PI: Smith, Kevin P.
PI's E-mail: smith376@tc.umn.edu
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PROJECT 1 ABSTRACT
(1 Page Limit)

Fusarium head blight (FHB) is the most serious disease in decades to plague the malting barley crop of the upper Midwest. Our work has focused on identifying quantitative trait loci (QTL) for resistance to FHB and accumulation of deoxynivalenol (DON) in germplasm relevant to Midwest barley improvement. We have established a long term research program to characterize the genetics of FHB resistance from promising new sources and develop molecular marker tools that can be used in research to enhance our understanding of host genetics of resistance and to develop FHB resistant barley varieties. To realize this goal, we are systematically identifying new sources of FHB resistance to be used in QTL mapping studies. We are identifying and validating markers that are linked to important FHB QTL and making that information available for deployment in breeding programs. In parallel, we are developing an SSR allele database of relevant resistant and susceptible germplasm. This information can be merged with other databases and used to facilitate the exchange of germplasm via marker assisted selection (MAS). This is particularly important to barley since effective levels of resistance will likely require the accumulation of multiple genes from different resistant sources likely identified in different research programs. To date, we have identified and validated four promising QTL for FHB in the varieties Chevron and Frederickson. We are currently conducting fine mapping studies to attempt to separate resistance QTL from other linked genes controlling undesirable or confounding traits such as grain protein and maturity. These studies will locate QTL more precisely and provide better markers for MAS. The Vrs1 locus (controlling 2-rowed/6-rowed spike morphology) is of particular interest since many sources of FHB resistance are 2-rowed and it is not clear whether this resistance is due directly to spike morphology (pleiotropy) or to linked resistance genes. Recent research investigating the segregation of resistance and markers linked to known FHB QTL in breeding populations using new sources of resistance has identified several new sources as likely containing previously unknown genes for FHB resistance. We have initiated a study to map one of these sources, Atahualpa, and should complete this study by the end of the FY03 funding period. **Specifically, research in outlined this proposal will produce: fine maps and tightly linked markers in three FHB QTL regions, sets of near isogenic lines for FHB QTL, fine map and QTL analysis of the Vrs1 region, and a QTL analysis of the new resistant source Atahualpa.** The desired outcome of this research project is to generate genetic information and a set DNA marker tools that will facilitate germplasm enhancement of FHB resistance in barley. This project is relevant to the U.S. Wheat and Barley Scab Initiative and fits within the biotechnology area of research.