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## STATUS OF WHEAT BREEDING AT GLOBAL LEVEL FOR COMBATING Ug99 – A REVIEW

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### ABSTRACT

Stem rust in wheat remained under control for several decades all over the earth by the mid-1990's resulting in less emphasis on breeding for resistance to this disease and had not been priority in research for considerable era. The manifestation and expansion of races of *Puccinia graminis* f. sp. *tritici* commonly known as Ug99 with virulence for the *Sr31* resistance gene in 1998 in Uganda renewed interest in breeding for resistance to stem rust of wheat. Wheat community responded instantaneously. Global Ug99 stem rust screening services were launched in 2005 under the shade of Borlaug Global Rust Initiative (BGRI) in Kenya and Ethiopia with purpose to recognize auxiliary sources of resistance. Screening in Kenya and Ethiopia of wheat materials from Asian countries carried out in 2005-06 disclosed a very low frequency of lines resistant to Ug99 and its variants. Considerable achievements have been attained identifying diverse race-specific resistance and adult plant resistance (APR) genes that can be exploited to improve wheat germplasm to contest the hazard. Four more genes namely *Sr55*, *Sr56*, *Sr57* and *Sr58* along with the *Sr2* gene, now have been characterized to confer slow rusting. New perspectives on rust control in the future through the development of multiple resistance gene cassettes through cloning of some rust resistance genes opens. The strain spread to eastern and southern Africa and in Iran. Meanwhile evolution has also been observed in the strain generating new variants. Currently, 10 variants in the Ug99 race group have been perceived in twelve countries. SAARC wheat disease trap nursery has been developed in the vicinity of Iran where Ug99 was perceived in 2007. Data designates that *Pgt-Ug99* (TTKSK) reported from Iran in 2007 has not evolved further, nor has it extended to adjacent Pakistan or India to impose any crop failure.

**Keywords:** Black stem rust, *Puccinia graminis* f. sp. *tritici*, *Triticum aestivum*, Ug99, wheat.

### INTRODUCTION

Wheat (*Triticum aestivum* L.) plus rice and maize is executing fifty percent of the calories requirement of the globe (Mateen *et al.*, 2015). Wheat holds the status of 'King of cereals' due to the acreage, productivity and the position in the international food grain trade. Many biotic and abiotic factors affect yield components of wheat responsible for the gap between potential and actual yield. The most important restraint to sustainable wheat cultivation is rust diseases. These diseases have been addressed the most, leading to discovery of various principles of breeding for disease resistance (Biffen, 1905; Cragie, 1927; Caldwell, 1968; Flor, 1971). The rusts is a group of fungi that are among the most vicious

disease causing agents equipped with potential to depress yield considerably (Park, 2007). It is estimated that annually cereal rusts reduce approximately 10 percent total grain yields and have caused food crisis under epidemic conditions (Agrios, 2005). All three rust pathogens have caused severe epidemics both historically as well as recently (Roelfs, 1977; McIntosh *et al.*, 1995; Leonard, 2001; Hodson, 2011). The triumph of these pathogens in an agricultural environment is owing to their capacity to extend by the wind over long distances and their talent to adapt to host resistance (Kolmer, 2005). Several cases exist where these pathogens overcame new resistant wheat varieties only few years after they were first cultivated at large scale in the field (Bayles *et al.*, 2000; Jin *et al.*, 2008). After the collapse of *Yr9* resistance gene in the final decade of the last century, numerous cultivars were released with the

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incorporation of resistance gene *Yr27*. One such important cultivar in Pakistan is Inquilab-91, is highly vulnerable to stripe rust (Singh *et al.*, 2004).

Optimum temperature requirements in three rusts are not similar. Stem rust grows in the warm (2-40 °C) temperatures and stripe rust requires the cool (0-15 °C), whereas leaf rust has mild temperature (2-35 °C) requirements (Roelfs *et al.*, 1992). Though their optimum environmental conditions are slightly different, these rusts are present globally, wherever wheat is grown. They are present simultaneously in one field frequently, during different stages of the wheat development and in different severities. Wheat producing regions are differentially apposite, for the development of three rust diseases (Saari and Prescott, 1985). The pathogens causing these diseases are highly specific with conical host array (Hodson, 2011).

