Genetic Relationship of Adult Plant Resistance to Wheat Rusts and Validation of Stem Rust QTL

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Cereal rusts are among the most important fungal diseases worldwide and pose a major threat to global food security. Wheat is attacked by three rusts known as stripe rust, leaf rust, and stem rust caused by fungal pathogens, *Puccinia striiformis*, *Puccinia triticina*, and *Puccinia graminis* respectively. These pathogens are widely distributed across the world, produce spores with the ability to travel long distances, rapidly multiply under favorable environmental conditions, and evolve new races that overcome the resistant genes in cultivated varieties. The rapid appearance of new races of rust pathogens with virulence for the major seedling resistance genes in wheat has intensified the focus to breeding for durable resistance (Singh and Rajaram 1992; Singh *et. al.*. 2000). Durable rust resistance is more likely to be of adult plant type rather than seedling type and not associated with the genes conferring hypersensitive reaction (McIntosh 1992, Bariana *et. al.*, 2001). Genetic studies conducted at the International Maize and Wheat Improvement Centre (CIMMYT) in Mexico have shown that at least 10-12 different genes are involved in adult plant resistance (APR) in CIMMYT germplasm, and by accumulating 4-5 minor genes, a near–immunity resistance level can be achieved in terms of yield losses. However, 2-3 genes in a line provide moderate level of resistance (Singh *et. al.* 2005, 2009). Most of these genes are undesignated except *Lr34/Yr18/Sr57*, *Lr46/Yr29/Sr58*, *Lr67/Yr46/Sr55* and *Sr2/Yr30* which are also linked with phenotypic markers, leaf tip necrosis (*Ltn1*, *Ltn2*, *Ltn3*) and pseudo black chaff (PBC), respectively. Therefore, identification and characterization of novel durable resistance genes using genotyping by sequencing (GBS) and quantitative trait loci (QTL) mapping will provide an excellent way to understand the genetic relationship/mechanism of adult plant resistance in the process of varietal development by using the advanced breeding approaches for sustainable production.

Two different projects were developed to identify and map the genetic sources and dissect the mechanism of adult plant resistance to rusts. The first project utilizes a bi-parental mapping population derived from a cross of COPIO x Apav#1. It consists of 178, F_4:F_5 recombinant inbred lines (RIL) developed at CIMMYT in Mexico. ‘FH6-1-7’ is a line from Ethiopia, having resistance to all three rusts including the Ug99 variant at the adult plant stage. The advanced

wheat line COPIO (CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7) carries this parent and is likely to become a wheat variety in Ethiopia (R.P. Singh, Personal communication). So, adult plant resistance to all three rusts is unique in parent "COPIO" which has not been mapped to date. The other parent, 'Apav#1', is derived from a cross of Avocet x Pavon and is susceptible to all three rusts. The objectives of this research are to:

1. Evaluate the mapping population derived from the cross of the COPIO x Apav#1 for APR to all three rusts under artificially inoculated field conditions.
2. Map the novel durable resistance genes in wheat line "COPIO"
3. Understand the genetic relationship of APR genes conferring resistance to all three rusts.

This mapping population was planted in the field at the CIMMYT summer research station in Toluca, Mexico for stripe rust (*Yr*) field testing and seed multiplication during 2015. F_4:F_5 lines will be subsequently used for phenotyping and genotyping. Screening for *Yr* will be repeated in Toluca during 2016 and final results will be available by the end of October, 2016. Testing for stem rust Ug99 will be conducted in Kenya in 2016 (off-season and main-season). Leaf and stem rust testing will be carried out in Obregon, Mexico and St. Paul, Minnesota during the 2015-2016 and 2016-17 crop seasons. The mapping population will also be planted in Pakistan at WRI-Faisalabad, CDRI-Karachi and CCRI-Pirsabak to evaluate for leaf, stem and stripe rust respectively, during 2015-16 and 2016-17. The mapping population will also be screened against selected single races of leaf and stem rust especially the Ug99 lineage group races to ensure it does not carry any valuable seedling resistance genes.

A one-meter long row will be planted at all locations with perpendicular border of susceptible check varieties. All nurseries will be artificially inoculated to ensure high disease pressure and scored for infection type and severity using the modified Cobb scale (Peterson *et al*., 1948). For seedling testing, the population will be planted in small pots and inoculated at the 2-3 leaf stage with single races. Rust will be scored 14 days after inoculation based on 0-4 scale as described by Stakman *et al.*, 1962. Genotyping of the RILs will utilize GBS, which has been successfully used in the Anderson lab on common wheat (Bajgain *et al*., 2014) and the outcrossing perennial *Thinopyrum intermedium* (Zhang et al., 2014). Detection of genomic regions and markers associated with resistance to the rusts will utilize QTL analysis software QTL Cartographer for the RIL population.

The second project involves the validation of stem rust APR QTL on 2B chromosome in a Sabin/MN06113-8 wheat mapping population. The wheat breeding program at the University of Minnesota mapped a large effect stem rust APR QTL on chromosome 2B in a spring wheat bi-parental population RB07/MN06113-8 (Bajgain *et al*., 2015). This QTL is effective against the North American, Kenya and Ethiopian stem rust races. *Sr2* is the only known stem rust adult plant resistance gene and widely used in wheat breeding programs across the world. So, this newly identified large effect QTL will potentially be another genetic addition for the wheat community to cope with this devastating fungal pathogen. This QTL validation population will

be phenotyped in Africa during 2016 and 2017 following the same procedures outlined for the first project. The validation population will be genotyped with DNA markers that span the 2B QTL region and further development of diagnostic markers will facilitate the marker assisted selection.

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