeted breeding. Comparative analyses have also revealed fungal virulence genes providing fungal targets for disease control in host-produced RNA silencing approaches. This technology not only suppresses fungal development of various cereal rust species, but also allows for functional analysis of specific target genes during infection.

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<sup>1</sup>Agriculture and Agri-Food Canada, Pacific Agri-Food Research Center, Summerland, BC V0H 1Z0, Canada; <sup>2</sup>Agriculture and Agri-Food Canada, Cereal Research Center, Winnipeg, MB R3T 2M9, Canada; <sup>3</sup>USDA-ARS-HWWGRU, Manhattan, KS 66506, U.S.A.; <sup>4</sup>Trent University, Peterborough, ON K9J 7B8, Canada. **Email: Guus.Bakkeren@agr.gc.ca**

## 30. Development of SNP markers to infer evolutionary relationships of *Puccinia triticina*

M. Liu and J. Kolmer<sup>1</sup>

Previous studies on *Puccinia triticina* based on SSR markers revealed tremendous genetic differentiation among world-wide populations collected from common wheat, and also between isolates collected from durum and common wheat. To further infer the evolutionary relationships among the populations with the aid of coalescence theory and DNA sequences data, SNP markers of high resolution are needed. We examined three strategies for this purpose: 1) SNPs in intron regions of house-keeping genes; 2) SNPs in SSR marker flanking regions; 3) SNPs in random hypovariable regions through the IGV (Integrated Genome Viewer). For house-keeping genes, fragments of 800-900 bp for RNA polymerase II largest subunit (RPB1), the 2<sup>nd</sup> largest unit (RPB2), and elongation factor 1 (EF1-alpha) were examined. Each of these regions contains 3 - 4 introns. With a panel of seven tested samples, DNA sequence variation ranges from 2 - 4 SNPs/Kb (per 1,000 base pairs). Among 16 SSR-flanking regions, seven loci were successfully sequenced revealing variation ranging from 2 SNPs/Kb to 11 SNPs/Kb. Through the whole genome viewer, hypovariable regions with variation from 20 to 50 SNPs/Kb were examined. SNP markers from the different regions represent different evolutionary rates. Therefore using a combination of these markers to infer evolutionary relationships would eliminate to some extent, expectation bias.

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<sup>1</sup>USDA-ARS Cereal Disease Laboratory, 1551 Lindig St., St. Paul, MN 55108, USA. **Email: miao.liu@ars.usda.gov**

## 31. A method to linearize Stakman infection type ratings for statistical analysis

*D. Zhang<sup>1</sup>, R. Bowden<sup>2</sup> and G. Bai<sup>2</sup>*

Cereal rust seedling infection types (ITs) are often recorded using the Stakman 0 to 4 scale. However, ITs recorded with this scale can include special annotations and complex ranges that make it difficult to analyze statistically. We propose a conversion algorithm that results in linearized scores on a 0 to 9 scale. First, simple infection types are converted as follows: 0, 1<sup>-</sup>, 1, 1<sup>+</sup>, 2<sup>-</sup>, 2, 2<sup>+</sup>, 3<sup>-</sup>, 3, and 3<sup>+</sup> are coded as 0, 1, 2, 3, 4, 5, 6, 7, 8, and 9, respectively. The symbol for hypersensitive fleck (;) is converted to 0 and IT 4 is converted to 9. Special annotation codes C and N are ignored. Double minus and double plus annotations are converted to single minus and single plus, respectively. Complex ranges such as ;12<sup>+</sup> are first collapsed to ;2<sup>+</sup>. Then the first and last ITs of the range are converted and averaged, with the first IT double-weighted because the most prevalent IT is listed first. Mesothetic infection types X, Y, and Z are more problematic to convert. We suggest that X<sup>-</sup>, X, and X<sup>+</sup> be converted to linearized scores of 4, 5, and 6, respectively. Y and Z ITs are treated similarly. The typical purpose of the Stakman scale is accurate description of infection phenotypes for recognition and postulation of particular resistance genes. However, the linearized Stakman scale enables the use of Stakman ITs for other purposes such as association mapping or ranking of resistance levels.

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<sup>1</sup>Department of Agronomy, 2004 Throckmorton Hall, Kansas State University, Manhattan, KS 66506, USA; <sup>2</sup>USDA-ARS Hard Winter Wheat Genetics Research Unit, 4008 Throckmorton Hall, Kansas State University, Manhattan, KS 66506, USA. **Email:** [robert.bowden@ars.usda.gov](mailto:robert.bowden@ars.usda.gov)