

## Lecture 2

### *Puccinia graminis tritici* race Ug99 and the re-emergence of stem rust research

#### Introduction

Much of our knowledge of cereal rust genetics was based on wheat stem rust, a major problem in many regions in the first half of the C20<sup>th</sup>

The reasons for the international decline in stem rust incidence and consequential damage after the 1960s appear to be varied:

- barberry removal
- changed agronomy; earlier maturity, less inoculum carry-over
- resistant varieties in the worst-affected areas

Whatever the reasons for the initial decline, it is likely that the long-term, widespread use of *Sr31* played a stabilising role in restricting stem rust outbreaks and in reducing inoculum carry-over in many areas.

*Sr31* was derived from wheat x Petkus rye hybrid material that was produced before the Second World War. Following the division of Germany at the end of the War, the materials were also divided between the West and the East, and were then independently used to develop varieties on both sides. These varieties were used in Western Europe, and the East German materials went on to Russia and China, and eventually to CIMMYT where the Bezostaya-derived lines Kavkaz and Aurora were widely used in the Winter X Spring crossing period. Many CIMMYT varieties, such as Bobwhite, Veery and Kauz and derivatives, were developed and distributed throughout the developing world where they became very significant and widely grown cultivars.

In 1998, stem rust was found on *Sr31*-carrying varieties in Uganda. Virulence on genotypes with *Sr31* was confirmed in laboratory tests in South Africa by Pretorius et al. (2000). The isolate used was designated Ug99, which became the famous name that we all recognise currently. Although the race may have been earlier in Kenya, it is known to have caused damage in Kenya and Ethiopia in 2003 and thereafter.

Ug99 was confirmed in Yemen in 2006 and at two sites in Iran in 2007. These observations tended to confirm the predicted likely migratory pathways based on the study of weather patterns, and past experience with the likely movement of a *Yr9*-virulent race of *P. striiformis* from East Africa to the Indian subcontinent. Saari and Precott (1985) documented the migration of a X8156 (Mexipak 65, Kalyansona, etc.) attacking race of *P. striiformis* from Turkey to the Indian subcontinent. Thus there was precedent to believe there could be an inevitable migration of Ug99 to the India and possibly beyond.

#### Why is Ug99 so feared?

Ug99 is not only virulent on wheat lines with *Sr31*, but also possesses virulence for certain genes present in lines that are resistant in other countries. These genes include *Sr30* and *Sr38*. Mutant derivatives with separate virulences for *Sr24* (TTKST) and *Sr36* (TTTSK) have appeared in Kenya, and the former has caused losses in cultivar Kenya Mwamba with *Sr24*. Genes *Sr36* and *Sr24*, which have provided resistance in Australia

for many years, were originally seen as being potentially useful in the obtaining resistance to Ug99, but their rapid loss of effectiveness was a major disappointment. Ug99 seems to be a very competitive race. How did Ug99 arise?

**Table 1** Four gene sets and letter code system for designating races *P. graminis* f. sp. *tritici* according to the North American system. Avirulences for TTKSK are shown in bold

|            | Four gene differential sets |             |             |                     |
|------------|-----------------------------|-------------|-------------|---------------------|
|            | <i>Sr5</i>                  | <i>Sr21</i> | <i>Sr9e</i> | <i>Sr7b</i>         |
|            | <i>Sr11</i>                 | <i>Sr6</i>  | <i>Sr8a</i> | <i>Sr9g</i>         |
|            | <b><i>Sr36</i></b>          | <i>Sr9b</i> | <i>Sr30</i> | <i>Sr17</i>         |
|            | <i>Sr9a</i>                 | <i>Sr9d</i> | <i>Sr10</i> | <b><i>SrTmp</i></b> |
| Pgt letter | <b><i>Sr24</i></b>          | <i>Sr31</i> | <i>Sr38</i> | <i>SrMcN</i>        |
| B          | L                           | L           | L           | L                   |
| C          | L                           | L           | L           | H                   |
| D          | L                           | L           | H           | L                   |
| F          | L                           | L           | H           | H                   |
| G          | L                           | H           | L           | L                   |
| H          | L                           | H           | L           | H                   |
| J          | L                           | H           | H           | L                   |
| K          | L                           | H           | H           | H                   |
| L          | H                           | L           | L           | L                   |
| M          | H                           | L           | L           | H                   |
| N          | H                           | L           | H           | L                   |
| P          | H                           | L           | H           | H                   |
| Q          | H                           | H           | L           | L                   |
| R          | H                           | H           | L           | H                   |
| S          | H                           | H           | H           | L                   |
| T          | H                           | H           | H           | H                   |

This system assigns a letter for each four-gene set of differential lines based on the pattern of low (L) and high (H) seedling responses, where L = avirulent and H = virulent on each specific Sr gene line.

