

A Turkey-ICARDA Regional Cereal Rust Research Center in Izmir, Turkey

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Once again, wheat stripe (yellow) rust struck the “wheat-belt” in Central, West Asia, and North Africa (CWANA), East Africa, the Caucasus region, and South Asia in 2013. Unusual early infections were observed in several countries with serious outbreaks on susceptible wheat cultivars. These outbreaks were caused by a combination of factors, including conducive climatic conditions, wide-scale monoculture of ‘mega-cultivars’, susceptible local cultivars with inadequate resistance, and a combination of virulence factors overcoming deployed yellow rust resistance genes in commercial fields. This situation continues to pose a serious threat to food security in these regions, driven by changing climatic patterns that support rust prevalence in areas where rust was not previously a problem. While crop losses due to the 2013 epidemic were less than in 2010, the 2013 outbreaks threaten some previously stripe rust-resistant cultivars and breeding germplasm, including some cultivars that are resistant to *Pgt* race Ug99. Considering the transboundary nature of rust pathogens, no single country can successfully control a rust epidemic, and surveillance and cooperation between countries is a vital component of a regional rust management strategy. Remarkable recent progress largely supported by the Durable Rust in Wheat project and BGRI has been made in surveillance and breeding for stem rust resistance. Despite limited progress, the implementation of a similar coordinated system for stripe rust is a high priority. Along with the Global Rust Reference Center (GRRC) in Denmark, there is an immediate need for a regional rust center in the developing world. This need is critical as regional race analyses currently very much depend on a few national laboratories and advanced rust centers in Denmark, France, and the USA. With their expertise on wheat stripe rust, Turkey and ICARDA are well positioned, both geographically and scientifically, to monitor pathogenic changes in rust pathogens in this region. In 2013 the Ministry of Food, Agriculture and Livestock of Turkey and ICARDA agreed to establish the “Regional Cereal Rust Research Center” in the Aegean Agricultural Research Institute (<http://www.etae.gov.tr>) in Izmir. The new center will serve as the regional rust research center allowing race analysis of rust samples from the Central & West Asia and North Africa (CWANA) region, under bio-containment conditions. It will also facilitate regional rust surveillance and an early warning system, and provide field screening facilities at various ‘hot spots’ for national breeding programs. International wheat rust trap nurseries will also be distributed from the center. The current International Agricultural Research and Training Center (<http://www.utaem.gov.tr>) in Izmir, provides a significant opportunity for improving capacity on wheat rust among scientists and agricultural professionals from developing countries. It will deliver international training courses and related capacity building activities. In this presentation we will provide an update on recent developments of the Turkey-ICARDA rust collaborative activities and the Regional Cereal Rust Research Center in Izmir.

Early warning and mitigation planning: Epidemiological models add value to surveillanceD.P. Hodson¹ and C.A. Gilligan²¹CIMMYT-Ethiopia, PO Box 5689, Addis Ababa, Ethiopia; ¹Epidemiology and Modelling Group, Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge CB2 3EA, UK**E-mail: cag1@cam.ac.uk**

Considerable progress has been made in the development and implementation of a global surveillance and monitoring system for wheat rusts. Uniquely for a major crop-disease problem of global importance a functional, trans-boundary, surveillance system is now operational. In the space of five years, a standardized surveillance network covering 40 countries has been created, a comprehensive data management platform developed and important pathogen changes, e.g. the Ug99 race group, have been tracked. The rust surveillance activities have permitted the identification of current disease hotspots for stem rust, leaf rust and stripe rust across the key wheat growing regions of Africa and Asia. Through interlinked data resources (e.g. CIMMYT Wheat Atlas, GRIS, BGRI screening nursery database) increasing amounts of information are being obtained relating pathogen data to host distributions and responses. The existing surveillance platform provides a good foundation, but important information gaps still remain if effective planning and control strategies for wheat rusts are to be achieved. Partnerships with advanced UK research institutes, Cambridge University and Rothamsted Research, are adding increasing value to the existing surveillance platform. Epidemiological modelling provides a powerful means of integrating current knowledge and comparing the effectiveness of different potential strategies before they are implemented in practice, e.g. optimal deployment strategies for rust resistant cultivars or the most effective chemical control strategies. Building upon accumulated current knowledge an epidemiological model is being developed for stem rust. The model will permit insights into likely epidemic development over space and time in different environments and cropping systems. Based on this epidemic model, so called hazard maps can be developed. Such hazard maps quantify the size of the epidemic for each point on a map resulting from an introduction of one or more *Pgt* races at that place. The hazard maps can be combined with data on likely points of introduction from natural air-borne movements or accidental human-borne transmission to produce risk maps. Hazard and risk maps together with epidemiological models will form the basis for the early detection, efficient monitoring systems as well as a basis for optimal mitigation planning. Current status of the rust surveillance and the epidemiological modelling activities will be described.

