

**PI: Gonzalez, Jose**

**PI's E-mail: jose.gonzalez@sdstate.edu**

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**Project Title: Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region.**

### PROJECT 1 ABSTRACT

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The widespread FHB (scab) epidemics causing extensive damage in the wheat and barley production areas of the Northern Great Plains of the U.S. is well documented (Bai and Shaner 1994; Saylor 1997) and there is no need to re-state that information to this audience.

Traditional QTL mapping using recombinant inbred lines is slow (4-5 years), and in many cases is disengaged from breeding applications. Recently, association mapping using a set of unrelated lines, has caught the attention of scientists, however this approach has several limitations including sensitivity to population structure, potential loss of power if multiple resistance genes are present in the set of lines, and lack of direct application to breeding because this approach does not develop new material .

We propose to use a novel approach to identify the major loci controlling resistance to FHB in two novel sources of resistance to FHB; SD3934 and Mult757. The proposed approach is based on the method used in human genetics to identify genetic loci controlling genetic disorders in human families. This type of pedigree-based genetic analysis is based on the co-transmission of the phenotypic trait and molecular markers in several families affected by the trait (Jannink and Walsh, 2002).

DNA-based molecular markers have been used to map quantitative trait loci (QTL) and their subsequent use in marker aided selection (MAS). Traditionally in self-pollinated species mapping populations are bi-parental cross of distantly related parents and most commonly fixed lines after 4-5 generations of selfing. Traditional approaches have three important limitations, the markers are not available on time to plant breeders and the identified markers may not be applicable to other genetic backgrounds then tested, and as such a mapping population rarely gives rise to a new cultivar. So using plant breeders' populations for mapping purpose has caught attention. Plant breeding populations in self pollinated crops include larger number of families with small family size derived from crosses between large numbers of related founders. The objective of this study is to test applicability of family-pedigree based linkage and association mapping techniques commonly used in human genetics to plant breeding populations. These techniques were applied to map a well characterized QTL, *Qfhs.ndsu-3BS*, for Fusarium head blight resistance derived from Sumai 3. Breeding population developed by spring wheat program during 2005-2007 which included 83 families consisted of 793 individuals with average family size of 9 members. Resistance to Fusarium head blight was evaluated under greenhouse condition by artificially inoculating a most virulent SDSU isolate. Genotyping was done using mapped markers 3B and other chromosomes. QTL-marker linkage analysis was done using variance component based parametric linkage analysis and pedigree-wide regression. QTL-marker association analysis was done using quantitative transmission disequilibrium test (QTDT) developed for extended pedigrees. All of the approach could map the location of QTL as suggested by previous studies with high probability value. The best fit markers could explain 40-50% of the phenotypic variation. Moreover, QTDT was more stringent to detect markers associated with the QTL. The result shows the usefulness of human genetics the approach to detect relatively large effect QTLs earliest possible in breeding program and subsequent use in MAS.

We plan to optimize this approach and use to study the resistance in SD3934.