BGRI 2013 Technical Workshop

19–22 August, New Delhi, India



Index to Posters

Adoption or Rust Resistant Wheat

- 1 Accelerated women's participation in promotion of rust resistant wheat varieties in hills of Nepal, S. Sharma et al.
- 2 **Nepal-CIMMYT collaboration in increasing food security through wheat research and development,** *D.B. Thapa et al.*
- 3 Going beyond component technologies to integrated systems for enhancing the adoption of rust tolerant wheat varieties: Experience of EAAPP in Ethiopia, *M. Yami et al.*
- 4 Determinants of adoption of rust resistant improved wheat varieties in the Robe and Digelu Tijo districts of Oromiya region, Ethiopia, *T. Solomon et al.*

New Tools for Breeding

- 5 A consensus map for race Ug99 stem rust resistance loci in wheat, *L.-X. Yu et al.*
- 6 **Closely linked markers for** *Yr51***: From discovery to implementation,** *M.S. Randhawa et al.*
- 7 **Development of a wheat core germplasm set for precision breeding,** *A. Tiwari et al.*
- 8 Evaluation of design strategies for genomic selection training populations: A wheat stem rust resistance case study, J. Rutkoski et al.

Mapping and Molecular Dissection of Rust Resistance

- 9 Sources of resistance to stripe rust identified using molecular markers, J.P. Jaiswal et al.
- 10 Genetic analysis of resistance to leaf rust and stripe rust in Indian wheat cv. Sujata and NP876, C.X. Lan et al.
- 11 **Resistance to leaf rust and stripe rust in common wheat cv. Francolin#1**, *C.X. Lan et al.*
- 12 Identification and mapping of genetic factors controlling stripe and leaf rust resistance in spring wheat, *A. Singh et al.*
- 13 Molecular mapping and improvement of leaf rust resistance in wheat breeding lines, *T. J. Tsilo et al.*
- 14 Identification and mapping of genetic factors controlling stem rust resistance in spring wheat and the study of their epistatic interactions across multiple environments , *A. Singh et al.*

BGRI 2013 Technical Workshop • Poster Abstracts • m.globalrust.org

- 15 Genomic localization and genetic mapping of race-specific stem rust resistance in the Synthetic W7984 x Opata M85 double haploid population, *S.M. Dunckel et al.*
- 16 Seedling resistance to wheat leaf rust in Thatcher isolines carrying race specific and race non-specific genes, *S. Dugyala et al.*
- 17 Breeding high yielding micronutrient-rich wheat varieties with resistance to rusts, G. Velu et al.
- 18 Leaf tip necrosis, lesion mimic genes and resistance to spot blotch in spring wheat, *P.S. Yadav et al.*
- 19 **Molecular marker assisted accelerated improvement of wheat varieties with multiple rust resistances,** *Vinod et al.*
- 20 Comparison of GBS vs. SNP-chip approaches for mapping Ug99-effective APR QTLs, P. Bajgain et al.
- 21 Deciphering single nucleotide polymorphism using Next-Generation Sequencing data in hexaploid bread wheat, *S. Chandra et al.*
- 22 Characterization of recombinant *Lr34* protein: A putative wheat ABC transporter involved in leaf rust resistance, *R. Nandhakishore et al.*
- 23 *In silico* identification, annotation and expression profiling of wheat WRKY transcription factors in response to leaf rust pathogenesis using Next Generation Sequencing data, *L. Satapathy et al.*
- 24 Functional characterization of a wheat WRKY transcription factor with protective role in leaf rust pathogenesis and AFM imaging of the protein-DNA complex, *D. Kumar et al.*
- 25 Mining, annotation and characterization of stress responsive transcription factor genes ZIM, GRAS and HSF in wheat, *Poonam S. and K. Mukhopadhyay*
- 26 Evidence of *Yr36*-mediated partial resistance at low temperatures, *V. Segovia et al.*
- 27 Validation of a candidate barley stem rust susceptibility gene determining the recessive nature of rpg4-mediated Ug99 resistance, *D. Arora and R. Brueggeman*
- 27.1 Genome-wide association analysis on seedling and adult plant resistance of stripe rust in elite Pacific Northwest spring wheat lines, K. Ando and M. O. Pumphrey