Understanding the genetic landscape of *Puccinia graminis* f. sp. *tritici*, from a global to country perspective

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With the recent sequencing of the wheat stem rust pathogen (*Puccinia graminis* f. sp. *tritici*, *Pgt*) genome, an array of molecular tools has now become available to characterize the genetic variation of *Pgt* and develop new diagnostic methods for identification and detection of the Ug99 race group. The *Pgt* Genotyping Project is currently comprised of collaborators on five continents and collections from 18 countries. Two different genotyping platforms are being used, genome-wide re-sequencing and a SNP chip. Analysis of approximately 150 *Pgt* isolates has defined at least 10 distinct clades. Several of the clades contain isolates from different continents supporting that global movement of *Pgt* has occurred. The Ug99 race group forms a distinct clade and shares a common lineage with isolates from Africa, Australia and Europe. In addition, this project has demonstrated that a single race phenotype often contains multiple genotypes. The South African *Pgt* population is divided into two clades. The first clade represents the historical *Pgt* ancestry whereas the second consists of four members of the Ug99 race group. TTKSF was the first Ug99 race to be detected in South Africa in 2000. It is proposed that TTKSF entered South Africa as an exotic introduction and subsequently established itself as the dominant race within the population. Annual stem rust surveys and race analyses done by the ARC-SGI monitor the distribution and migration of races within and between the major wheat growing areas. Collected isolates are identified using infection type data on standard wheat differentials. To improve race identification, SNP and SSR technology was used to classify isolates collected during the 2010, 2011 and 2012 surveys. Results indicated a strong correlation between traditional and DNA based identification methods. The addition of the DNA methods serves as an example of how wheat stem rust research with a global aim, i.e. the molecular characterization of the Ug99 race group, adds value to understanding and describing pathogen variability in South Africa.

A North-South partnership identifies genetic biodiversity for durable rust resistance in African wheat genotypes

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Since 1996 Prins, Boyd and Pretorius have characterised stripe rust resistances in South African wheat varieties. In 2008 the team was awarded a SARID grant (UK: BBSRC-DfID initiative), expanding their research to include genetic characterisation of stem rust resistance, to build DNA marker capacity, and to train a PhD student. The SARID project had three goals: (1) to fine map stripe rust adult plant resistance (APR) QTL on chromosomes 2B and 4A identified in the South African variety Kariëga, (2) to genetically analyse stripe rust APR derived from the European variety Cappelle-Desprez, and (3) to assess genetic diversity for stem rust and stripe rust resistances within the John Innes Center African wheat collection. The fine mapping of the Kariëga QTL resulted in the establishment of new marker technology within the South African team, developing markers for single nucleotide polymorphisms (SNPs) within wheat genes identified through comparative cereal genomic analyses. These SNP markers defined each QTL to a smaller genetic interval, proving highly valuable for marker assisted selection (MAS), with one SNP marker being diagnostic for the valuable 4A QTL. One major and 3 minor QTL for stripe rust APR were identified in the Cappelle-Desprez-derived line Yr16DH70, providing a valuable resource for wheat stripe rust resistance breeding within South Africa. These QTL and associated DNA tools are now being used by South African wheat breeders. To identify new sources of stripe rust and stem rust APR a genetic association analysis (GAA) was undertaken in a collection of African wheat lines. This project established a new and highly successful collaboration between Prins and Dreisigacker (CIMMYT) and introduced GAA into wheat research in South Africa. The stem rust screens were particularly valuable, identifying seedling and APR effective against the Ug99 race group. Two wheat lines with APR to stem rust were crossed with a susceptible parent and doubled haploid populations were developed to validate the GAA analysis.

Wheat Productivity Enhancement Program (WPEP) for Pakistan – A U.S. and Pakistan Partnership including CIMMYT and ICARDA focused on mitigating the threat of *Pgt* race Ug99

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WPEP is an outcome-driven science collaboration begun in 2010 involving USDA, CIMMYT, ICARDA, and 11 Pakistani scientific organizations working in all provinces of Pakistan. The primary coordinating partner in Pakistan is the Pakistan Agricultural Research Council (PARC). WPEP's overarching goals are to enhance and protect the productivity of wheat in Pakistan by increasing the capacity of Pakistani scientific institutions to minimize adverse effects of wheat rusts (including *Pgt* race Ug99). WPEP originated from needs identified by U.S.-Afghanistan-Pakistan Regional Food Security meetings, and a USDA-sponsored Pakistan Ug99 workshop in 2009. An early, related outcome of those meetings was the provision of 150 tons of a high-yielding, Ug99-resistant variety (Maquwim-09) into Afghanistan's formal seed system in 2010. That seed (Misr-1) was developed by Egypt's Agricultural Research Center and shipped to Afghanistan by the U.S. in a partnership with CIMMYT, FAO, the USAID Famine Relief Ug99 seed project, and the Government of Afghanistan. WPEP is strengthening Pakistan's capacity to collect, store, and characterize rust pathogen culture collections in support of wheat rust resistance breeding. WPEP also seeks to provide breeders with information on the nature of rust resistance genes in Pakistani wheat germplasm. USDA-ARS researchers in Minnesota, North Carolina and Washington are collaborators in host plant resistance, pre-breeding, and rust-race characterization aspects of WPEP. Other WPEP objectives include accelerated breeding, accelerated seed multiplication, and enhanced farmer adoption of better crop management. Early results of this project include the release of the first Pakistani varieties with Ug99 resistance, upgrades at the Pakistan Cereal Rust Laboratory at Muree, renewed national Traveling Wheat Seminars and Annual Planning Meetings through the leadership of PARC, improved use of off-season nurseries, and upgrading of the methods employed in field phenotyping.

