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Project ID: **FY12-NW-011**	**ARS Agreement #:** **59-0206-1-114**
Research Category: **VDHR-NWW**	**Duration of Award:** **1 Year**

Project Title: **Improved Breeding for FHB Resistance by Advanced Genetic and Phenotypic Characterization of Soft Winter Wheat.**

PROJECT 3 ABSTRACT

(1 Page Limit)

The objective of this project is to develop populations, knowledge of the genetics of FHB resistance, and breeding methodologies for rapid improvement of FHB resistance in soft winter wheat (SWW). Genetics studies in SWW suggest that there are several unique sources of FHB resistance that are controlled by several QTL with moderate to small effects, thus complicating traditional MAS approaches. Consequently, recurrent selection is likely to be an effective breeding tool to accumulate favorable alleles. We propose to develop knowledge of the types of resistance, the genetics of this resistance, and efficient breeding methodologies for improving FHB resistance in SWW. Specifically, we will determine the genetic structure of FHB resistance in SWW, develop models to implement genomic selection (GS) for multiple FHB traits, and characterize RKI and RTA in SWW. Our approach will be to phenotype and genotype a set of 70 elite SWW lines that have good FHB resistance and 1034 families derived from those elite lines. The population will be phenotyped for multiple FHB traits (INC, SEV, IND, , DON) in field trials. The data will be used in an association analysis (AA) to determine the genetics of resistance in SWW to estimate the effect of QTL on multiple mechanisms of FHB resistance and the frequency of favorable alleles in the SWW. The data will also be used to develop a GS model that predicts the breeding value of individuals using estimated gene effects from the entire genome. The model can be used in subsequent selection cycles to choose superior parents with little or no phenotyping. Collectively, AA and GS will allow us to 1) select parents that are fixed for the same major genes, 2) design crosses that facilitate combining different genes and multiple mechanisms of FHB resistance, and 3) allow selection of superior individuals without phenotyping thereby reducing time per breeding cycle.