New Sources of Resistance

- 28 Wheat-alien chromosome addition lines for stem rust and yellow rust resistances, *M. Rahmatov et al.*
- 29 Inheritance of Ug99 resistance in spring wheat landrace PI 374670, E.M. Babiker et al.
- 30 **Reaction of Turkish wild and landrace wheat and barley accessions to African** *Pgt* **race TTKSK**, *B. Steffenson et al.*
- 31 Introgression of resistance to African Pgt races from Sharon goatgrass (*Aegilops sharonensis*) into wheat, *E. Millet et al.*
- 32 Identification of novel genes for resistance to African Pgt races in Aegilops spp., J. Manisterski et al.
- 33 Stem rust resistance in Aegilops spp., P.D. Olivera and Y. Jin
- 34 Genetics of resistance to African *Pgt* races in Sharon goatgrass, *B. Steffenson*
- 35 Stem rust and leaf rust resistances in wild relatives of wheat with D genomes, V.K. Vikas et al.
- 36 Sources of resistance to stem rust in durum wheat, A.N. Mishra et al.
- 37 Identification of new sources of resistance to wheat rusts, Satish-Kumar et al.
- 38 A novel gene for leaf rust resistance in Tunisian durum wheat, S. Berraies et al.
- 39 **Yield evaluation of wheat lines carrying stem rust resistance genes derived from alien species,** *I. Dundas et al.*
- 40 **Preliminary evaluation of Ethiopian emmer landraces to wheat rusts and** *Septoria tritici* blotch in **southeastern Ethiopia**, *B. Hundie*
- 41 **Reactions of Turkish wheat landraces to** *Pgt* **race TTKTF**, *K. Akan et al.*

BGRI 2013 Technical Workshop • Poster Abstracts • m.globalrust.org

42 Reactions of some Turkish *Aegilops* and *Triticum* materials to *Pgt* race TTKTF, *K. Akan et al.*

National and Regional Efforts toward Wheat Rust Resistance

- 43 Genetic mapping and QTL analysis of leaf rust resistance genes in Australian wheat cultivar 'Cook', A. Akhmetova et al.
- 44 **Breeding for durable rust resistance in Texas hard red winter wheat using synthetic-derived wheat lines,** *B. Reddy et al.*
- 45 **Resistance to** *Pgt* **race TTKSF in the wheat cv. Matlabas,** *Z. Pretorius et al.*
- 46 **Development of wheat lines with complex resistance to rusts,** *L. Herselman et al.*
- 47 **Stripe (yellow) rust resistant spring bread wheat genotypes for the CWANA region,** *W. Tadesse et al.*
- 48 Variation in seedling response to North American *Pgt* and *Pt* races in an inclusive East African bread wheat panel, *M. Godwin et al.*
- 49 **Evaluation of bread wheat germplasm from the CGIAR Centers against** *Pgt* **race Ug99 in 2012**, *Z. Tadesse*
- 50 Yield performance and rust reactions of Ethiopian bread wheat genotypes, Y.S. Ishetu et al.
- 51 Zakia: A new Ug99-resistant variety for the heat stressed environments of Sudan, *I.S.A. Tahir et al.*
- 52 **Resistance of some Turkish bread wheat genotypes to yellow rust and stem rust,** *L. Çetin et al.*
- 53 Seedling and adult plant resistance to stripe rust among winter wheat commercial cultivars and advanced breeding lines in Uzbekistan, Z. Ziyaev et al.
- 54 Molecular breeding for leaf rust resistance in wheat, A. Kokhmetova et al.
- 55 Characterization of Afghan wheat landraces for response to rusts, A. Manickavelu et al.
- 56 **Stem rust reactions of candidate wheat lines under artificially inoculated and natural conditions in southern Pakistan**, *K.A. Khanzada et al.*
- 57 **Response of wheat cv.Seher-06 to leaf rust in Pakistan**, J.I. Mizra et al.
- 58 Wheat cultivation in Bhutan: Prospects and challenges, S. Tshewang and Doe Doe
- 59 Genetics of rust resistances in Nepalese wheats, B.N. Mahto et al.
- 60 Determining rust resistance genes in Nepalese wheat lines using SSR markers, S. Baidya et al.
- 61 **Rust resistant wheat varieties released in Bangladesh,** *N.D.C. Barma et al.*
- 62 HD-2189: A bread wheat variety undefeated by *Puccinia triticina* for 25 years in India, *G.S. Arunkumar* et al.
- 63 Yield reductions caused by stripe rust in a diverse group of Indian wheat genotypes, *R. Tiwari et al.*
- 64 Screening Indian germplasm for leaf rust resistance, A.L. Bipinraj et al.
- 65 Utilization of Australian germplasm for enhancing stripe rust resistance in popular Indian wheat cultivars, *R. Chatrath et al.*
- 66 Marker assisted pyramiding of stem rust resistance genes *Sr24* and *Sr26* in Indian wheat breeding, *B.K. Das et al.*
- 67 Adult plant leaf rust resistance in Indian bread wheat accessions bearing leaf tip necrosis, *J Kumar et al.*
- 68 Assaying stem rust resistance genes in Indian wheat varieties using molecular markers, *R. Malik et al.*
- 69 An accelerated breeding approach to pyramid resistance genes as a means of addressing wheat rust threats in India, *M. Sivasamy et al.*