Effect and interaction of wheat leaf rust adult plant resistance genes in Uruguay

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Achieving durable resistance to leaf rust (LR) in wheat has been a major objective of breeding programs for a long time. The durability of resistance to LR is considered to be associated with adult plant resistance (APR) genes that are inherited quantitatively. The objective of this study was to analyze the presence, effect and interaction of durable resistance genes *Lr34*, *Lr68* and *Lr-Sr2* in the presence of *Lr46* using linked molecular markers in two BC₁F₅:F₆ populations, viz. Parula/2*LE2304 and Parula/2*ORL99192. APR was evaluated in two inoculated locations in Uruguay during 2012. *Lr34* and *Lr46* were fixed and *Lr68* and *Lr-Sr2* segregated in the Parula/2*LE2304 population; there was a 33% reduction in disease severity (DSR) when both genes were combined. The effect of *Lr-Sr2* on LR response was minor (4–12% DSR) whereas *Lr68* showed a stronger effect (21–29% DSR). The combined effect of *Lr34*, *Lr68* and *Lr-Sr2* segregating in Parula/2*ORL99192, led to the highest DSR (48%). The effect of *Lr68* was significantly higher (14–31% DSR) than the effect of *Lr34* (11–21% DSR) and *Lr-Sr2* (3–8% DSR). *Lr68* and *Lr34* had significant additive effects in reducing LR severity at the adult plant stage. *Lr68* expressed higher levels of resistance to LR than *Lr34* in Uruguay and is therefore a key gene to be used in breeding for durable LR resistance in this country. It was confirmed that several APR genes need to be combined in order to achieve effective levels of resistance.

This abstract is one of three selected for presentation at the Competitive Graduate Student Symposium plenary session of the BGRI 2013 Technical Workshop. A full paper describing the Silva et al. research is available on globalrust.org.

Genome-wide association mapping of adult plant resistance to stripe rust in synthetic hexaploid wheat

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Stripe (yellow) rust, caused by *Puccinia striiformis tritici* (*Pst*), is a major threat to wheat production in many wheat growing areas. In Ethiopia, substantial yield losses occurred in 2010 due to the breakdown in resistance of the *Yr27* carrying mega-cultivars widely grown by farmers. Use of adult-plant resistance (APR) is seen as an efficient approach to provide durable protection from the disease. To identify new APR genes, 181 synthetic hexaploid wheats (SHWs) were evaluated for resistance at Meraro-Ethiopia and Tel-Hadya-Syria in 2009-2010 and 2010-2011 cropping seasons under field conditions. These were analysed with 4040 polymorphic single nucleotide polymorphisms (SNPs) markers using Mixed Linear Models that accounted for population structure and kinship relationships. Twenty six SNP markers in 14 genomic regions on chromosomes 1AS, 1AL, 1BS, 1DS, 2AS, 2DS, 3AS, 3AL, 3BL, 3DL, 4AL, 4DL, 5A and 6BL were significantly ($p < 0.01$) associated with APR to stripe rust in SHWs. The 26 SNPs explained individually between 3.4 to 8.1% of the genetic variance, while all SNPs together explained 80% of phenotypic variation for APR. Additional to confirming previously reported loci associated with APR, this study uncovered new loci and linked SNP markers to APR in SHWs on chromosomes 3AS, 3AL and 3DL. Of these, the novel locus on 3AS was most strongly associated with APR to stripe rust and was annotated as an 'ABC transporter,' a defence response gene similar to APR gene *Lr34/Yr18*. These provide additional loci that can be used to improve APR for stripe rust in wheat.

This abstract is one of three selected for presentation at the Competitive Graduate Student Symposium plenary session of the BGRI 2013 Technical workshop. A full paper describing Zegeye et al.'s research is available on globalrust.org.

Quantifying stripe rust reaction in wheat using remote sensing based handheld NDVI sensor

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Wheat crop production and productivity is significantly affected by the rusts with losses that impinge on national food security. A study for quantitative stripe rust reaction was performed on 120 Indian wheat genotypes representing released varieties, elite genotypes, genetic stocks and local landraces obtained from the Germplasm unit of the Directorate of Wheat Research, Karnal. Stripe rust epiphytotics were created with the *Yr27*-virulent *Pst* race 78S84. Rust reactions were recorded four times at seven day intervals. Area Under the Disease Progress Curve (AUDPC) values ranged from 0 to 2077. Since stripe rust infection affects foliar pigments through discoloration of the green color, we attempted to improve the precision of disease scoring by collecting data with a remote handheld Normalized Difference Vegetation Index (NDVI) sensor. This instrument reads the color of several plants and delivers an average value. The NDVI values for the genotypes used in the present experiment varied from 0.46 to 0.69. A significant regression coefficient ($r^2=0.63$) was observed between AUDPC and NDVI data. The results indicate that temporal ground-based NDVI data could be effective in quantitative rust reaction studies.

