Capturing new genetic variation for rust resistance among the Watkins collection of pre-Green Revolution wheats - discovery to deployment and cloning

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The Green Revolution involved the deployment of reduced height (*Rht*) genes to generate shorter wheat varieties with increased grain yields. It also contributed to a reduction in genetic diversity in the modern gene pool. Therefore, the pre- Green Revolution tall wheat landraces may provide a reservoir of genetic variation for economic traits such as rust resistance. Considering the breakdown of a suite of rust resistance genes through the emergence of currently predominant pathotypes (e.g. Ug99 and high temperature adapted isolates of the stripe rust pathogen) after three decades of Green Revolution, the discovery, characterisation and deployment of diverse sources of resistance remains a high priority. We have screened the Watkins wheat landrace collection and discovered, characterised and formally named a suite of new rust resistance genes including *Yr47*, *Yr51*, *Yr57*, *Yr63* and *Sr49*. In addition, genotypes carrying potentially new genes for resistance to three rust pathogens are currently being investigated by students from seven nations representing three continents (Australia, Asia and Africa). *Yr47*, *Yr51*, *Yr57* and *Lr52* have been backcrossed into modern cultivars including the widely adapted cultivar PBW343 (Atilla) using markers developed in our research program. Development of triple rust resistant derivatives in modern wheat backgrounds is in progress. Stocks carrying *Yr47*, *Yr51*, *Yr57* and *Lr52* have been mutated to facilitate cloning of these loci for their eventual use in development of multi-gene cassettes for transformation.

Rapid isolation and increase of virulent *Pgt* races and evaluation of germplasm in single-race field nurseries in Ethiopia

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Wheat stem rust is one of the major wheat yield limiting factors in Ethiopia. A stem rust epidemic occurred in the wheat belts of Arsi and Bale zones in the 2013-2014 crop season caused by *Pgt* race TKTTF that is virulent to the widely grown Ug99-resistant variety Digelu. This epidemic highlighted the need for wheat varieties with resistance to multiple *Pgt* races. This study was therefore, carried out to evaluate the reaction of the major Ethiopian varieties and advanced breeding lines against the dominant *Pgt* races in Ethiopia. Races TKTTF, TTKSK, TRTTF and JRCQC were isolated from field samples and multiplied on the susceptible cultivar McNair starting in May 2014. Four wheat stem rust nurseries, each inoculated with a single *Pgt* race, were established at Kulumsa and monitored from July through October, 2014. Each nursery included 34 entries in two replicates and 137 entries in a single replicate, augmented with six sets of five repeating checks. An additional nursery established at Debre Zeit, containing 551 entries in an augmented design, was evaluated with the epidemic *Pgt* race TKTTF. These entries included the most relevant Ethiopian bread and durum wheat breeding lines and cultivars, and 34 seedling-susceptible lines to evaluate the race-specificity of adult plant resistance. Stem rust severities for the four races ranged from trace to 80 %. Out of all entries evaluated, 10 were resistant to all four *Pgt* races, while 11 entries were effective to three of the four races. At Debre Zeit, 31.4% of the entries were resistant to *Pgt* race TKTTF. This study showed that rapid isolation and increase of *Pgt* races in Ethiopia is possible to facilitate field screening of breeding lines to select for candidate cultivars with resistance to multiple virulent races of *Pgt*.

Using 'speed breeding' to harness rust resistance: faster, cheaper and easier

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A new method for rapid generation advance, called 'speed breeding', has considerable advantages over DH technology for spring wheat because it provides increased recombination during line development and enables selection in early generations for some traits. The system has been refined over the past 8 years at The University of Queensland, utilizing controlled temperature regimes and 24-hour light to accelerate plant growth and development. The low-cost management system enables up to 6 plant generations of wheat annually – just like Arabidopsis. Currently, three of the six wheat breeding companies in Australia are exploiting speed breeding, and elite lines developed using the technology are in the final stages of yield evaluation.