Research and advisory activities have been influenced substantially by fiscal and community disorders from crop losses following epidemics. The world has largely been unhurt from stem rust for over three decades (Singh *et al.*, 2008) exceptional case is in Ethiopia during 1993 and 1994 (Shank, 1994) resulted in a decline in research activity against the malady. It is not astonishing that there are many wheat scientists who have not seen this disease in the field. In 1999, a new strain of the stem rust pathogen, commonly referred to as Ug99 (formally known as race TTKSK), virulent on previously resistant wheat cultivars was documented in Uganda. Later Ug99 and its lineage have spread within eastern Africa, across the Red Sea into Yemen and into Iran. Accordingly, attention has been drawn to novel strain of black rust at global level virulent to good number of the commercial wheat varieties cultivated worldwide (Singh *et al.*, 2006).

**Nature of the dilemma:** Eastern Africa has played a critical role in relation to stem rust epidemiology constantly most likely due to ecological location and climatic conditions of the region, and the continuous cultivation of the wheat during the year providing green-bridge for survival of inoculum. The environmental condition prevailing in highlands of eastern Africa facilitates populations of stem rust to persist throughout the year and these conditions provide support to the evolution of new physiological strains. In 2006, a variant of Ug99 with added virulence on stem rust gene *Sr24* has further enhanced the susceptibility of wheat to stem rust globally (Jin *et al.*, 2008). A considerable area (18 million

hectares) in south Asia has suitable conditions for a stem rust epidemic (Reynolds and Borlaug 2006). These regions fall along the potential migration path of the Ug99 race and account for roughly one fourth of global wheat acreage and one fifth of global production.

Ug99 is distinguished by virulence for gene *Sr31* famous to be situated in the translocation 1BL.1RS (Singh *et al.*, 2006). This translocation not only conferred resistance against wheat rusts but affected the yield parameters as well as quality. Once in the CIMMYT's spring wheat germplasm seven varieties among ten inherited 1BL.1RS has now decreased up to three in more recent advanced lines. The *Sr31* ensured security against stem rust until the emergence of the Ug99 (Pretorius *et al.*, 2010). With the emergence of Ug-99 numerous important stem rust genes became ineffective that were otherwise resistant such as *Sr38* transferred from *T. ventricosum* Ces. (syn. *Aegilops ventricosa* Tausch.), and *Sr24* from *Agropyron ponticum* Nevski (Singh *et al.*, 2006). Moreover, many of the resistant lines possessed *Sr24* and *Sr36* (Jin *et al.*, 2007, 2008) to which races TTKST and TTTSK are virulent, respectively. It seemed that Ug99 will spread like a tsunami from CEA across the world resulting crop collapse and gloom in the overpopulated subcontinent (Singh *et al.*, 2006, 2008a, 2011). The disease is threatening 20% the world's wheat in Central and North Africa, the Middle East and Asia (Dixon *et al.*, 2009).

**World war against Ug99:** Wheat scientists and research leaders responded to the global threat from Ug99 positively participating in the global effort to mitigate the threat. Research is needed to improve our comprehension of stem rust in the context of contemporary cropping practices, wheat cultivars, and pathogen populations as much of our current understanding is based on more than fifty year-old data, which must be updated. This is essential because circumstances have changed completely as a result of green revolution in 1960's.

Identification and molecular characterization of innovative resistance genes remains of paramount imperative to augment resistance assortment and stability in wheat germplasm, since the dangerous races of stem rust pathogen persist to cause (Basnet *et al.*, 2015).

The Borlaug global rust initiative ([www.globalrust.org](http://www.globalrust.org)) was instigated to facilitate to take action against this severe hazard to the globe's wheat production. The Initiative has been maintained by a number of

international institutions and foundations and has led to organized action at an international scale (Wellings, 2011). BGRI attained several achievements (Hodson *et al.*, 2012). Singh *et al.* (2006, 2008, 2011, 2015) documented the evolution and geographical spread of the Ug99 race group at regular intervals in a series of reviews. South Asian Association for Regional Cooperation (SAARC) has developed a SAARC wheat disease trap nursery (Prashar *et al.*, 2010) to keep conscious with the prevailing situation of threat in the region.

