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Project Title: Developing Marker Information for Genetic Diversity and FHB Resistance in Barley.

PROJECT 1 ABSTRACT
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We are conducting research to enhance our understanding of resistance to Fusarium head blight (FHB) in barley and develop molecular marker tools to exploit resistance genes from diverse sources of resistance. We are engaged in mapping and validating quantitative trait loci (QTL) for FHB in three sources of disease resistance (Chevron, Frederickson, Atahualpa). Resistance alleles at two QTL associated with FHB that were identified in the Chevron mapping population are linked with other traits that are undesirable for breeding (late heading and high grain protein). We are fine-mapping both of these regions to determine whether the coincidence of QTL in these regions is due to tight linkage of genes or pleiotropy. Markers that are identified to be tightly linked to FHB QTL will be made available for breeding. We are similarly fine-mapping two FHB QTL identified in the Frederickson mapping population. In this case one QTL is linked to heading date and the other to the v-locus, which determines two-rowed/six-rowed spike morphology. In this funding period, we propose to construct linkage maps for both regions and complete QTL analysis on the v-locus region. We have identified Atahualpa as a source of resistance that is genetically distant from other sources of resistance that are currently being researched. We have a partial map of an Atahulapa/M81 population and disease data from four environments. We anticipate completing the QTL analysis of this population in the first quarter of FY04. Markers linked to novel QTL for FHB will be validated and made available for marker assisted selection. We have recently discovered a novel QTL for DON accumulation in single floret inoculated barley plants. This QTL has been validated and the allele from the low DON accumulating parent reduces toxin concentration 2.5 fold. We developed a set of near-isogenic lines (NILs) for this QTL and have crossed these NILs to develop a fine mapping population. We propose to screen ~1500 F2's to identify recombinants in a 7 cM region that contains the QTL. We will then use these recombinants to develop a fine map of the region and identify a set of NIL that span the region to fine map the QTL. We will also screen a diverse set of barley germplasm with five simple sequence repeat markers that span the QTL region to assess genetic diversity and identify a set of haplotypes that will be investigated to identify new DON accumulation alleles. Information on genetics of resistance and markers linked to resistance QTL that are identified in the course of this research will be valuable for managing multiple disease resistance genes in barley breeding programs.