This abstract is one of three selected for presentation at the Competitive Graduate Student Symposium plenary session of the BGRI 2013 Technical workshop. A full paper describing the Arora et al. research is available on globalrust.org.

Waste not, want not: The importance of being earnest about gene stewardship

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The shortage of stem rust resistance genes effective against the Ug99 group prompted recent efforts to increase the number of resistance genes available to breeders. We are fortunate that many new and/or cytogenetically improved rust resistance genes are now being shared with the global wheat breeding community by their developers. If we are poor stewards of these resources, the new resistance genes will eventually be defeated, and we will waste the efforts and investments that have been made. However, if we are good stewards, we should have enough resistance to achieve sustainable, durable resistance.

Stewardship can be defined as the careful and responsible management of something entrusted to one's care. What should we do to safeguard the new resistance genes? Diversification of resistance is often suggested as a way to reduce the risk of large scale epidemics. Although diversification is generally a good idea, it cannot be at the expense of leaving new genes exposed and vulnerable. A durable combination (pyramid) must be designed so that the component genes protect each other. They should reduce the probability of simultaneous pathogen mutations to virulence and they should avoid stepwise erosion of the pyramid by preventing significant reproduction of any new race that is virulent on component genes. We need pyramids to be immune or nearly immune not only to current races, but to anticipated mutants. This objective should be achievable with three or more major genes or a combination of major and minor genes.

Successful gene stewardship will depend on several things. On the technical side, we will need very good markers for each gene. Each breeding program will require strong genotyping support to assemble and then validate pyramids. Most importantly, successful stewardship will require that we organize our user community to cooperate more closely. We will need to decide which genes require special stewardship and which do not. Every user of the stewardship pool resource will need to participate in earnest. It only takes one cultivar with an unprotected gene to give the pathogen a stepping stone to greater virulence. As they say, a chain is only as strong as the weakest link.

Perspectives on applied aspects of breeding for rust resistance

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Wheat breeding is largely conducted by the public institutions in Asia, Africa and Latin America; however, private sector engagement in South America and South Africa is substantial and is increasing in some other countries. A dynamic breeding program must target crossing by considering the situation that will prevail in 8-10 years when the derived varieties will be grown. A successful variety is the sum of various traits and resistance to a particular rust is just one but a crucial trait for focus. Therefore, a strategy that prolongs the effectiveness of resistance is of extreme importance in enhancing productivity gains while protecting the environment and farmers' incomes. There are numerous breeding programs worldwide and most operate with constraints. The capacity of a program to breed for rust resistance is enhanced when breeders, geneticists, pathologists and molecular biologists set goals together, and collaborate and work in harmony. Choice of resistance, race-specific or partial, and their utilization will depend on the commitment of individual breeding programs. It is often easier to use single race-specific resistance genes with large effects in breeding programs with limited resources; however, larger and more resourceful programs must commit to utilizing resistance genes more responsibly, i.e. using them in combinations or switching to more complex adult plant resistance (APR) based on multiple slow rusting, minor genes. Limited availability of effective race-specific genes, and tightly-linked molecular markers, usually leads to the utilization of the same genes by many breeding programs in time and space. This often leads to higher genetic vulnerability and losses across large areas when virulent races develop and spread. Maintaining diversity is therefore the key to overcoming “boom-and bust” episodes if dependence on race-specific resistance is to prevail. The CIMMYT bread wheat breeding program has been successful in developing high-yielding wheats that possess near-immune to adequate levels of APR to all three rusts. Large scale deployment of varieties with APR and removal of susceptible varieties from cultivation should lead to sustainable long-term control of rusts.

A wheat breeding strategy for durable resistance in stripe rust-prone areas of Sichuan, China