“Borlaug Global Rust Initiative” is working upon following approach to alleviate the potential of epidemics,

- 1) Monitoring the spread of race Ug99
- 2) Identification of resistant sources through screening of existing germplasm
- 3) Distributing selected material for breeding or to utilize as varieties directly
- 4) Incorporation of resistance from diverse sources into high yielding through breeding

**Monitoring the spread of race Ug99:** Presently, Ug99 (race TTKSK) is the only known pathotype substantiated outside of Africa. Airflows out of Yemen exhibited the same general pattern as in previous years, i.e. wind movement from Yemen to south Iran (Nazari *et al.*, 2009). One divergence with preceding years was a tendency for wind to move in a northwestern direction from Yemen. Stem rust incidence was reported from Israel and Lebanon in 2010; but incidence of Ug99 was not confirmed (Singh *et al.*, 2008). Ug99 races carrying combined *Sr31* + *Sr24* virulence are spreading quickly throughout Africa and it is considered likely that expansion of geographical distribution of Ug99 related races in the future. Additionally, virulence to the *SrTmp* gene has now been attained by the latest variants detected in Kenya (races TTKTT and TTKTK). One of these variants (TTKTK) appears to spreading quickly, also being detected in 2014 in Egypt, Eritrea, Rwanda and Uganda (Patpour *et al.*, 2015). This is the earliest report of Ug99 race group in Egypt. Attempts should be exaggerated in affected countries as well as in neighboring regions. So far, 10 variants in the Ug99 race group have been detected in twelve countries (Patpour *et al.*, 2015).

Sound distributed precipitation in the Rift Valley Epidemiological Zone and the continuous availability of the main host or the green bridge appear to provide

favorable environment (Zadoks and Rijsdijk, 1984). This situation is in stark contrast with that in the Iranian Epidemiological Zone and in the Indian Punjab Epidemiological Zone, where *Pgt*-favorable weather does not prevail for most of the time and the pathogen moves to cooler areas to survive the hot summer months. In the Rift Valley Epidemiological Zone, *Pgt* is endemic as the urediniospore survives in situ in the same area and re-occurs each season. Since the *Pgt* is in continuous contact with the main host or green bridge, the pathogen is able to quickly evolve new variations. For example, *Pgt*-Ug99 (PTKS) was first detected in Uganda in 1999 and from adjacent Kenya; by 2007 three more new variations namely TTKSK, TTKST and TTTKS were reported. In contrast, *Pgt*-Ug99 (TTKSK), reported from Iran in 2007, has not evolved further till 2013. A series of studies (Nagarajan *et al.*, 2012, 2013, 2014) has demonstrated that, apart from various other epidemiological impediments, the sowing time, growth and maturation of wheat varies widely within and between the three epidemiological zones and this will check the *Pgt* spread over a large area. During previous two decades two “mega-cultivars” ‘PBW343’ and ‘Inquilab 91’ were being cultivated on large area in South Asia, both of which were susceptible to Ug99. Occurrence of stem rust in Pakistan in 2009 alarmed of Ug99 attack. Investigations were carried out at Murree in Pakistan and at the Cereal Research Centre, Winnipeg, AAFC, Canada. Analyses of all isolates were recognized as race RRTTF. This race has also been branded in Ethiopia (2007) and in Yemen (2007, 2008). RRTTF has reported virulence on *Sr13*, *Sr36* and *SrTmp*. It is avirulent on *Sr8a*, *Sr9e*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr31*, *Sr32*, *Sr39*, *Sr40*. Sealed urediniospores were also tested in PBI, Sydney University, Australia for DNA fingerprinting and negative results were acquired for Ug99. Combined analyses nullified prevalence of Ug99 in Pakistan (Mirza *et al.*, 2010). The *Pgt*-Ug99 (TTKSK) reported from Iran in 2007 neither evolved further, nor it spread to Pakistan or India to inflict any crop loss.

**Identification of resistant sources:** By the end of 2006, the screening included germplasm from 22 countries in the region with more detailed resistance/susceptibility ratings obtained on varieties covering an estimated 75 million ha. Only 5% of the commercial cultivars were resistant (Singh, 2015). Considerable progress has been achieved. The screening facility offered by the Kenyan Agricultural Research Institute (KARI), is playing an

important role in identifying resistance against Ug99. CIMMYT's role in evolving these varieties is adequately obvious as several of them materialized from this organization. The seed multiplication and delivery of these lines is being done involving both public and private sector (Wheat Atlas by CIMMYT, Int.). Postulation data indicates 21.5% of the lines carry various race-specific resistance genes (Singh *et al.*, 2015). Much of the research effort is directed at identifying and utilizing durable sources of resistance. Durable Rust Resistance in Wheat project is to recognize sources of resistance from gene pools, introgression and cytogenetic manipulation of new sources of resistance to determine of combinations of resistance genes, and develop germplasm (Pumphrey, 2012).