Recently, we developed methods adapted for use in the speed breeding system, which permit year-round high-throughput screening for adult plant resistance (APR) to rust pathogens that attack wheat. In this presentation, we describe the protocols, explain how phenotypes are related to field-based measures and highlight how the system can even handle diverse germplasm, such as winter types and landraces. Our 'triple rust' screening methodology enables selection for APR to all three rust pathogens and crossing of selected plants within a single plant generation. We applied the technique to rapidly introgress rust resistance into several Australian cereal cultivars.

The technology is also a useful tool to accelerate rust research efforts. RIL populations designed for mapping novel APR genes can be developed within 12–18 months. Experiments to understand gene function in terms of temperature stability and onset of resistance can be performed year-round and if combined with sequencing technologies, such as RNAseq, transcripts involved in rust defence can be rapidly identified and harnessed via the speed breeding system.

We will also reveal our current activities aiming to integrate the system with other plant breeding technologies to maximise genetic gain for wheat.

A decade of stem rust surveillance: How far have we come and where are we going?

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In response to the threat posed by Ug99 (race TTKSK) and a global expert panel assessment, the Borlaug Global Rust Initiative (BGRI) was formed in 2005. This represented one of the most comprehensive global programs to address an emerging crop pathogen threat. For the last decade, surveillance and monitoring has been a key component of the BGRI. Progress in rust surveillance and monitoring over the last ten years is critically reviewed, with a focus on stem rust. The transition from a data poor environment regarding stem rust to a fully functional, comprehensive crop pathogen surveillance system is a notable success. Key components and status of the current system are described, including; the surveillance network, the data management and information platforms, and pathogen tracking. The application of the existing surveillance and monitoring system and the current status of important stem rust races are described. The role that new technologies are playing in the monitoring and tracking of stem rust is highlighted. Recent stem rust epidemics in East Africa provide stark warning of threat that the disease poses and the clear need to continuously monitor evolving stem rust populations. Shortcomings of the existing system are examined and future directions for the surveillance and monitoring system are outlined.

Population structure of *Puccinia striiformis* f.sp. *tritici* at the southern part of Pakistani Himalayan region

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The Himalayan region of Pakistan has been shown to be the centre of diversity of wheat yellow rust pathogen *Puccinia striiformis* f.sp. *tritici* (*Pst*) with a probable role of sexual reproduction in the population temporal maintenance. However, the populations of southern part of Pakistani Himalayan region remains unexplored, where wheat yellow rust is an important disease on rainfed wheat. The current study was thus carried out to assess the disease status and population structure of *Pst* prevalent in the southern part of Pakistani Himalayan region, mainly the districts of Kohat, Karak, Bannu, Lakki-Marwat and DI-Khan. A high disease pressure was observed during wheat season in 2013 in the region, where the level of severity ranged from 5% to 100% depending upon the variety tested. Microsatellite genotyping of 102 isolates with 18 SSR markers revealed a high diversity ranging from 0.86 (for DI Khan) to 1.00 (for Karak). The recombination signature was lower compared to the Himalayan populations. Analyses of the population subdivision revealed no clear evidence of spatial structure, with the maximum F_{ST} value of only 0.081. The overall diversity was higher in the region as compared to European clonal population, though it was still lower than the recombinant Himalayan populations, which could be attributed to their distance from *Berberis* spp. plantation zone.

The cereal *Mla* locus is a rich source of effective resistance genes: cloning the *Sr50* gene from rye