- 70 **Exploring untapped variability for stripe rust resistance in indigenous wheat germplasm,** *C.N. Mishra et al.*
- 71 Identification of slow ruster wheat genotypes for stripe and leaf rusts under artificially inoculated conditions, *M.S. Sarahan et al.*
- 72 **Evaluation of barley genotypes for stripe rust (***Puccinia striiformis* **f. sp.** *hordei***) resistance in India,** *R. Selvakumar et al.*
- 73 A need to diversify *Lr24*-based leaf rust resistance of wheat in central India, *T.L. Prakasha et al.*
- 74 **Frequency of Ug99 resistant wheat lines derived from segregating populations selected under the Mexican and Mexico-Kenya shuttle breeding schemes,** *J. Huerta-Espino et al.*

Breeding Rust Resistance Durum Wheat

- 75 Stem rust resistance in durum wheat, P.D. Olivera et al.
- 76 **Breeding for leaf rust resistance in durum wheat in Morocco,** *N. Nsarellah et al.*
- 77 **Preliminary characterization of resistance to stripe rust from six elite durum lines,** *A. Loladze and K. Ammar*
- 78 **Leaf rust resistance in landraces and wild relatives of durum wheat from the Caucasus region,** *A. Loladze and K. Ammar*
- 79 **Characterization of leaf rust resistance of durum wheat lines derived from crosses with wild relatives,** *A. Loladze et al.*
- 80 Mitigating the threat of leaf rust to durum yield stability in new, *Septoria tritici* blotch resistant, germplasm in Tunisia, *M.S. Gharbi et al.*
- 81 Identification and mapping of markers linked to leaf rust resistance in Indian durum genotype Malvilocal, *A.L. Bipinraj et al.*

Global Surveillance Tools

- 82 Wheat rust information resources: Integrated tools and data for improved decision making, *D. Hodson et al.*
- 83 **FAO Global Wheat Rusts Program strengthens national capacities to manage wheat rusts,** *F.Dusunceli et al.*
- 84 An SMS network tool for rapid surveillance of wheat rusts through extension offices: A pilot initiative in Turkey, *F.Dusunceli et al.*
- 85 A new early-warning system for stripe rust affecting wheat and triticale: Host-pathogen interactions under different environmental conditions, J. Rodríguez-Algaba et al.
- 86 Inferring the origin and trajectories of recent invasions of wheat yellow rust strains from worldwide population structure, *S. Ali et al.*
- 87 **Screening for stem rust resistance in East Africa: A global effort to mitigate the threat of Ug99,** *S. Bhavani et al.*

National Surveillance Efforts

- 88 SSR analysis of herbarium specimens of *Puccinia graminis* f. sp. tritici in South Africa, B. Visser et al.
- 89 **Variation among** *Puccinia graminis* **f. sp.** *tritici* isolates from wheat in South Africa, 2011 and 2012, *T.G. Terefe and Z.A. Pretorius*
- 90 The rusts of *Secale africanum* in South Africa, C.M. Bender et al.

