

Germplasm Enhancement of South Dakota Wheat for Resistance to Biotic Stresses

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Importance to South Dakota:

Biotic stresses are one of the most important limitations for wheat production. Scab is, at this time and without a doubt, the most important disease in SD especially for its double impact in yield and in quality. Other disease such as leaf and stem rust and tan spot are also regularly found in wheat fields with variable impacts. Leaf and stem rust resistance genes are occasionally overcome by new changes in the pathogen making necessary the continuous incorporation of additional resistance genes. Orange wheat blossom midge (OWBM) has become one of the key pests in wheat production and in the last decade there have been infections of economic impact in the northern plains.

Preemptive development of germplasm with 'novel' resistance genes in multiple combinations and genetic backgrounds is seen as the best and more economical mitigation to the impact of biotic stresses in wheat production in South Dakota.

Objectives:

- Introgression and pyramiding of 'novel' resistance genes to different biotic stresses generating multiple early generation germplasm for both SD wheat breeding programs (spring and winter wheat).
- Continue to provide support for Marker Assisted Selection in South Dakota spring and winter spring wheat breeding programs for known disease resistance genes.
- Study the genetics of resistance to the orange wheat blossom midge (OWBM) using mapping and genomic approaches. Developing adapted early generation germplasm with the resistance gene.

Justification:

This project, based in the Seed Technology Laboratory, strives to work with the Spring and Winter wheat breeding programs as well as the Crop Quality Lab and Plant Pathologists to develop and use molecular genetics approaches to improve the efficacy in the development of improved cultivars for South Dakota. Biotic stresses are one of the most important limitations for wheat production in South Dakota. Scab and other disease such as leaf and stem rust and tan spot are also regularly found in SD wheat fields with important impacts in the bottom line. Fusarium Head Blight resistance genes do not provide a full resistance to this important disease making the pyramiding of multiple genes a necessity. Leaf and stem rust resistance genes are occasionally overcome by new changes in the pathogen making necessary the continuous incorporation of additional resistance genes.

Progress Report:

Haplotyping work is well advanced. We have found some difficulties replicating the original references, but this is not completely out of the ordinary to study the genetics of resistance to the orange wheat blossom midge (OWBM), we have run 50+ DNA markers including ~25 single nucleotide polymorphisms (SNP) and have been placed on the linkage map. Additional SNP markers were developed and sent for genotyping to Kbioscience, unfortunately these did not yield any polymorphisms given the close relationship between the founding parents of the mapping population. Several crosses have been made to introgress the OWBM resistance gene in chromosome 2B into South Dakota adapted germplasm and segregating populations are being advanced.

We established a working relationship with Dr. Marion Harris at North Dakota State University. Dr. Harris has developed a method for infestation in greenhouse conditions. The method is labor intensive and only allows for

few plants to be assayed at a time and depends on availability of the insect eggs collected from infested fields in the previous growing season. Her participation has allowed us to use greenhouse infestations to generate ribonucleic acid (RNA) samples from infested and non-infested embryos from resistant and susceptible genotypes. We are currently preparing some of these samples for RNA sequencing using pyrosequencing platforms from the University of Illinois. This approach will allow us to sample most of the genes being expressed in those samples, thus providing us with a detailed view of the metabolic processes related to resistance.

Materials and Methods:

Objective 1. We are using a novel family pedigree based approach in plant genetics to validate and pyramid resistance genes that have not been deployed in adapted germplasm. The proposed approach is based on the method used in human genetics to identify loci controlling genetic disorders in human families. This type of family-based genetic analysis is based on the co-transmission of the phenotypic trait and molecular markers in several families affected by the trait. Funding from the USDA Scab Initiative has allowed us to greatly expand our efforts pyramiding multiple FHB resistance quantitative trait loci (QTLs). The main advantages of this approach is the faster turnaround compared to ‘traditional’ QTL analysis where one has to wait 2+ years to begin the analysis. The source of resistance is introgressed into multiple adapted genetic backgrounds that can be used in further varietal development. We have proven the power of this approach using a well-validated QTL in wheat and a publication in *Theoretical and Applied Genetics*.

Objective 2. For this objective we have leveraged funding from a USDA-AFRI (Agriculture and Food Research initiative) grant secured in 2010 by Dr. Berzonsky and participated by Dr. Glover, Dr. Stein, Dr. Grady (Sunflower breeding) and Dr. Gonzalez to study the physiological effects of pyramiding multiple rust resistance genes in wheat and sunflower.

Objective 3. We are using an available recombinant inbred lines already phenotyped. It is known that the gene in question is located in the short arm of chromosome 2B; however perfect markers are not available. This makes it difficult to use this gene in breeding programs since an accurate phenotype is tough to produce. Selected recombinant lines from this population have been crossed to elite SD germplasm to generate early generation germplasm that is being advanced through selfing to develop larger mapping populations.