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The stem rust resistance genes *Sr31* and *Sr50* in wheat were both derived from translocations of the short arm of chromosome 1 from rye and conferred resistance to all field isolates of *Puccinia graminis* f. sp *tritici* (*Pgt*) for many years, preventing their distinction as different resistance specificities. We now show that *Sr50* confers resistance against the Ug99 strain that overcomes *Sr31*, whereas a mutant *Pgt* strain virulent towards *Sr50* is avirulent towards *Sr31.* Because lack of recombination between wheat and rye chromosome arms precludes genetic mapping and so map-based cloning of *Sr50*, we used a combination deletion mutagenesis and large DNA fragment cloning in bacterial artificial chromosome (BAC) vectors to define this resistance locus. Sequence analysis of a BAC contig spanning the smallest deletion detected with DNA markers at the *Sr50* locus identified six **c**oiled **c**oil **n**ucleotide **b**inding site **l**eucine-**r**ich **r**epeat (CC-NB-LRR) genes and a chymotrypsin inhibitor gene closely related to genes at the orthologous barley powdery mildew resistance locus, *Mla*. Sequencing of these genes from two EMS-induced mutants that had lost no DNA markers revealed mutation in one of the CC-NB-LRR orthologs of *Mla*. Transgenic complementation tests in stem rust susceptible wheat proved this gene to be *Sr50.* A survey of a set of rye accessions identified several carrying the gene but occurring in different *Mla* gene haplotypes based on DNA gel blot patterns and copy number of *Mla* orthologs. Several different powdery mildew and rust resistance genes including *TmMla1* from *T. monococcum*, 23 *Mla* alleles from barley and stem rust resistance genes *Sr33* from *Aegilops tauschii* and *Sr50* from rye are all members of the *Mla* clade of cereal R genes.

The gene Sr50,was initially thought to be allelic to *Sr31*, however, appearance of Ug99 showed that this is a different gene and is rye ortholog of barley Mla powdery mildew resistance gene. The cloning of *Sr50* gives us an opportunity to screen the rye germplasm for presence of *Sr50* and allows us to now do functional analysis of the various domains and understand the mechanism of resistance. The cloning also helps to add very effective resistance to gene cassette. *Sr50* is effective against all the stem rust isolates around the globe

Quantification of atmospheric dispersion and identification of likely airborne transmission routes of emerging strains of wheat stem rust

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Use of large-scale computational resources has permitted the first quantitative study of airborne migration routes of fungal spores between numerous key epidemiological hot-spots of wheat stem rust in Africa, the Middle East and the Indian subcontinent. By coupling a state-of-the-art Lagrangian particle dispersion model (NAME) with mechanistic epidemiological models, we simulate turbulent atmospheric transport of large ensembles of fungal spores from source sites. The models use highly resolved global meteorological datasets from the UK Meteorological Office. We consider release of *P. graminis* uredinospores from numerous source locations over an 11 year period (2003-2014) and simulate atmospheric trajectories over a 10 km^2 spatial sampling grid to elucidate spore deposition rates at national, regional, and continental spatial scales.

Our systematic exploration permits the first quantitative perspective and ranking of likely airborne transmission routes of wheat stem rust. We identify migration trends within and between the "Rift valley epidemiological zone", the Middle East, the Indian Subcontinent, as well as South Africa. Our results indicate (I) consistent seasonal dispersal patterns, (II) likely airborne transmission of stem rust from the Middle East to North-East Africa, and (III) suggest that there is considerable risk of spread of Ug99 or other virulent races from Eastern Yemen to the Indian subcontinent. Model results indicate that over the 11 year study period, viable spore deposition occurred between Eastern Yemen and Pakistan on average 22 days per year during overlapping wheat growing seasons. The validity of the modelling framework has been successfully tested by comparison with survey data from the 2013 epidemic outbreak in Ethiopia, and was recently used as a risk assessment tool to provide rapid response advice in different East-African countries. Known stem rust race distributions are also supportive of the model outputs.

The research we have been doing allows a quantitative perspective on likely airborne transmission routes of Ug99 or other virulent races of wheat rust. By that we hope to provide new insights and recommendations for future risk assessment, survey and control strategies and also to contribute to fundamental understanding of epidemiological spread on regional and continental scales.

The work we would like to present is the result of a joint effort of Dr Laura Burgin and Dr Matt Hort from the UK Meteorological office, Dr Dave Hodson from CIMMYT, and Dr James Cox, Matthew Hitchings and me from the Epidemiology and Modelling group of Prof Gilligan in Cambridge.

