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

Project ID: FY10-HW-010 **FY10 ARS Agreement #: 59-0790-8-066**

Research Category: **HWW-CP** **Duration of Award: 1 Year**

Project Title: Simultaneously Pyramiding and Validating Multiple FHB Resistance QTLs in Different Hard Winter Wheat Backgrounds.

PROJECT 1 ABSTRACT

(1 Page Limit)

The goal of this project is to deliver early generation germplasm (~50 different genetic backgrounds combining multiple resistance genes) to the winter wheat breeders in this region. This will include active collaboration with winter wheat breeders in the Northern Great Plains of the U.S. and will make breeding material available to the breeders without restrictions. Breeders will be able to make their selections according to their target environments. Each breeder will submit parental elite lines with Fhb1 to be used in the crossing scheme, ensuring in this way that Fhb1 is the base level of resistance. This project makes use of a novel family based pedigree mapping approach to validate and pyramid new major loci controlling resistance to FHB in different sources of resistance to FHB; Freedom, Dream, Arina, Ernie and Lyman. The proposed approach is based on a 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). Traditional QTL mapping using recombinant inbreed lines is slow (4-5 years), and in many cases is disengaged from breeding applications. Recently, we have demonstrated that utilizing a family-based mapping protocol can accurately identify QTL in wheat breeding populations (Rosyara et al., 2009). Furthermore, simulation studies of the family-based mapping protocol have identified a means to optimize this procedure further (Rosyara et al., in review), specifically that to increase the power to detect QTL it is better to; use four way crosses, increase the marker density and increase the size of the population by having more individuals per family rather than more families.

The approach consist in developing pedigrees based on the basic crossing scheme were 3-4 resistance sources are crossed to a set of adapted lines (~20), the resulting F_1's are crossed to each other producing a 4-way F_1. These 4-way F_1s will be genotyped using an ABI genetic analyzer (as well as nondenaturing polyacrylamide gels) for markers around the putative QTLs. The selfed progeny of these 4-way crosses will be bulked and phenotyped for FHB resistance to rpvide a phenotypic value for the previous generation. Figure 1 shows the basic crossing scheme described above. Adapted germplasm carrying Fhb1 will be the base of the crossing scheme. Every family will have at least one parent carrying this resistance gene from Sumai 3.