BGRI 2013 Technical Workshop • Poster Abstracts • m.globalrust.org

- 91 Wheat rusts: Distribution and virulence analysis of stem rust in the major wheat growing regions of Ethiopia in 2012 and 2013, *G. Woldeab et al.*
- 92 **Occurrence of wheat rusts in Algeria and strategies to reduce crop losses,** *A. Benbelkacem and H.J. Braun*
- 93 The rusts on winter wheat in southeastern Kazakhstan, Y. Dutbaev et al.
- 94 Wheat stem rust research in Georgia, Z. Sikharulidze et al.
- 95 Wheat rust virulence in southern Russia, G. Volkova et al.
- 96 Phenotypic and genotypic analyses of Turkish Pgt samples collected in 2012, M. Newcomb et al.
- 97 **Epidemics and adult-plant responses of Iranian wheat genotypes to the** *Yr27***-virulent** *Pst* **race in 2013**, *F. Afshari et al.*
- 98 Puccinia striiformis f. sp. tritci races and their distribution in Syria during 2008 and, S. Kharouf et al.
- 99 **Physiologic specialization of** *Puccinia triticina* **on durum wheat in Syria in 2010,** *M. Kassem and M. Nachit*
- 100 Virulence spectra of wheat rusts in Pakistan during 2012-13, A.R. Rattu et al.
- 101 Status of stripe rust and virulence patterns of Pst in Pakistan, J.I. Mirza et al.
- 102 Current status of Pgt virulence in Pakistan, J.I. Mirza et al.
- 103 Surveillance of wheat rusts in Bangladesh, P.K. Malaker et al.
- 104 **Prevalence and distribution of wheat stripe rust in Jammu and determination of sources of resistance**, *V. Gupta et al.*
- 105 Stripe rust of wheat: An Indian puzzle, S.C. Bhardwaj et al.
- 106 Virulence analysis of Pst isolates collected from western Canada, H.S. Randhawa et al.
- 107 Physiological specialization of Puccinia triticina on wheat in Argentina in 2011, P. Campos
- 108 **Upgrading knowledge of Chilean hexaploid wheat yield losses caused by stripe rust and leaf rust,** *R. Madariaga and I. Matus*

Barberry Surveillance

- 109 **Barberry rust survey: Developing tools for diagnosis, analysis and data management,** *A.F. Justesen et al.*
- 110 Survey of barberry and associated rust pathogens in Nepal, M. Newcomb et al.

Characterizing Wheat Rusts

- 111 EMS mutagenesis of avirulent *Puccinia graminis* f. sp. tritici urediniospores, G. Singh et al.
- 112 Analysis of simple sequence repeats in genic regions of the wheat rust fungi, R. Singh et al.
- 113 Analysis of effector proteins from the flax rust and wheat stem rust pathogens, P. Dodds et al.
- 114 Genome analyses of the wheat yellow (stripe) rust pathogen *Puccinia striiformis* f. sp. *tritici* reveal polymorphic and haustorial expressed secreted proteins as candidate effectors, D.G.O. Saunders et al.
- 115 Next-generation sequencing to characterize Pst races from western Canada, A. Laroche et al.
- 116 Identification and characterization of microRNAs and their putative target genes in *Puccinia* spp., *B. Pandey et al.*
- 117 Characterization of seedling yellow rust resistance in wheat commercial cultivars, landraces and elite genotypes from Syria and Lebanon, *R. Al Amil et al.*

EMS mutagenesis of avirulent Puccinia graminis f. sp. tritici urediniospores

G. Singh¹, J. Nirmala² and M.N. Rouse^{1,2}

¹Department of Plant Pathology, University of Minnesota, 485 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA; ²USDA-ARS Cereal Disease Laboratory, 1551 Lindig Street, St. Paul, MN 55108, USA

