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PROJECT 3 ABSTRACT

(1 Page Limit)

Rapid deployment of Fusarium head blight (FHB) resistant barley varieties is essential to maintain barley production in the Upper Midwest. Successful FHB resistance breeding is dependent on finding useful sources of resistance and employing effective selection strategies to identify resistant lines. Identification of quantitative trait loci (QTL) for FHB in barley will lead directly to marker assisted selection strategies to improve the efficiency of breeding and accelerate the delivery of new resistant varieties. We have conducted genetic mapping studies that have identified and validated two important QTL regions on chromosomes 2(2H) and 6(6H). In each of these regions, resistance is associated with an undesirable trait. Late heading is associated with resistance on chromosome 2(2H) and high grain protein concentration (GPC) with resistance on chromosome 6(6H). Preliminary evidence suggests that resistance can be separated genetically from these associated traits. Work on this is still in progress. In addition, we have identified a QTL on chromosome 3(3H) that is associated with DON accumulation and appears to be independent of resistance to infection and therefore represents a novel mechanism of resistance. All three of these QTL regions warrant further investigation to elucidate the genetics of resistance to FHB in barley and provide the tools and information necessary to exploit genetic resistance in breeding. We propose to continue fine mapping work on each of these three QTL regions. We are completing the research on chromosome 2(2H) and have isolated recombinants that are early heading and resistant. We will continue fine mapping this region to identify markers that are less than 1 cM away from the resistance gene as the first step towards map-based cloning. For the chromosome 6(6H) region, we propose to continue the fine mapping study that is in progress by improving the marker saturation of the region and evaluating the population for FHB and GPC in three field trials in 2006. For the chromosome 3(3H) QTL associated with DON accumulation, we will evaluate a fine mapping population in the greenhouse using the single-kernel inoculation method and more precisely map the position of the QTL. Work on the genetics of this DON accumulation QTL will be carefully coordinated with concurrent research on this QTL using gene chip experiments (Dr. Gary Muehlbauer) and field disease experiments (Dr. Ruth Dill-Macky).