Three principles for more informative virulence surveys for wheat rusts

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To inform breeders and growers of important changes in virulence and to facilitate development and deployment of resistant cultivars, isolates of wheat rust fungi are routinely evaluated on seedlings of a set of differential wheat lines containing different resistant genes. However, the methods used to evaluate and report virulence changes in most regions of the world seem inadequate for accomplishing these goals and could be improved by adherence to three principles. Firstly, for each region, the resistance genes in the set of differentials should match the effective genes in contemporary cultivars and breeding lines. Most differential sets contain several resistance genes that have been ineffective for decades and do not contain genes found in cultivars and breeding lines. Given the importance of genes for race-specific adult-plant resistance, these should be included in differential sets. Secondly, intermediate reactions on differential lines that had been highly resistant are important warnings of gradual increases in virulence. Naming races requires isolates to be either virulent or avirulent on each line in a fixed set of differentials and is a hindrance to identifying gradual changes in virulence on currently effective genes. Utilizing virulence formulae with a designation for intermediate virulence (e.g. parentheses around the gene or differential) seems to be a simple solution for both documenting partial virulence and for easily changing differentials to match genes in cultivars and breeding lines. Thirdly, the method for evaluating virulence against a particular differential should predict the result of that host-pathogen interaction in the field. Growth stage and environmental conditions are important for expression of some resistance genes, and all currently effective genes are not likely to be expressed under the same conditions. Following these principles will make virulence surveys more predictive of important changes in the field and thereby contribute to more effective management of rust diseases.

New variants in the Ug99 race group found in Kenya in 2013 and 2014

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Since 1998, when *Pgt* race TTKSK (Ug99) was first identified in Uganda, seven variants in the Ug99 race group have been reported in nine countries in eastern and southern Africa. Five of these variants (TTKSK, TTKST, TTTSK, PTKSK, and PTKST) have been observed in Kenya. Increased surveillance efforts in recent years have enabled detection of new virulence combinations that threaten wheat production. Three new variants in the Ug99 race group were identified from samples collected in 2013 and 2014 in Kenya. A new race, TTHST that is identical to TTKST but avirulent on *Sr30* (IT 2-), was identified from a sample collected in the Central Rift Valley Region in 2013. In 2014, two new races, TTKTK and TTKTT, were identified from a total of nine samples (six collected from cv. Robin, and one from each of Eagle10, NJRBW II, and barley) in multiple regions. These two races are of special concern as both are virulent on *SrTmp*, a gene that is effective against all previously known races in the Ug99 group. Resistance gene *SrTmp* is postulated to be the source of TTKSK resistance in cv. Robin (released in 2011 in Kenya, also postulated to have *Sr2*) and cv. Digalu (released in 2005 in Ethiopia). The presence of new races with virulence on *SrTmp* may explain the high levels of stem rust severity observed in wheat cultivar Robin in Kenya in the past two years. Genotypic relationships between these new races and known races in the Ug99 race group are being characterized using SNP markers. Cultivars and elite breeding lines from Kenya, CIMMYT, and the US are being evaluated for seedling reactions to race TTKTT. With the detection of these new races, there are a total of eight variants in the Ug99 race group in Kenya.

Durable rust resistance: From gene to paddock, continent and beyond

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The concept of durable resistance was introduced by Dr Roy Johnson about 40 years ago, following a breakdown in the slow rusting or adult plant resistance of several English winter wheats to stripe rust, including Joss Cambier, and continued effectiveness of resistance in several other cultivars including Cappelle Desprez and Hybrid de Bersee. The resistance in the latter was referred to as durable, and durable resistance defined as "resistance that remains effective when a cultivar is grown widely in environments favouring disease development".
Durable resistance is a descriptive term; it does not provide any explanation of the causes underlying long lasting resistance. It does, however, contain two conceptual elements, one being that there may be any of several underlying causes for durable resistance and the other that resistance that has remained effective for a long period of widespread use may not necessarily continue to do so in the future.

This paper will discuss the role of durable resistance in achieving sustained control of cereal rust diseases. In view of the complexity of host : pathogen interactions, genetic diversity must be seen as a key ingredient in large scale sustained control of plant diseases. It has been argued that even where specific or major resistance genes are used, genetic diversity can be used as insurance against lack of durability and hence as a means of reducing genetic vulnerability. Above all, responsible use of resistance genes depends upon an understanding of the resistance genes present in cultivars and breeding populations, and monitoring pathogen populations with respect to deployed resistances, are crucial in ensuring that the genetic bases of resistances are not narrowed.

