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PROJECT 2 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. Current screening methods have produced breeding lines with improved levels of resistance, but the progress has been relatively slow. Expanded use of marker assisted selection (MAS) has the potential to accelerate this process and produce new resistant varieties more quickly. Quantitative trait locus (QTL) studies have identified and validated two QTL regions on chromosomes 2(2H) and 6(6H) that are reasonable targets for MAS in barley. We have identified each of these QTL regions using two different sources of resistance. The map resolution of these studies does not permit us to determine whether there is a single QTL in each region. Therefore, allelism tests will be necessary to resolve this question. We propose to evaluate a set of crosses in barley to both pyramid multiple QTL for FHB resistance and test allelism at two specific regions. If crosses for allelism tests produce independent segregants for FHB QTL within the same region, then we will use those recombinants that carry both genes in further crosses to pyramid those genes. We will screen large F2 populations with markers flanking the QTL target regions using the facilities at the USDA genotyping center. After producing lines that are fixed for two or more FHB QTL we will conduct phenotypic selection in later generations (F3-F4). This strategy will quickly fix resistance alleles at known mapped QTL and allow for phenotypic selection of resistance alleles at unmapped loci. We are currently making crosses in the greenhouse that will allow us to pyramid resistance alleles at FHB QTL in elite malting quality backgrounds. We will also include three elite parents that trace back to resistant sources that have not been mapped to build on that resistance as well. We have set up an incomplete diallel to generate populations segregating at 2 QTL regions. After making initial two-way cross combinations this fall, we will make selected three- way combination crosses in the winter to produce lines with the maximum potential for resistance. Two-way populations will be screened with markers at the F2 stage in the summer of 2006, while three-way populations will be screened with markers in the fall of 2006. This project will generate hundreds of breeding lines produced by MAS, fixed at multiple resistance loci, which will be evaluated in the summer of 2007 for FHB resistance and other important traits. We will also include some lines from each cross that are selected for the susceptible allele to assess the effectiveness of MAS. In addition, we will determine whether QTL mapped in similar regions from different sources of resistance are the same or separate loci. This should significantly increase the number of resistant lines that move through our program and ultimately end up as potential new varieties.