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Major FHB epidemics have occurred in 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. Similarly, little is known on interaction between Fhb1 and other QTL in adapted backgrounds and allele distribution in adapted breeding materials. Association mapping is an effective strategy for generation of such information. In this proposed project, we are using association mapping to search QTL in US HWW and study interaction between major QTL from China and minor QTL from US HWW. The identified resistant materials will be directly used in US HWW breeding programs in the Great Plains. We collected 196 HWW accessions including native sources of resistance (e.g. Henye, Lakin, Hondo, Harding, 2174, Arapahoe, Everest, Overland, Camelot, Settler CL, Lyman, Art, Hitch, etc); high DON accumulators (e.g. Harry and Trego); a series of backcross lines (Fhb1 and/or Fhb3 containing Trego, Wesley, Harding, Overley, Jagger and Overland); purified germplasm of 2008 to 2010 HWW Southern and Northern Regional Performance Nurseries, Observation Regional Germplasm Nursery, Tri-States FHB Nursery. All accessions will be phenotyped for FHB infection and spread in the greenhouses and irrigated FHB nurseries in KS, NE, and SD. All accessions will be analyzed with 200 genome-wide SSR markers for structure analysis. Mean while, SNP will be analyzed for high-resolution mapping using 9K SNP chip from Illumina. A database with all marker allele information will be developed for all 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 genetic levels bypasses the length of time needed to create biparental mapping populations to directly identify new QTL in HWW, builds upon the considerable previous investment in identifying and transferring known QTLs to adapted HWW, and will elucidate the interaction of known FHB QTL with the background and environment. It also builds up a database with rich marker and QTL information for the materials studied, and all breeders in cooperation with the Genotyping Center will directly use the database to select parents to make cross and use markers for marker-assisted breeding (milestones: 1.1, 1.8, 2.1, 2.4).