Detection of significant new races of the wheat stem rust pathogen in Africa and Middle East

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Stem rust caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*) is a destructive disease on bread and durum wheat. Following the identification and distribution of Ug99, major national and international efforts have been made to detect additional spread and emergence of new *Pgt* races. Since 2011, GRRC has accepted to receive live samples of stem rust year round, and up to 2014, a total of 428 dried samples of *Pgt* infected wheat tissue were received from 15 African and Asian countries, i.e., Azerbaijan, Egypt, Ethiopia, Iran, Iraq, Kenya, Lebanon, Nepal, Rwanda, Sudan, Tanzania, Turkey, Uganda, Yemen and Zimbabwe. Additional samples were received from Germany, Sweden and Denmark, where wheat stem rust re-emerged in 2013-2014. Recovery procedures using susceptible seedlings of cv. Morocco was done upon arrival and a total of 269 samples were successfully recovered, multiplied and stored in liquid nitrogen until further use. To date, 140 *Pgt* isolates have been pathotyped based on the method of Jin et al. (2008). Subsets of isolates were selected for molecular characterization including SNP genotyping and shipped to USDA-ARS, Cereal Disease Lab (CDL). The *Pgt* race TKTTF was widely distributed and found in ten countries including Egypt, Ethiopia, Iran, Iraq, Lebanon, Sudan, Turkey and the three European countries. Races of the Ug99 lineage were frequently observed in Africa. Clear indication of a new race in the Ug99 race group with additional virulence for *SrTmp*, TTKTK, was observed in samples from four African countries in 2014. PCR diagnostics developed by CDL confirmed the new race being member of the Ug99-lineage. The experimental work was supported by the DRRW project and new research facilities were funded by Aarhus University.

Phenotyping adult plant resistance to leaf rust in wheat under accelerated growth conditions

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Leaf rust (LR), caused by *Puccinia triticina*, is among the most important diseases of wheat (*Triticum aestivum* L.) crops globally. The most sustainable method for controlling rust pathogens is deployment of cultivars incorporating durable forms of resistance, such as adult plant resistance (APR). However, phenotyping breeding populations or germplasm collections for LR resistance in the field is dependent on weather conditions and limited to only once a year. In this study, we report a protocol for phenotyping APR to LR incorporating 'speed breeding' technology, which utilizes controlled temperature regimes and 24-hour light to provide accelerated growth conditions (AGC) – enabling up to 6 plant generations of wheat per year.

A panel of 22 genotypes, including disease standards carrying known APR genes along with a diversity panel comprising 300 accessions (including winter types and landraces) were characterized for resistance to LR under AGC and in the field. Analysis of genotypes displaying APR revealed that disease response expressed on flag–2 leaves under AGC was highly correlated with field-based measures ($R^2 = 0.76$). Analysis of the diversity panel indicated that APR was expressed by plants that had obtained the stem elongation stage (i.e. GS≥30) prior to inoculation. Despite the high degree of genetic diversity in the panel, strong correlations between LR response under AGC and the field were observed, and were further improved when field response was adjusted based on growth stage ($R^2 = 0.81$). The diversity panel was also screened with DNA markers for known APR genes (*Lr34*, *Lr46* and *Lr67*), which identified 22 accessions carrying potentially novel sources. This method integrates assessment at both seedling and adult growth stages and requires only seven weeks to complete, enabling up to seven consecutive assays annually. When coupled with 'speed breeding', this approach could also accelerate introgression of resistance genes into adapted wheat cultivars.

