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A consensus map for race Ug99 stem rust resistance loci in wheat

L.-X. Yu¹, R. Singh², S. Bhavani², A. Morgounov², J. Huerta-Espino³, R. Wanyera⁴, H. Barbier¹ and M. Sorrells¹

¹Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853, USA; ²International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico; ³Campo Experimental Valle de México INIFAP, Apdo. Postal 10, 56230 Chapingo, Edo de México, Mexico; ⁴Kenya Agricultural Research Institute, Njoro, PO Private Bag, Njoro 20107, Kenya

E-mail: mes12@cornell.edu

The global effort to identify sources of resistance to *Pgt* race Ug99 has resulted in numerous studies reporting putatively new resistance loci. The purpose of this study was to combine available information on stem rust resistance loci and their map locations. The map locations from various sources were analyzed with our recent association mapping projects involving 608 spring and winter wheat breeding lines from CIMMYT and the IWWIP, and other populations from different groups. The map contains DArT, SSR and other markers and thus provides a useful resource for developing the consensus map. Marker loci associated with stem rust resistance were placed on the map and most of them have been mapped in more than one population. Several markers appeared to be linked to known *Sr* genes, while other significant markers were located in chromosome regions where no *Sr* genes were previously reported. This consensus map and related information will be made available on the BGRI web site and periodically updated with all loci associated with Ug99 resistance in wheat.

Closely linked markers for Yr51: From discovery to implementation

M.S. Randhawa¹, U.K. Bansal¹, M. Valarik² and H.S. Bariana¹

¹The University of Sydney Plant Breeding Institute Cobbitty, PMB 4011, Narellan, NSW 2567, Australia; ²Centre of the Region Hana for Biotechnological and Agricultural Research, Institute of Experimental Botany, Sokolovska 6, 77200 Olomouc, Czech Republic

E-mail: mandeep.randhawa@sydney.edu.au

Stripe rust resistance gene Yr51, identified in wheat landrace AUS27858, is effective against preand post-2002 Australian *Puccinia striiformis* f. sp. *tritici* (*Pst*) pathotypes. Post-2002 *Pst* pathotypes are very similar to North American pathotypes reportedly adapted to warmer temperatures. Yr51 is also effective against Indian *Pst* pathotypes. Bulked segregant analysis using DArT markers placed Yr51 in chromosome 4AL. DArT-based STS markers and SSR markers previously mapped in chromosome 4AL were used to saturate the region containing Yr51. Based on marker analysis, the wheat composite and deletion bin map information from the GrainGenes database, Yr51 was mapped in deletion bin 4AL4-0.80-1.00. EST-derived STS markers from this deletion bin and gene based markers (Jakobson et al. 2012, Theor Appl Genet 125:609-623) were used for further enrichment of the genomic region carrying Yr51. Yr51 was flanked by markers *owm45F3R3* and *sun104* at 1 cM and 2.5 cM proximally and distally, respectively. Studies are in progress for map-based cloning of Yr51. Yr51 is currently being backcrossed into Australian and Indian wheat cultivars through marker assisted selection. This work is supported by a John Allwright Fellowship funded by the Australian Centre for International Agricultural Research in an Indo-Australian collaborative project.

Development of a wheat core germplasm set for precision breeding

A. Tiwari, M. Devare, J. Warade, A. Swami, V. Dalvi, A.M. Rao, B. Char, U. Zehr and V. Mikkilineni

Mahyco Research Centre, Maharashtra Hybrid Seeds Company Limited, Jalna-Aurangabad Rd, PO Box 76, Dawalwadi, Jalna, MS 431203, India

E-Mail: anshuman.tiwari@mahyco.com

Wheat is an important cereal crop around the world. Genetic variation is essential for any crop improvement program. Diversity analysis of germplasm estimates the extent of variability among genotypes, and estimates of genetic distance enable us to choose diverse parental lines for hybridization in order to maximize favorable epistatic effects in a line development program and for improving the chances of heterosis in a hybrid breeding program. Therefore, a thorough understanding of genetic diversity in germplasm will enable precision breeding. Genetic diversity analysis will help in identification and introgression of desirable alleles from non-elite donors and would also identify associations of markers and traits. In this report, we will present results of a diversity analysis of 1,152 wheat germplasm lines. Qualitative traits were used for phenotypic diversity analysis. Microsatellite markers distributed across the genome were used in molecular analysis, thereby generating phenotypic and molecular marker data. We have so far found that the phenotypic and genotypic diversity of the germplasm is in the range of 46% and 94%, respectively. The lines were classified into four major classes and more than 40 minor classes. The genetic diversity data suggests that there is considerable genetic variation between wheat genotypes and its exploitation should enable capture of favorable epistatic/heterotic effects from parents with different alleles. A core germplasm set will be identified based on genetic distance values and desirable agronomic and phenotypic traits. The efficiency of the set will be further validated in experimental crosses.

Evaluation of design strategies for genomic selection training populations: A wheat stem rust resistance case study

J. Rutkoski¹, R.P. Singh², J. Huerta-Espino³, S. Bhavani⁴, J. Poland⁵, J.-L. Jannink⁶ and M.E. Sorrells¹

¹Department of Plant Breeding and Genetics, 240 Emerson Hall, Cornell University, Ithaca, NY 14853, USA; ²International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 El Batan, Mexico; ³Campo Experimental Valle de México INIFAP, Apdo. Postal 10, 56230 Chapingo, Edo de México, Mexico; ⁴CIMMYT, ICRAF House, United Nations Avenue, Gigiri, Village Market-00621, Nairobi, Kenya; ⁵United States Department of Agriculture; Agricultural Research Service (USDA-ARS) and Department of Agronomy, Kansas State University, 4011 Throckmorton Hall, Manhattan, KS 66506, USA; ⁶USDA-ARS and Department of Plant Breeding and Genetics, Cornell University, 240 Emerson Hall, Ithaca, NY 14853, USA

E-mail: rutkoski.jessica@gmail.com

Genomic selection (GS) is a method that enables breeding value prediction based on genomewide markers. A "training set" composed of phenotyped and genotyped individuals is used to train a model in order to predict breeding values of new individuals closely related to the training set. The use of historical data for model training is attractive because it can reduce GS start-up costs, however the utility of historical data for prediction of new selection candidates (SCs) is not clear and evaluating a subset of SCs may be optimal for model training. Using stem rust adult plant resistance in wheat as a case study, we evaluated prediction accuracies of three model training strategies: 1) use pre-existing historical data (TP-H), 2) evaluate a subset of the SC population and use for model training (TP-SC), and 3) use a combination of these two sets (TP-H+SC). All three strategies were evaluated using empirical data given various levels of heritability, training population sizes, and training population optimization algorithms to identify scenarios favoring each strategy. This study found that TP-H was favorable only when the heritability was substantially higher than that of the SC population and the historical training set was large or optimally sub-sampled using an optimization algorithm. Surprisingly, TP-H+SC. generally did not lead to accuracies above those obtained using either TP-H or TP-SC. Further work to develop decision support tools integrating genetic distance between training and validation sets, heritability, and size of the training set is warranted.