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

Project Title: Using Association Mapping to Identify and Validate New FHB Resistance QTL and Integrate the QTL into HWW.

PROJECT 2 ABSTRACT

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Problem Addressed and Rationale: Major scab epidemics have occurred in the HWW region. Genetically improved seed coupled with appropriate management practices are the quickest and most cost effective way to reduce DON in the grain supply. However, little is known concerning the genetic basis of native resistance in the Great Plains germplasm and how best to effectively utilize it. Using association mapping techniques, we will be able to validate reported QTL and identify new QTLs in HWW germplasm, and move from molecular mapping to marker-assisted breeding.

Approach: ***Materials:*** For this research we plan to use selected line from numerous sources that we have identified as being important in the creation of FHB tolerant lines. The key to this research will be to maximize the information we are already collecting from our existing FHB screening nurseries, such as, advanced regional lines and lines that being testing in our state variety trials. Our goal will be to use 188 wheat lines including native sources of resistance (e.g. Henye. Lakin, Arapahoe, Everest, Overland, Settler CL, Lyman, Art, Hitch); DON accumulators (e.g. Harry and Trego); a series of backcross lines (Fhb1 and/or Fhb3 in Trego, Wesley, Harding, Overley, Jagger and Overland), and some accessions with various levels of FHB resistance from China and/or Japan (to look for new alleles and increase our diversity). ***Phenotypic data:*** All accessions will be phenotyped for FHB resistance by needle and spray inoculation in the greenhouse at KSU and SD, respectively and irrigated FHB winter wheat nurseries in KS, NE, and SD using three replications. Bulk samples from these phenotpying nurseries will be submitted for objective FHB evaluation and DON analysis (in cooperation with Dr. Floyd Dowell). ***Genotyping Using Molecular Markers:*** For marker analysis, all accessions will be analyzed for structure analyses with at least 100 genome-wide SSR markers at the USDA Genotyping Lab in Manhattan. We will also genotype the accessions using all reported markers linked to known FHB QTLs (about 100) and DArT markers for higher resolution QTL mapping. DArT markers will be analyzed by Triticarte, Pty Ltd. (related to Diversity Array Technology, Pty. Ltd.) in Australia. The diversity of lines should be adequate for association mapping studies and allow most important alleles to be identified, as well as some of their epistatic interactions. We believe that between the SSR and DArT markers (as well as some STS and SNP markers linked to QTL) we will have adequate genome coverage for association mapping. ***Data Analysis:*** The data will be analyzed using the software developed by Dr. Dong Wang to identify major genes and epistatic gene interactions that control FHB tolerance and help reduce DON. PowerMarker software will be used to calculate values of gene diversity, and distance-based cluster analysis using the UPGMA algorithm. A model-based (Bayesian) software package Structure 2.1 (Pritchard and others 2000) will be used to assess the number of subpopulations among all accessions. Information on marker distribution in wheat genomes was obtained from the consensus map Somers et al 2004. Pair-wise LD will be calculated using TASSEL 1.9.4 (http://www.maizegenetics.net). A database with all marker allele information will be developed for all the evaluated accessions and breeders will use them to select appropriate parents for crosses. We have chosen this approach because it directly compares our native sources of resistance (including our commercial lines), with known Asian sources of resistance at both phenotypic and genotypic levels.