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China is the largest producer and consumer of wheat in the world and regularly suffers from stripe rust epidemics with significant yield losses. Sichuan and Gansu provinces are considered major provinces where new races of the stripe rust fungus evolve. Breeders have successfully developed and deployed resistant varieties, but have depended largely on race-specific resistance genes with large effects. These genes are often used simultaneously by many breeding programs within a province or region due to open sharing of improved wheat materials among breeders. Loss of widely deployed race-specific resistance genes to new virulent races therefore causes susceptibility of multiple varieties and breeding materials. In 2000 a shuttle breeding program was initiated between SAAS and CIMMYT to incorporate minor gene-based adult plant resistance (APR) from CIMMYT germplasm into adapted Sichuan wheat varieties. Results were very positive and 11-39% of the 669 advanced breeding lines evaluated in official multi-environment stripe rust trials in 2007-2009 had consistently high levels of resistance. Recently a new stripe rust race, V26, with virulence to gene *Yr24* evolved in China and caused susceptibility of the popular variety Chuanmai 42 released in 2003. In our 2013 field trials, inoculated with a mixture of V26 and other races, 23 parental lines with CIMMYT APR genes and 54 second generation advanced APR lines (derived after completing two breeding cycles with Sichuan parentage) showed high resistance levels compared to the high susceptibility of Chuanmai 42 and other checks. The key breeding strategy we applied could be summarized as follows: 1) establishing a special breeding program without major gene resistances to introduce and create locally adapted APR parents; 2) using high-yielding, adapted susceptible materials as single backcross parents until several highly resistant (APR) wheat lines became available; 3) growing large segregating populations ($BC_1F_1 > 200$, $BC_1F_2-4 > 3,000$ plants) and selecting under high rust pressure; 4) retaining plants with moderate resistance levels ($< 20\%$ severity) during early generations and only highly resistant plants in later generations; and 5) using a selected bulk method to increase the efficiency of the breeding program. We have demonstrated that development of high-yielding varieties with high levels of APR is possible. Deployment of varieties with complex APR should lead to durable resistance in our region of China where stripe rust is endemic and continuously evolving.

Development of *Pgt* race Ug99 resistant wheat cultivars in Iran: Achievements and prospects

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Rusts are important biotic constraints to wheat production in Iran. Stripe (yellow) rust is the greatest threat, especially in humid seasons and the 1993 epidemic caused losses of 1.5 million tonnes (Torabi et al. *Cereal Rusts and Powdery Mildews Bulletin* 23: 9-12). The release of resistant irrigated wheat varieties during the last two decades has considerably reduced the threat of stripe rust. Leaf rust and stem rust also have the potential to cause devastating losses, especially in northern Caspian Sea region where humidity and temperatures are favorable. Although there were reports of *Pgt* race Ug99 in Iran in 2007 (Nazari et al. 2008, *Seed and Plant Journal* 24: 207-213, in Persian), no damaging epidemics have occurred. Iranian wheat breeding programs started to send germplasm to Kenya for APR assessment against Ug99 in 2007, in conjunction with seedling assessments made in local greenhouses. Following receipt of the first evaluation results the NARS programs started to breed for resistance to race Ug99 by incorporating identified sources of resistance into breeding materials. Evaluations on promising germplasm in Kenya as a short term strategy has led to the release of several bread wheat varieties, including Parsi, Sivand, Bam, Arg, Morvarid, Akbari, Gonbad, Sistan, Sirvan, Ofogh and Pishgam with acceptable levels of resistance/tolerance to stem rust in addition to other attributes. A hybridization and gene pyramiding strategy is being undertaken to develop new populations of wheat lines using the above-mentioned genotypes as parents to ensure durability of resistance in future materials. Where possible, molecular tracking of resistance genes is being undertaken to characterize resistant varieties. Regional networking and scientific interactions expedite collaborative activities and enhance the breeding effort in developing new resistant varieties.

Breeding for rust resistance in Kenya: Successes, setbacks and future approaches

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Over the last decade wheat has become an important food crop in Kenya with demand increasing to 6% annually; however, the annual production increases have remained below 1% leading to imports of 0.6 million tonnes each year. The slow growth could be attributed to a number of constraints such as drought, diseases and changed land use. Stem rust and yellow rust are rated as the most important biotic constraints in Kenya, and Kenyan wheat farmers have been fighting the Ug99 race group of the stem rust fungus since 2001. KARI, together with CIMMYT and other institutions, accepted the challenge, joined BGRI and established the critical screening facility at Njoro where over 300,000 wheat accessions from more than 20 countries/institutions were introduced and evaluated since 2005. The initial attempt in Kenya to address the challenge posed by Ug99 through deployment of effective race specific genes was not successful as the deployed gene *Sr24* was defeated by a variant of Ug99 that caused widespread losses. The introduction of adult plant resistance (APR), largely based on the “*Sr2*-complex” present in some of the CIMMYT and old Kenyan varieties, into breeding materials has resulted in a few adapted wheat lines which resist Ug99 in the Kenyan environment. The first Ug99 resistant varieties, Robin and Eagle 10, were released in 2009, and since then six more resistant varieties were released for commercial production with diverse combinations of race-specific and APR genes. Seed was multiplied and supplied to farmers through seed companies and individual farmers, and seed multiplication of new varieties is currently underway. In the future, breeding for rust resistance will focus on combining both major and minor genes for maximum protection and durability. The use of molecular markers to increase efficiency will aid selection of complex resistances. KARI is collaborating with CIMMYT and the National Institute of Agricultural Botany (NIAB) in a BBSRC funded project to improve molecular laboratory facilities in Kenya so as to implement marker assisted breeding strategies. Training courses organized at KARI every year under the DRRW project are designed to train wheat breeders from the public and private sectors in Africa, the Middle East and Central and South Asia, who wish to learn about stem rust, evaluation of germplasm, and standardization of note taking, as well as to update themselves with the global knowledge and innovative techniques that can enhance progress and efficiency in their breeding activities. The interaction of Kenyan scientists with the international wheat research community has increased our capacity to handle the wheat rust problem by facilitating testing and rapid release of Ug99 resistant varieties not only in Kenya but also in different wheat growing regions of the world.

