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Project Title: Marker Assisted Selection for FHB Resistance in Barley.

PROJECT 1 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 are generating a set of crosses in barley to both pyramid multiple QTL for FHB resistance and test allelism at these two specific regions. To accomplish this we will screen large F2 populations with markers flanking the QTL target regions using the facilities at the USDA genotyping center. This project will produce sets of breeding lines with various combinations of resistance alleles that will allow us to measure the effects of these alleles alone and in concert with other alleles. Specifically in this funding period we will develop:

- Elite breeding lines carrying different combinations of resistance source (Chevron, Frederickson, Hor211) alleles at FHB QTL on chromosome 2(2H) and 6(6H)
- A recombinant breeding line in a Lacey background that carries the Chevron alleles for FHB resistance on chromosome 6(6H) and Lacey levels of GPC
- A set of recombinants between two resistance sources at two QTL regions that can be used to conduct allelism tests in subsequent funding periods.