Metabolomics and plant physiology during the wheat-stripe rust interaction

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Stripe rust is one of the major diseases of wheat worldwide. The causative fungus, *Puccinia striiformis* f.sp. *tritici* (*Pst*), keeps the infected tissue alive even after sporulation phase, a strategy that is referred to as biotrophy. The compatible interaction is divided into three phases; colonization, growth, and sporulation, the last occurring ~14 days after germination of spores. During the growth phase plant apoplast is completely occupied by hyphae, and the fungus develops special invasive structures called haustoria within plant cell. Both hyphae and haustoria are thought to take up nutrients from the host, but haustoria are specialized for this role. However, it is still unknown how the fungus obtains nutrients; perhaps by direct manipulation of host metabolic pathways related to photosynthesis or by changes in whole plant metabolite fluxes by acting as a sink. Also, it is unclear why wheat plants do not detect either the fungus itself, or the consequent loss of nutrients. The aim of this study is to understand the changes during the three phases of infection, comparing metabolites and plant photosynthetic efficiency in healthy and infected tissue, and correlating this with fungal growth. The results show that CO2 assimilation rates decreased only at the sporulation phase, which correlates with a reduction in transitory starch accumulation. However, glucose and fructose levels were lower only during colonization phase. Interestingly, although the infection alters the nutrient balance, this did not seem to affect the development of young leaves. In addition to these results, we found that stripe rust grows faster in younger leaves, which might be related to their morphology and the nutrient availability and fluxes within the leaf. This research suggests that the fungus is undetected until sporulation, and will aid future studies to understand the mechanisms of adult plant resistance conferred by transporter proteins.

The research will aid future studies to understand the dynamic of adult plant resistance conferred by transporter proteins. The knowledge in wheat physiology and metabolism during rust infection could help to explain the role of transporter proteins during wheat-stripe interaction in different plant growth stages.

Training agricultural scientists for a more globalized world: Monsanto's Beachell-Borlaug International Scholars Program after 7 years

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Monsanto's Beachell-Borlaug International Scholars (MBBIScholars) Program was established on March 25, 2009, on Dr. Norman Borlaug's 95th birthday. Monsanto initially funded the MBBIScholars program for $10 MM ($2 MM per year for 5 years) and extended the program with a second grant for $3 MM ($1 MM per year for 3 years). As of February 2015 (6 Years of funding) the program has supported 70 students. The 70 MBBIScholars were selected from 359 applications. MBBIScholars are from 25 countries with India having 20 scholars. MBBIScholars from other countries are – Argentina 3, Bangladesh 2, Brazil 2, China 4, Columbia 4, Ecuador 1, Egypt 1, England 1, Ethiopia 4, Kenya 2, Korea 2, Iran 3, Italy 1, Mali 1, Nepal 2, Pakistan 1, Philippines 1, Syria 2, Tajikistan 1, Thailand 1, Tunisia 1, USA 4, and Uruguay 2. Forty scholars studied wheat breeding and 30 studied rice breeding. Twenty seven scholars were young ladies. Applications for the 7th round were due on or before February 1, 2015. A unique feature of the MBBIScholars Program is the requirement that scholars must complete part of their PhD program in both developed and developing/transition countries. Scholars have worked with developed country scientists as follows – Australia 4, Canada 3, USA 43, and Western Europe 20. The program pays for the MBBIScholars to participate in a 3 day Leadership course prior to attending the World Food Prize during their first 2 years. It has been a good experience to see MBBIScholars gain self-confidence after attending the Leadership Course and World Food Prize, and as they study and conduct research in developed and developing/transition countries. They also gain many lifelong contacts in the plant breeding community. Based on the current funding agreement with Monsanto, the final round of MBBIScholars will be selected from applications due February 1, 2016. In view of the great success of this model of training international plant breeders, it would be highly desirable for donors to support and extend this PhD training program to include additional crops of interest in developed and developing countries.