Approaches to breeding for rust resistance at Sensako, South Africa

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South Africa's total wheat consumption is in excess of 3.64 million tons per annum with local production contributing 53% of the demand in 2012. This shortfall can be attributed to a significantly reduced cropping area, as a result of reduced profitability since deregulation of the wheat industry in 1998. With looming food shortages and the challenge to become more self-sufficient in wheat production, it is crucial to improve the value of the crop. To achieve this, yields have to be increased, input costs reduced, and prices increased for delivered grain. These are key objectives for Sensako, a privately owned South African wheat breeding company, currently owning approximately 75% of the local wheat market share. Among other traits, resistances to leaf rust, stem rust and stripe rust are extremely important in the South African context where wheat is produced in a range of environments differing in elevation, rainfall patterns and soil types. This variation allows for classifying production regions in terms of risk of rust epidemics and thus prioritising resistance breeding for particular regions. In this paper Sensako's approach to rust resistance breeding will be addressed taking into account the economic importance of the rusts and measures taken to alleviate their effects.

Outcomes of the Wheat Futures Convening: Envisioning possibilities for wheat improvement

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In April 2013, a group of fifteen early-career wheat scientists convened for a two-day meeting at the Bill & Melinda Gates Foundation (BMGF) in Seattle, WA, to brainstorm and deliberate about the future of wheat improvement. Hailing from nine countries and 14 different research institutions, the fifteen participants represented both the public and private sectors and a diversity of academic and geographic perspectives. By focusing on early career scientists, the sponsors of the meeting (BMGF and the Durable Rust Resistance in Wheat Project at Cornell University) were seeking innovative ideas with the potential of catalyzing the efforts of the broader wheat research community.

In terms of group composition, the 2:1 female-to-male ratio was striking, given the traditional over-representation of men in the agricultural sciences; and the participants agreed that this was a positive indication of the current and future demographic shift in wheat science. The group acknowledged that recognizing and developing the expertise of both male and female scientists will be critical to achieving long-term wheat improvement objectives.

Despite the fact that the group was composed almost exclusively of rust pathologists, molecular geneticists/genomicists, and breeders, there was widespread acknowledgement that the future of wheat improvement depends critically upon renewed and vigorous investments in agronomic research, extension, capacity building, on-farm innovation, and locally-optimized Integrated Crop Management (ICM) practices. This assertion came as bit of a surprise, given the professional composition of the group; and the lack of agronomic, agroecological, and extension expertise at the table was roundly recognized as a deficit in the discussion.

Participants also concluded that future wheat improvement will require a strong, ongoing commitment to open exchange of information, tools, and germplasm among the global wheat

research community. If grounded in and continually vetted against the articulated needs of wheat researchers in target regions around the world, the group posited that shared information management and decision support resources, clear data standards, young scientist training, and shared research facilities (particularly specialized phenotyping and genotyping facilities) are necessary to meet future wheat productivity goals.

In terms of both building collaborative relationships among early career wheat scientists and providing space for open and critical dialogue about the challenges facing wheat researchers, this first Wheat Futures Convening was a valuable experience for the participants and will hopefully spur further discussion within and across the broader wheat research, extension, and production communities.

Wild *Triticum* and *Aegilops* species: A mine of rust resistance genes for future harvest

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The importance of genetic diversity for crop breeding programs is well recognized. The breeding process, particularly in wheat, tends to converge the available diversity into elite genotypes. The germplasm of wild progenitor and non-progenitor related species and genera comprises immense genetic diversity, but a large proportion of this variability remains unutilized. The variation in wheat germplasm needs to be constantly explored and introgressed into cultivated wheats to ensure food and nutritional security for the ever-increasing global population. About 1,000 wild germplasm accessions of wheat and its relatives comprising 4 *Triticum* and 18 *Aegilops* species have been extensively evaluated under laboratory and field conditions for resistance to various wheat diseases, including the rusts, powdery mildew, Karnal bunt and cereal cyst nematode. Potentially useful sources of resistance have been identified in the primary, secondary and tertiary germplasm pools. Some accessions of non-progenitor *Aegilops* species with the C, U and M genomes were found to be useful sources of multiple disease resistance. We have transferred 20 disease resistance genes from 10 different sources to the highly susceptible bread wheat cultivar WL711. Three of these genes were designated as *Lr57*, *Lr58* and *Yr40*. Progenitor species as donors offer advantages in terms of relative ease of transfer to wheat. Among the progenitor species, *Ae. tauschii* (the D genome donor) and *T. monococcum*/*T. boeoticum* (closely related to the A genome donor) are rich reservoirs of genetic variation. All *T. monococcum*, most *T. boeoticum* and a few *T. urartu* accessions are completely resistant to leaf rust. Most of the *T. monococcum* accessions have moderate to complete resistance to stripe rust, most *T. boeoticum* accessions show complete resistance, and the majority of *T. urartu* accessions are highly susceptible. Resistances to leaf rust, stripe rust, powdery mildew and cereal cyst nematode have been transferred from A-genome species to cultivated wheats and mapped. The D genome of *Ae. tauschii* has much greater genetic diversity than the D genome of *T. aestivum* and new sources of leaf rust and stripe rust resistance have been identified in *Ae. tauschii* germplasm and are being exploited via bridging crosses. Advances in molecular cytogenetic and chromosome isolation techniques combined with genome sequencing, could make it feasible to dissect the genomes of wild relatives of wheat in order to discover new resistance genes and to transfer them to wheat.