E-mail: rous0089@umn.edu

Pgt race TTKSK has been recognized as a major threat to the world's wheat crop. The emergence of virulent races such as TTKSK warrants further understanding *Pgt* avirulence genes and their ability to mutate and overcome resistance in wheat varieties. *Pgt* mutants defective in avirulence activity will serve as valuable resources for cloning avirulence genes and understanding wheat resistance. In this study, we are attempting to isolate virulent mutants of North American *Pgt* races MCCFC and RKQQC that are normally avirulent to the wheat stem rust resistance genes *Sr21* and *Sr35*, respectively. To this end, we have screened different concentrations of EMS (Ethyl Methane Sulfonate) (0.005 M, 0.008 M, 0.010 M, 0.040 M and 0.080 M) to determine the effects on germinating urediniospore viability. Preliminary results indicate that EMS concentrations of 0.010 - 0.015 M confer 50% urediniospore viability. This concentration is being used to mutagenize race MCCFC on monogenic wheat line 'T.monoc.deriv./8*LMPG (*Sr21*) and race RKQQC on line DV92 (*Sr35*). Virulent pustules from the EMS treatments are being isolated and inoculated to the stem rust differential set to distinguish between mutants and contaminants.

Analysis of simple sequence repeats dynamics in the genic regions of wheat rust fungi (*Puccinia* sp.)

R. Singh, B. Pandey, R. Chatrath, I. Sharma

Directorate of Wheat Research, Karnal, 132001, India

E-mail: rajenderkhokhar@yahoo.com

Simple sequence repeats (SSRs) or microsatellites are one of the valuable sources for genetic markers because of their abundance and inherent potential for determining extensive allelic variation in the genomes. In this study, we analyzed and compared the abundance and organization of SSRs in the genic region of three important fungal pathogens of wheat, brown or leaf rust (Puccinia triticina), black or stem rust (Puccinia graminis f. sp. tritici), yellow or stripe rust (Puccinia striiformis). The total number of SSR ranged from 4026 to 5844 representing 0.3% of genic region. The relative abundance and SSR density was highest in stem rust followed by stripe rust and leaf rust. The distribution pattern of different SSR motifs provides the evidence of greater accumulation of dinucleotide followed by trinucleotide in leaf and stripe rust, but the frequency of dinucleotide and trinucleotide repeats was same in stem rust. AG dinucleotide repeats are more frequent. Among trinucleotide repeats, ACC repeats are more frequent in leaf rust with a frequency of 12.51 SSR/Mb. AAC and ATG repeats are more frequent in stem rust and stripe rust, respectively with a frequency of 27.12 SSR/Mb and 17.99 SSR/Mb. The information about the frequency, relative abundance, relative density and variation in length of different SSR motifs in *Puccinia* sp. will be useful for developing markers that can be used for analysis of genetic diversity, population genetics, race identification and acquisition of new virulence.

Analysis of effector proteins from the flax rust and wheat stem rust pathogens

P. Dodds¹, N. Upadhyaya¹, R. Mago¹, J. Ellis¹ and R. Park²

¹CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia; ²Plant Breeding Institute, University of Sydney, PMB 4011, Narallen, NSW 2570, Australia

E-mail: peter.dodds@csiro.au

Stem rust caused by *Puccinia graminis tritici* (Pgt) is one of the most serious diseases in wheat and is combated mainly through the use of resistant varieties. Because the fungus evolves virulence towards previously resistant varieties, continuous breeding and identification of new sources of resistance is necessary to combat the threat of epidemics. Our work on the flax rust model system has provided insights into how the plant immune system recognises and responds to rust pathogens. These obligate parasites produce specialised infection structures called haustoria that penetrate infected cells and are the main sites of nutrient extraction. A suite of disease effector proteins are secreted from haustoria into the host cells where they promote infection. However these effectors can also be recognised by host immune receptors, known as resistance (R) proteins. To find effectors from Pgt that are recognised by wheat R genes, we used genome and transcriptome sequencing to predict ~ 400 candidate effector genes from Australian Pgt race 21-0. To screen for R gene recognition, we developed a bacterial Type III Secretion System delivery assay using *Pseudomonas fluorescens*. We screened candidate effectors on a set of 18 wheat cultivars carrying 22 different R genes and identified one effector that induces a cell death response specifically on a wheat genotype carrying Sr22. We are also analyzing sequence variation in effector candidates between clonal field isolates that have mutated to overcome resistance genes deployed in agriculture.

