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PROJECT 1 ABSTRACT
(1 Page Limit)

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). We are fine mapping two FHB QTL that were identified in the Chevron mapping population and are linked with other traits that are undesirable for breeding six-rowed malting barley (late heading and high grain protein). 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 vrs1 gene, which determines two-rowed/six-rowed spike morphology. We are have developed or are developing high-resolution linkage maps for all the regions and collecting phenotypic data to map the positions of the coincident traits. 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.