Maximizing the potential for sustainable and durable resistance to the wheat stripe rust

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Wheat stripe (yellow) rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), was recently dubbed one of "wheat's worst enemies" and continues to be a major threat to global food security. The appearance of new and more aggressive *Pst* strains at the beginning of the 21st century and their rapid spread has resulted in severe yield losses in recent years. To date, pathologists and breeders have focused on the host plant by deploying resistance genes in new varieties. Recent innovations in sequencing technologies provide us with the unprecedented opportunity to start understanding how *Pst* changes at the molecular level. Improved knowledge of the pathogen's biology and how it evolves to overcome resistance genes will complement and augment these efforts.

Our aim is to understand the molecular basis of *Pst* pathogenicity and to exploit the information to design effective breeding strategies that maximize the potential for durable disease resistance in the field. During this first year, we have sequenced over 30 isolates and have established a *Pst* population genomics platform to characterize the pathogenicity arsenal of *Pst*. We are now taking the first steps to understand how *Pst* evolves in time across regions. Data stemming from the project is being made available through the www.yellowrust.com website.

We have also evaluated Triticeae germplasm for yellow rust response (and stem and leaf rust responses) in Ethiopia, Kenya, UK and India to characterise both seedling and adult-plant resistance. This includes ~800 landrace accessions from the Watkins collection for which >100 single-seed descent populations are being currently developed in a sister project led by colleagues in the UK (<http://wisplandrappillar.jic.ac.uk/>). We have identified sources of major and partial resistances based on the screens performed across different continents and we will now validate these in further trials and advance mapping populations. We are also working on using next-generation sequencing to rapidly identify SNP markers closely linked to these resistance genes.

Through this work, we also seek to create and consolidate partnerships between researchers and breeders and enhance the scientific capabilities of all partners.

Unraveling the *Rpg1*-mediated stem rust resistance signaling in barley

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Stem rust (caused by *Puccinia graminis tritici*) has re-emerged as a threat to barley and wheat via the widely virulent race TTKSK (aka Ug99) and its variants bringing renewed interests in stem rust resistance genes and their function. The barley stem rust resistance gene *Rpg1* confers durable resistance to the stem rust pathogen. We identified two novel *Pgt* effectors that interact with RPG1 within 5 minutes after spores land on the leaf surface, revealing the existence of a unique mechanism. The effectors are completely conserved at the amino acid level among avirulent races, but differ from virulent races by a few amino acids, which abolish their ability to phosphorylate, degrade and interact with RPG1. The two effectors fail to enter plant cells during the critical phase when RPG1 is recognized and activated. These discoveries have opened up novel strategies to control rusts on cereals.

Thank you Charles Darwin: A description of candidate wheat genes that may control wheat rust, derived from an evolutionarily based approach

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We identified a small subset of protein-coding genes of wheat that have undergone positive selection during adaptive evolution. These genes were derived from pairwise comparisons of the transcriptomes of several different wheat species/genotypes to that of *Triticum monococcum*. Positive selection is here narrowly defined as changes in protein sequence that have occurred as a response to selective pressures, rather than simply as a result of stochastic fixation of random amino acid replacements. Positively selected changes give rise to novel protein conformations and thus new functions. Wheat transcriptomes were queried for positive selection on protein-coding regions, using the Ka/Ks algorithm in an automated, high-throughput fashion. (Molecular-level positive selection can be detected in protein-coding genes by pairwise comparisons of the ratios of nonsynonymous nucleotide substitutions per nonsynonymous site [Ka] to synonymous substitutions per synonymous site [Ks]). Two genes with strong positive selection were detected. These displayed Ka/Ks ratios >1 with statistical support. In one candidate, the full-length coding sequence gave rise to Ka/Ks ratios >1, which is quite rare and strongly suggests the action of episodic positive selection. Such episodes may occur when naïve plant populations are challenged with novel pathogens/diseases, or, less frequently, during domestication events.

Each putative positively selected candidate was cloned from multiple wheat genotypes and carefully sequenced, thus permitting phylogenetic analysis to confidently assign orthology/paralogy. Genes thus demonstrated to be truly orthologous were then sampled from additional wheat genotypes.