Wheat stripe and stem rust situation in Egypt: *Yr27* and *Sr31* virulence

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Wheat stripe (*Puccinia striiformis* f. sp. *tritici*,=*Pst*) and stem (*Puccinia graminis f. sp. tritici* =*Pgt*) rusts are the most important wheat disease in Egypt as well as present in all wheat growing areas. This study to evaluate a set of tester lines of wheat carrying stripe *Yr's*, stem *Sr's* rust genes and selected Egyptian varieties have been studied for their response to *Pst* and *Pgt* at adult plant stage under field conditions in Sakha Agriculture Research Station, during the 2011 to 2014 growing seasons. The results revealed that stripe rust, it has been observed that the new race *Yr27*-virulence to *Pst*. In addition pathotypes were virulent for *Yr2, Yr6, Yr7, Yr8, Yr9*, *Yr27*, while *Yr18* showed moderate susceptibility. On the other hand, *Yr1, Yr5, Yr10, Yr15, Yr17, Yr32* and *YrSP* exhibited high levels of resistance. Regarding, evaluation of resistance genes sources of stem rust on ICARDA, CIMMYT wheat germplasm, and Egyptian wheat varieties released *i.e.* Misr1 and Misr2 which having Ug99_resistance genes *Sr2* and *Sr25* were found susceptible to *Pgt*, also *Sr31* recorded infection moderately susceptible to susceptible at adult stage. Genes *Sr2* complex, *Sr24, Sr26, Sr27,* and *Sr32* were resistant at adult plant stages. The combination of *Sr26* with *Sr2* and *Sr25* provided stem rust resistance in some CIMMYT wheat germplasm. The objectives of this work are: race analysis of wheat stem and stripe rust disease, evaluation the level and distribution of wheat stripe and stem rust in Egypt, and identification the resistance genes in commercial varieties or new promising lines using standard and molecular genetic markers.

Egyptian germplasm such as Misr1, and Misr2 and others tester lines of wheat carrying stem rust *Sr's* were evaluative under field condition at adult stage in Egypt during 2014 growing season, Egyptian cultivars Misr1 and Misr2 were susceptible rated 10S-20S and *Sr31* rated MS-S. that results clearly presence a new *Sr31*-virulence. On other hand, genes *Sr2* complex, *Sr24*, *Sr26*, *Sr27* and *Sr32* were resistant and combination of *Sr26* with (*Sr2* and *Sr25*) produced stem rust resistance in some CIMMYT wheat germplasm. **Shahin *et al.,*** 2015, in APS Annual Meeting, Aug. 1-5, Pasadena, CA, US, (*In Press*).

Breeding durable adult plant resistance to stem rust in spring wheat- progress made in a decade since the launch of Borlaug Global Rust Initiative (BGRI)

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A key objective of BGRI is to breed high yielding, stem rust resistant spring wheat germplasm suitable for releases as successful varieties in wheat growing countries of Africa, Middle East, Asia and Latin America. High emphasis was given to select adult plant resistance (APR) to stem rust in achieving this goal that is especially important in East African highlands where various variants belonging to the Ug99 race group and other lineages of stem rust fungus are now known, disease is endemic and present throughout the year on wheat crops. Recent molecular mapping studies show that combinations of partially effective APR gene *Sr2* with 3 to 4 additional APR genes such as *Sr55, Sr56, Sr57, Sr58* and other undesignated quantitative trait loci confer adequate to high levels of resistance to stem rust. A 'Mexico-Kenya shuttle breeding scheme' was initiated in 2008 to select APR to stem rust under high disease pressures at Njoro, Kenya while selecting for resistance to other rusts, yield, agronomic and quality traits in Mexico. This selection scheme, combined with phenotyping of advanced lines for multiple seasons in Kenya has resulted in identifying a small frequency of high yielding lines that possess a high level of resistance with a stable and low stem rust severity performance over seasons/locations under high disease pressures. These near-immune wheat lines are the best candidates for release in East Africa to achieve durable disease control and simultaneously curtail, or reduce, further selection of new virulences. A significantly higher proportion of wheat lines were also developed with moderate levels of resistance that is considered suitable for deployment in wheat growing areas where rust builds up later in the season. The worldwide distribution of the wheat lines derived from Mexico-Kenya shuttle breeding initiated in 2012 through the international yield trials and nurseries from CIMMYT.

Potential releases and cultivation of these lines in different countries together with a reduction in area sown to susceptible varieties are expected to reduce the threat from stem rust.

