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Project ID: FY10-NW-010	**FY10 ARS Agreement #: 59-0790-6-061**
Research Category: **VDHR-NWW**	**Duration of Award: 1 Year**
Project Title: FHB Resistant Soft White and Red Wheat Varieties for Michigan and Region.	

PROJECT 1 ABSTRACT
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The overall goal of this project is to accelerate development of soft white and red winter wheat cultivars adapted to Michigan with improved resistance to Fusarium head blight (FHB) and deoxynivalenol (vomitoxin, VOM, DON). FHB has been an annual problem in Michigan for more than a decade. The majority of wheat cultivars grow in Michigan are susceptible to FHB. Michigan is the largest producer of soft white wheat in the Eastern U.S., and Michigan State University's wheat breeding program is one of two public programs in the Eastern U.S. (the other is directed by M.E. Sorrels at Cornell University) that focuses the majority of the program on soft white winter wheat. White wheat has been found to have higher levels of DON than red wheat when comparing varieties of comparable field symptoms, making the problem of FHB in Michigan especially serious.

Michigan State University has been actively involved in breeding for FHB resistance. Breeding with Chinese sources of FHB resistance has been strongly emphasized, but, yield trails have shown that the breeding lines produced have exhibit poor yield. Native sources of resistance may lend themselves more easily to higher yielding line. Some native sources of resistance have been used in crosses in the past, and we will create additional crosses with native sources of resistance, and work to combine native and Chinese sources of resistance.

In 2009, we began using Marker Assisted Selection (MAS) for Chinese sources of resistance to enrich populations from 3-way crosses, and select in early generations from 2-way crosses. By using MAS in early generations we are both 1) increasing our proportion of lines with desired resistance and 2) eliminating lines without the resistance. In addition, through early selection we also maintain as much variation as possible for other traits (such as yield) – making it more likely that we will be able to identify a higher yielding line in combination with resistance.

A brief overview of our plan of work is as follows: Crosses will be made between elite high yielding germplasm and FHB resistant germplasm. Marker Assisted Selection of known Quantitative Trait Loci (QTL) for resistance will be conducted in collaboration with the USDA/ARS Regional Small Grains Genotyping Lab (RSGGL, Raleigh, NC), and selections will be made based on these marker data. FHB phenotyping will be conducted in an inoculated and misted field nursery. Post-harvest assessment of Fusarium damaged kernels and DON will be conducted on selected lines/nurseries. Through these methods we expect to increase the FHB resistance in MSU's breeding lines, and have a greater change to develop commercial cultivars with both FHB resistance and high yield.

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Project ID: FY10-NW-002	**FY10 ARS Agreement #: 59-0790-6-061**
Research Category: VDHR-NWW	**Duration of Award: 1 Year**
Project Title: Coordinated Evaluation and Utilization of Marker Assisted Selection.	

PROJECT 2 ABSTRACT
(1 Page Limit)

The objectives of this project are to 1) evaluate the effectiveness of use of FHB-resistance QTL in the NWW breeding programs through marker assisted selection (MAS); 2) quantify the effects of these QTL in reducing FHB and DON; and 3) measure their impact on other key traits such as yield and milling and baking quality. Approximately 700-1000 partially inbred lines (RIL) from crosses with an array of parents homozygous for the resistance alleles at Fhb1 and other QTL have been planted in breeding nurseries in KY, MO, IN, IL, MI, OH and NY. These lines will be genotyped at Fhb1 and other resistance QTL during the spring and summer of 2010 at the USDA-ARS *Eastern Regional Small Grains* Genotyping Lab, Raleigh, NC. This material will be concurrently phenotyped for FHB traits, and in some cases yield and other agronomic traits in the individual Co-PI's scab and yield nurseries. Based on genotypic and phenotypic data, a number of pairs of sister lines, homozygous for resistance and susceptibility alleles at each QTL will be identified in each breeding program. Seed of these lines will be distributed to Co-PIs for planting in the fall 2010 and FHB phenotyping, yield testing and milling and baking quality analysis. Outputs will include information on the effect of genetic background on QTL expression, sharing of lines to use as parents, and possible identification of lines worthy of joint germplasm and/or cultivar release.

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Project ID: FY10-NW-009	**FY10 ARS Agreement #: 59-0790-6-061**
Research Category: **VDHR-NWW**	**Duration of Award: 1 Year**
Project Title: Coordinated Evaluation of FHB Resistance of Advanced Soft Winter Lines and Cultivars.	

PROJECT 3 ABSTRACT
(1 Page Limit)

The objectives of this project are to phenotype advanced breeding lines that are candidates for release, place FHB and other agronomic, disease resistance, and quality data in a database and report on purification and seed increase of the best lines. Regional uniform testing has stood the test of time as one of the best ways to evaluate and distribute new germplasm. Breeders benefit from both the extended testing in other environments and from access to superior lines from other breeding programs. The NUWWSN and PNUWWSN tests were created to specifically test FHB resistance of up to 120 entries and are coordinated by Ohio State University. The NUWWSN and PNUWWSN are also evaluated for milling and baking quality by the USDA Soft Wheat Quality Lab and are assessed for other diseases as they occur. Our most advanced lines are tested for yield and other traits in uniform tests coordinated by Harold Bockelman of the USDA or by breeders. In addition, each state has an Official Variety Test (OVT) of released cultivars that are evaluated for FHB resistance and make that information available to growers through the state extension service. Through these coordinated evaluation efforts, we can determine the FHB resistance of nearly all germplasm that is currently released, or likely to be released in the near future. We anticipate that all data from the trials of breeding lines will be placed in the database that we are developing in collaboration with Mark Hughes (USDA, CDL) who is designing interfaces that facilitate queries from breeders, growers, millers, and bakers.

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Project ID: FY10-NW-008	**FY10 ARS Agreement #:** 59-0790-6-061
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 4 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, FDK, 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.