I personally disagree with the designation TTKSK; in my opinion the designation should be PTKSK, because the differential with *Sr21* confers a high intermediate response and is resistant in the field in Kenya. Gene *Sr21* is originally from *Triticum monococcum*, but a hexaploid derivative was chosen as the differential. Genes transferred from levels of lower ploidy to higher ploidy often show diluted incompatibilities. In a survey of diploid wheats carried out by Rouse et al. (2009; BGRI Obregon Proceedings) diploid wheats with *Sr21* were classified as resistant, but the actual low infection type was somewhat intermediate and significantly higher than that seen with USA race MCCFC (race 56). Perhaps Ug99 is heterozygous for avirulence.

#### Addressing the Ug99 threat

After Ug99 began to spread in Kenya and Uganda, Dr N. Borlaug led an international campaign to attract attention to the threat and an effort to gain funding to address it. A

Global Rust Initiative (later BGRI) was established and Cornell University obtained significant funding for a “Durable Rust Resistance in Wheat” project involving North American and other research institutions in collaboration with CIMMYT and ICARDA, and government agencies in Kenya and Ethiopia. FAO became an additional significant participant in BGRI to enable the effort to include countries other than those covered by DRRW, as well as providing a greater coverage for pathogen surveillance and for seed production and distribution systems throughout the entire region under threat. Several national programs are now part of BGRI.

#### Main research projects of DRRW

The main research projects of DRRW were under three categories, with additional efforts aimed at training, and awareness issues.

#### **Surveillance**

It is important to know where the pathogen is right now, and where it is likely to go in the future. On the ground surveillance is a critical aspect of this. Real time meteorological data information can then be used to predict possible future occurrences, and this work, to be conducted at the FAO Office in Rome, is set up to link rust sampling on the ground, with climatic data, and the results of race analysis in the shortest possible timeframes. The on-ground work involves both rust surveys of farm fields and the use of trap plots using key genotypes to provide early indications of possible races. Race analysis will as much as possible involve local laboratories with facilities and expertise; otherwise it can only be done in Canada or the USA during limited periods in the northern winter. Greenhouse facilities will be established in Kenya and Ethiopia for local work in those countries.

Correctly identified genetic stocks will be essential for use in trap plots and as differentials for race analysis

At present there is no real scope for molecular methods of race analysis.

#### **Resistance**

- Very few ‘wheat’ genes are effective, and those that are effective are likely to provide only short term protection, e.g. *SrTmp*, *Sr13*, *Sr37*. *Sr36* and *Sr24* have already been overcome. Up to three new genes for resistance are indicated.

- Several alien resistance genes are effective, e.g., *Sr22*, *Sr26*, *Sr44*, *Sr45*, *Sr32*, *Sr33*.

- Many accessions of related species are resistant, but the extent of genetic variation is unknown. The most promising include *Aegilops* species in the sitopsis section, *Thinopyrum/Agropyron* species and *Secale* species. Should *Secale* be used as a source of resistance in wheat?

- Chromosome engineering projects are aiming to improve translocations already present in wheat, but unlikely to be exploited without reductions in the amount of alien chromatin.

- Some projects are focusing on slow rusting minor gene resistances. *Sr2* seems to be an important component of some resistances identified so far. Some lines with *Lr34* have resistance that seems to be based on complementary interaction; this resistance occurs in some Canadian varieties.

- What is the potential for genetic engineering? – using existing genes? Cloning resistance genes and transferring them from other species
- Can we utilize non-host resistance? What is non-host resistance?

### **Breeding for resistance to Ug99**

The DRRW project has provided funds for establishing screening nurseries in rust hotspots of Njoro in Kenya and at Kulumsa (bread wheat) and Debre Zeit (tetraploid wheat) in Ethiopia, in conjunction with the national agricultural organisations. These facilities are available to international breeding groups on a funded basis for some collaborators, or a fee-for service basis for developed countries.

Guidelines and protocols for the importation, growing and management of materials being sent to those countries have been established. Obviously, strict quarantine procedures and timelines must be applied to all activities. There are provisions for two generations per year.

With experience and a sound knowledge of the host pathogen genetics much of the breeding work should be possible in the absence of access to Ug99. Validation tests using Ug99 can be performed on selected materials.