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Research Area: **HGG** **Duration of Award: 1 Year**

Project Title: Fractional Analysis of Chromosome 2(2H) Fusarium Head Blight Resistance QTL.

PROJECT 1 ABSTRACT

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Our ultimate **goal** is to facilitate the development of malting barley cultivars with commercially acceptable FHB resistance. Towards this goal we are working to clone the gene (or genes) responsible for the major Fusarium Head Blight (FHB) resistance quantitative trait locus (QTL) found on barley chromosome 2(2H). This is a long-term goal and a more immediate goal is to develop isolines containing small CI4196 genomic regions in a commercially acceptable malting genomic background. This will facilitate map-based cloning, validate the FHB QTL and provide favorable germplasm for plant breeders. Another innovate approach is to use mutagenesis to identify genes that affect FHB resistance and/or susceptibility.

The specific objectives for this year are:

1) continue development of a saturated genetic and physical map of the chromosome 2(2H) FHB QTL region

2) screen a mutagenized population of CI4196 for increased susceptibility/resistance to FHB and morphological mutants that improve the agronomic qualities of CI4196. Characterize mutants selected during the 2006 grant year.

The work will be accomplished through continuing work already in progress. Development of a saturated genetic and physical map of chromosome 2H FHB QTL is in progress. However, this is a large region (in terms of DNA). Isolines with reduced QTL size already developed will facilitate this work. A fast neutron mutagenized CI4196 population was developed last year and screened for mutants this year (’06). Mutants relevant to agronomic qualities such as dwarf, semi-dwarf, 6-rowed, and early were selected and will be characterized. A new population was mutagenized with gamma rays and will be screened next year ('07). This work is directly relevant to the USWBSI goals to validate FHB resistance QTL/markers, develop BAC contigs and saturation maps for important QTL regions to facilitate MAS and map-based cloning efforts and select mutants for enhanced disease resistance and enhanced susceptibility to help identify genes involved in FHB resistance