Genome analyses of the wheat stripe (yellow) rust pathogen *Puccinia striiformis* f. sp. *tritici* reveal polymorphic and haustorial expressed secreted proteins as candidate effectors

D.G.O. Saunders¹, D. Cantu², V. Segovia³, D. MacLean¹, R. Bayles⁴, X.M. Chen^{5,6}, S. Kamoun¹, J. Dubcovsky^{7,8,9} and C. Uauy^{3,4}

¹The Sainsbury Laboratory, Norwich Research Park, Norwich, NR4 7UH, UK; ²Department of Viticulture & Enology, University of California, 1136 RMI North – 595 Hilgard Lane, Davis, CA 95616-5270, USA; ³John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK; ⁴National Institute of Agricultural Botany, Huntingdon Road, Cambridge, CB3 0LE, UK; ⁵Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430, USA; ⁶USDA-ARS-ADRU, 3003 ADBF, Washington State University, Pullman, WA 99164, USA; ⁷Department of Plant Sciences, University of California Davis, One Shields Ave, Davis, CA 95616, USA; ⁸Howard Hughes Medical Institute, 4000 Jones Bridge Road, Chevy Chase, MD 20815-6789, USA; ⁹Gordon & Betty Moore Foundation, 1661 Page Mill Road, Palo Alto, CA 94304, USA

E-mail: yellowrust@jic.ac.uk

To design effective breeding strategies that maximize the potential for durable disease resistance it is important to understand the molecular basis of pathogenicity. In particular, characterization of the structure, function and evolutionary dynamics of secreted effector proteins that are detected by host immune receptors can help guide and prioritize breeding efforts. However, to date, our knowledge of the effector repertoire of cereal rust pathogens is limited. We resequenced four *Pst* isolate genomes to identify effector candidates and relate them to their distinct virulence profiles. We implemented a bioinformatics pipeline to integrate genomics, transcriptomics, and effector-focused annotations to identify and classify effector candidates in PST. RNAseq analysis highlighted transcripts encoding secreted proteins that were significantly enriched in haustoria compared to infected tissue. The expression of 22 candidate effector genes was characterized using qRT-PCR, revealing distinct temporal expression patterns during infection in wheat. Lastly, we identified proteins that displayed non-synonymous substitutions specifically between UK isolates PST-87/7 and PST-08/21, which differ in virulence to two wheat varieties. Integration of genomics, transcriptomics, and effector-directed annotation of Pst isolates has enabled us to move beyond the single isolate-directed catalogs of effector proteins and develop a framework for mining effector proteins in closely related isolates and relate these back to their defined virulence profiles. This should ultimately lead to a more comprehensive understanding of the *Pst* pathogenesis system, an important first step towards developing more effective surveillance and management strategies.

Next-generation sequencing to characterize wheat stripe rust races from western Canada

A. Laroche, Byron Puchalski, A. Singh, Brent Puchalski, D. Gaudet, <u>H. Randhawa</u>, R. Graf and M. Frick

Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, T1J 4B1, Canada.