Segregation for aggressiveness in sexual offspring of the yellow rust pathogen *Puccinia striiformis*

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Recent events in worldwide populations of the fungal pathogen *Puccinnia striiformis*, which causes the yellow rust disease on wheat and other cereals, have suggested that other factors than shifts in virulence can lead to epidemic events. For instance, the spread of two strains across four continents that has occurred within the last 10-15 years seems to be a result of high temperature adaptation combined with a relatively short latent period (Hovmøller et al. 2008; Milus et al. 2009). Variation for quantitative traits like latent period has often been hypothesized to play a significant role in population shift but only very few experimental data have been generated. Here we report difference for components of aggressiveness which included latent period and lesion growth for 17 isolates derived from a selfing of an aggressive isolate using *Berberis vulgaris*. A group of offspring isolates had a significantly longer latent period and higher lesion growth than the parental isolate. Interestingly, the two traits were found to be positively correlated where a long latent period was correlated with a higher lesion growth rate. This may suggest a trade-off between latent period and lesion growth. All isolates were assessed on seedlings of two highly susceptible host varieties and the two hosts gave similar results. In a previous study the progeny isolates showed segregation for virulence/avirulence and SSR markers (Rodriguez-Algaba et al. 2014).

In conclusion, this study demonstrates genetically inheritable variability for latent period and lesion growth in *P. striiformis*, even within a single parental isolate. The results contribute to a better understanding of the ability of *P. striiformis* to adapt to new host varieties and changing environments at the quantitative level.

An integrated genomics approach to combat the wheat yellow rust pathogen

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We will present an update on the BBSRC-funded SCPRID project "Maximizing the potential for sustainable and durable resistance to the wheat yellow rust pathogen". This aims to understand the molecular basis of *Puccinia striiformis* f. sp. *tritici* (PST) pathogenicity and exploit this information to design effective breeding strategies that maximize the potential for durable disease resistance in the field. We have established a PST genomics platform through sequencing of PST genomes (UK, European, African, and Indian races) and analysis of expression time courses during infection (Cantu et al 2013). Using this platform we have characterised the PST effector complement, identified putative candidates and have begun their validation. The latest results of this will be presented. We have also evaluated a collection of hexaploid wheat landraces for resistance to PST across continents and have initiated single seed descent mapping populations and initial characterisation in $F_{2:3}$ populations. We will exemplify the use of new genomic technologies to develop closely linked markers to enable deployment of resistance loci in breeding programmes (Ramirez-Gonzalez et al 2014). We will also provide an update of a new technique, called Field Pathogenomics (Hubbard et al 2015). This method uses transcriptome sequencing of PST-infected wheat leaves to describe pathogen diversity and also identify the host variety. This analysis uncovered a dramatic shift in the PST population in the UK and suggests a recent introduction of a diverse set of exotic PST lineages that may have displaced previous PST populations.

- Hubbard et al (2015) Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. *Genome Biology* in press
- Ramirez-Gonzalez et al (2014) RNA-Seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. *Plant Biotech Journal*. DOI: 10.1111/pbi.12281
- Cantu et al (2013) Genome analyses of the wheat yellow (stripe) rust pathogen Puccinia striiformis f. sp. tritici reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. *BMC Genomics*. 14:270

Placement of South African stripe rust in a global context and development of diagnostic tools for genotyping field samples

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Stripe (yellow) rust, caused by the fungus *Puccinia striiformis* f. sp. *tritici* (PST), is a major global wheat disease. New PST strains that show higher infection rates and rapid adaptation to less favourable environmental conditions have been observed over the last 15 years. It has also continued to spread to areas where it was not previously recorded. In South Africa, stripe rust was first detected in 1996. In subsequent years three more PST races were observed, with what seemed to be a step-wise virulence gain. A better understanding of the South African PST pathotypes and how they fit in the global context is needed. We aimed to address this by sequencing the genomes of four historical PST isolates displaying the four distinct virulence profiles. This allowed us to characterise the genetic diversity between these stripe rust races and develop diagnostic markers to easily genotype current detections. We also placed the South African PST isolates in context with global PST isolates where sequence data was available. This analysis illustrates that the South African PST races are more closely related to PST from other African countries when compared to isolates from Africa, Europe and Asia. Through pairwise comparison of isolates, we identified 27 candidate effector genes showing specific polymorphisms between the four isolates that could be related to their distinct virulence profiles. We are currently undertaking gene expression profiling of these candidates to determine if these effectors are specifically upregulated during infection–a key characteristic of effector genes. This study has shed new light on the potential origin and adaptation of stripe rust in South Africa and provides tools for rapid genotypic classification of infections in the field.