**Distributing selected material:** Various institutes and organizations select many advantageous entries from the Stem rust screening nurseries (SRSN). Selection is multiplied to ensure that seed of high yielding, stem rust resistant materials is made available to as many farmers as possible to ensure that their wheat crop is not destroyed by stem rust (Mirza *et al.*, 2009; Sharma *et al.*, 2013; Bajgain *et al.*, 2015). This practice has helped to reduce area under Ug99 susceptible wheat cultivars.

**Wheat breeding for resistance against Ug99:** More than 50 resistance genes have been catalogued (Nazari *et al.*, 2008) merely a few are valuable against Ug99 (Singh *et al.*, 2006, 2008). Plants with some of these genes encompass unpleasant agronomic traits (McIntosh *et al.*, 1995). Despite the fact these genes have been introduced into wheat, have not been deployed in commercial cultivars (Yu *et al.*, 2011). *Aegilops speltoides* has been source of genes for stem rust resistance for example, *Sr32*, *Sr39*, and *Sr47* confer resistance to TTKSK (Jin *et al.*, 2007). Singh *et al.* (2008) advocate that lines with shortened or modified alien chromosome segments can be used successfully to substitute for chromosome fragments of wheat *boeoticum* chromosome segment carrying *Sr22* has limited the use of this gene in wheat breeding programs association of yield depression with the *T. monococcum* ssp. (The *et al.*, 1988). However, lines with *Sr22* and modified *T. monococcum* segments have been developed recently (Olson *et al.*, 2010).

Recently three pleiotropic APR genes have been identified to confer Adult Plant Resistance (non-race-specific durable resistance) along with other QTL Sr55

(=Lr67/Yr46/Pm46), Sr57 (=Lr34/ Yr18/ Pm38/ Sb1/Bdv1), and Sr58 (=Lr46/Yr29/Pm39) and a fourth gene Sr56 (Bansal *et al.*, 2014; Herrera-Foessel *et al.*, 2014; Singh *et al.*, 2012a, 2013). Presence of Sr2 in all resistant parents was an interesting feature. A high-yielding spring bread wheat germplasm developed and distributed worldwide by CIMMYT has adequate frequency of APR to all three rusts, including the Pgt Ug99 group (Singh, 2012).

Currently molecular markers associated to *Sr* genes are one of the focus areas of research. Markers linkage with genes *Sr2*, *Sr13*, *Sr22*, *Sr25*, *Sr26*, *Sr28*, *Sr32*, *Sr35*, *Sr39*, *Sr40*, *Sr47*, *Sr52*, *SrCad* and *SrWeb* have been documented (Spielmeyer *et al.*, 2003; Hayden *et al.*, 2004; Khan *et al.*, 2005; Mago *et al.*, 2005, 2009, 2011; Dundas *et al.*, 2007; McNeil *et al.*, 2008; Yu *et al.*, 2009; Hiebert *et al.*, 2010, 2011; Liu *et al.*, 2010; Niu *et al.*, 2011; Periyannan *et al.*, 2011; Qi *et al.*, 2011; Simons *et al.*, 2011; Klindworth *et al.*, 2012; Rouse *et al.*, 2012; <http://maswheat.ucdavis.edu/>). These markers will improve the potential of incorporating *Sr* genes into susceptible varieties to Ug99 but widely adapted and assist for the development of new elite lines resistant to Ug99 and its derivatives.

**Justification to continue research against wheat rusts:** However phenomenon of sexual recombination, mutation or somatic hybridization followed by selection whenever the new race has a selective advantage due to frequent evolution and selection of virulence in pathogen arise new strains of rust pathogens (Singh *et al.*, 2002). New races of wheat rusts complicate the struggle of wheat scientists to breed rust resistant wheat cultivars. New races may also be introduced into a new area through migration e.g. *P. striiformis* race with virulence for *Yr9* is understood to have migrated from the East Africa to South Asia (Hodson, 2011). Resistance could be conquered with the appearance of new races of the stem rust pathogen. Hence, it is important to be aware of the nature of resistance in these cultivars. Further sources of the potential genetic resistance need to be classifying to exploit.

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