E-mail: Harpinder.Randhawa@AGR.GC.CA

Wheat stripe (yellow) rust (*Puccinia striiformis* f. sp. *tritici*) is a highly aggressive pathogen of wheat quickly evolving new races that overcome existing resistance worldwide. The genome size of this pathogen is ≈ 110 Mb. New and highly virulent races of stripe rust already occur worldwide for which very limited genetic resistance exist and are a continuing threat to global food production thus posing a serious threat to wheat production around the world. The goals of the project are to identify stripe rust genetic elements related to strain aggressiveness and tolerance to high temperature and strain-specific sequences to further facilitate their recognition. A challenging issue has been to obtain enough single pustule isolated spores (300 mg) from this biotrophic organism to isolate sufficient DNA for sequencing (1 µg). So far, we have obtained Illumina sequencing information for 8 strains isolated from southern Alberta. Sequences were de novo assembled using Velvet and Geneious software as well as using data from PST-78 as a reference assembled genome (Dr. Cuomo, Broad Institute). Initial mapping of two contrasting strains against PST-78 suggested significant differences between these lines in both the mapped and unmapped sequence complements. Sequence representativeness between the output results of the HiRes and MiSeq instruments will be discuss as the later one requires only 50 ng of DNA. Results of assembled sequences will be discussed in function of their isolation dates (1990's vs. 2010's) and annotation of group specific genes' will be presented and discussed in term of temperature tolerance and aggressiveness.

Identification and characterization of microRNAs and their putative target genes in *Puccinia* spp.

B. Pandey¹, R. Singh¹, R. Chatrath² and I. Sharma²

¹Plant Biotechnology, Directorate of Wheat Research, Karnal 132001, India; ²Crop Improvement, Directorate of Wheat Research, Karnal 132001, India

E-mail: pandey.bharati15@gmail.com

MicroRNAs, small, single-stranded, non-coding RNAs with18 - 22 nucleotides, regulate gene expression post-transcriptionally. Although the role and targets of miRNA are extensively identified in diverse plants and animals, they remain largely uncharacterized in filamentous fungi; no miRNAs have been reported in rust fungi. Wheat is host to three different rust fungi, each of which is capable of causing serious losses to wheat production. In this study we identified and characterized miRNAs in the genomes of all three fungal pathogens using a computational pipeline. Contigs of genomic sequences of *Puccinia striiformis* were downloaded from the Broad Institute website (http://www.broadinstitute.org/). Most of the genes targeted by the predicted miRNAs were highly conserved across the three species, and were genes involved in transcription regulation, DNA binding, and ATP binding, but many were also hypothetical proteins. Our results provide new insights into regulatory and pathological functions of small RNAs and provide potential initiatives for study of plant pathogenic fungi. The study lays a foundation for understanding miRNA function in rust fungi and provides opportunities for exploiting RNA silencing in various applications, such as engineering plants resistant to fungal pathogens.

Characterization of seedling yellow rust resistance in wheat commercial cultivars, landraces and elite genotypes from Syria and Lebanon

R. Al Amil¹, M. Leconte², C. de Vallavieille-Pope², M.S. Hovmøller³, O. Abdalla⁴, K. Nazari⁴

¹Lebanese Agricultural Research Institute, Lebanon; ²INRA, UR1290 BIOGER, Grignon, France; ³Aarhus University, Slagelse 4200, Denmark; ⁴ICARDA, PO Box 5466, Aleppo, Syria

E-mail: k.nazari@cgiar.org

Multi-pathotype test on 87 elite line, 17 commercial cultivars, and 35 wheat landraces was carried out with 11 *Pst* pathotypes at INRA. *Yr1*, *3*, *4*, *6*, *7*, *9*, *17*, *25*, and *27* were postulated singly either in landraces, cultivars or in elite lines and gene combination of *Yr6+9*, *6+17*, *7+1*, *7+4*, *9+1*, *9+3*, *9+4* were only found in elite genotypes and the *Yr6+7* was only postulated in the landraces. *Yr27*, *7*, *6*, *3*, and *17* were the most common postulated genes in the cultivars, whereas the frequency of these genes were slightly different in elite lines. In landraces, *Yr25*, *Yr3*, and *Yr9* were the most frequent postulated genes. *Yr1* was only postulated in elite lines and *Yr4* was postulated in landraces and elite lines. Since the frequency of virulence *Yr1*, *Yr3*, and *Yr4* is low in the present *Pst* population in CWANA, utilization of these genes alone in large scale in farmer cultivars could result in increasing frequency of virulences and consequently devastating epidemics.