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

PROJECT 2 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 three quantitative trait loci (QTL). 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 have developed recombinant near isogenic lines to separate undesirable alleles from resistance alleles at these loci. We will develop a large segregating population from crosses between an NIL and the recurrent parent to generate recombinants and a high resolution map of the QTL region that will be useful for MAS and future map-based cloning efforts. We have recently discovered a novel QTL for DON accumulation in single floret inoculated barley plants. We have screened over 1500 F₂'s to identify recombinants in a 7 cM region that contains the QTL. We are using these recombinants to develop a fine map of the region. We are also screening a diverse collection of cultivated and wild barley for DON accumulation. If we uncover novel alleles that condition low DON accumulation, we will initiate genetic crosses. We will initiate research to use association genetics in breeding germplasm to identify novel FHB QTL. This research will leverage resources developed by the newly funded USDA-CSREES Barley CAP. 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.