Although we cannot yet ascribe with complete certainty the selection pressure that was responsible for the observed positive selection, our analysis of homology with known wheat gene/gene families suggested that each of our candidate genes are active in resistance pathways. We then compared our candidates with those resistance genes known to be ineffective against race TTKS; these candidates are novel. We plan now to genotype a sample of wheats that have been characterized for Ug99 resistance/sensitivity in order to use association analysis as a next step in validation of these candidates. We are looking for partners in this process.

GBS in wheat: Applications of genotyping-by-sequencing for wheat breeding and genetics

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Genotyping-by-sequencing (GBS) is a low-cost and flexible platform for whole-genome profiling of wheat breeding lines and genetic stocks. The abundance of molecular markers generated by GBS is excellent for a range of applications and different selection strategies in applied breeding. Here we focus on the intersection of the molecular marker platform and selection strategies for wheat breeding. We present three applications of GBS focused on breeding high-yielding durably resistant wheat: 1) genomic selection for grain yield, 2) genomic selection for quantitative adult plant rust resistance (APR), and 3) marker discovery and tagging of race-specific resistance genes (R-genes) in an approach suitable for gene pyramiding. As with any breeding program, focus on grain yield is a primary consideration. In the CIMMYT bread wheat breeding program we demonstrate the utility of GBS markers for genomic selection applications in wheat for yield and other associated agronomic traits. To develop durably resistant wheat cultivars a combined focus of selecting APR as well as pyramiding R-genes is proposed. Building on the genomic selection approach, we demonstrate the use of genomic selection for APR to stem rust and the application of this selection methodology in breeding programs. Finally, the use of effective R-genes in a breeding program can add additional layers of protection given the genes are deployed in pyramids to reduce pathogen fitness and avoid “breakdown”. Using near-isolines, we demonstrate rapid marker discovery for leaf rust R-genes. These GBS markers can then be used through applied bioinformatics approaches for gene pyramiding in the routine marker selection of the breeding program. Together, these implementations of molecular markers take an integrated approach to increasing the efficiency and selection power of the breeding program with the overall objective of speeding delivery of high-yielding durably resistant wheat varieties.

Using genomic selection in barley to improve disease resistance

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Genomic selection is a breeding method to predict the phenotype or breeding value of an individual using a large number of genome-wide marker effect estimates. It was shown to be effective for estimating breeding values for some quantitative traits and should substantially shorten the breeding cycle and increase genetic gain per unit time when employed in early breeding generations. We investigated the potential of genomic selection to improve resistance to *Fusarium* head blight (FHB) in barley and reduce the levels of the associated mycotoxin, deoxynivalenol (DON), in harvested grain. We fit models using training populations that have been genotyped and phenotyped for the traits of interest and calculate relative prediction accuracies as the correlation between the predicted and observed phenotype divided by the square root of the heritability for the trait. Initial studies using cross-validation indicate a relative accuracy of 0.78 for DON concentration using 384 SNP markers and training population of approximately 300 individuals. Generally the simplest model, random regression best linear unbiased prediction (RR-BLUP), resulted in prediction accuracies that are equal or similar to other more sophisticated models. In terms of optimizing prediction accuracy, the composition of the training population is more important than increasing the population size beyond 300 individuals. When we use a training population to predict the performance of breeding lines that are progenies of parents that are members of the training population, we observe a decrease in accuracy (0.58) compared to the cross-validation studies. We recently completed three cycles of genomic selection for FHB and are currently empirically assessing gain from selection. To assess the potential of using genomic selection to improve stem rust resistance in barley, we have characterized model accuracy using cross-validation with barley training populations that were evaluated for adult plant response in screening nurseries in Kenya. Obtaining good quality data from these off-site disease nurseries has proven to be a challenge and further highlights the potential value of using genomic predictions when reliable phenotypic data are unavailable.

The next fifty years of wheat rust research in India

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Wheat rusts are one of the most critical biotic stresses limiting wheat production in India. Ever since systematic wheat breeding started in 1908 researchers have continuously focused on developing varieties having inbuilt capacity to defend against rust pathogens. Consequently, India has not faced any major rust epidemic for more than three and half decades owing to systematic and extensive surveillance leading to pathotype identification and proper gene deployment strategies. However, this is no reason to be complacent as the three rusts may undergo significant changes due to pathogen evolutionary activity, varietal deployment patterns and climate change. Strategies are formulated to keep the rust menace at bay through multipronged approaches. New IT and remote sensing-based surveillance tools will assume greater significance to effectively monitor and track the spread of wheat rust diseases. Armed with a growing battery of molecular tools, a major reworking of the pathogen dynamics including epidemiology and evolution is definitely on the agenda. The theoretical underpinnings, in conjunction with rapid international developments in this area, are likely to accord greater space to quantitative aspects of rust-wheat interaction, thus shifting away from the conventional gene-for-gene paradigm, with practical implications for combining major-minor gene resistances. Characterization of race-specific effector molecules vis-à-vis R-genes on one hand, and availability of genome sequence of both host and pathogen on the other, would increasingly lead to a bioinformatics based meta-population approach to wheat-wheat rust relationship. The next fifty years hold a good prospect of keeping wheat rust free.