

PI: Gary Muehlbauer**PI's E-mail: muehl003@umn.edu****Project ID: FY16-BA-003****ARS Agreement #: 59-0206-4-021****Research Category: BAR-CP****Duration of Award: 1 Year****Project Title: Molecular Genetics Approaches to Developing Scab Resistant Barley.****PROJECT 1 ABSTRACT**

(1 Page Limit)

Fusarium head blight (FHB, scab), a fungal disease of small grain crops caused by *Fusarium graminearum*, threatens to reduce wheat and barley to economically unviable crops in the United States. The overall project goals are to develop genetic tools for increasing FHB resistance in barley. Three objectives will be addressed including: (1) fine map and characterize the chromosome 6H bin 7 FHB resistance QTL; (2) identify novel QTL associated with FHB resistance; and (3) field test transgenic barley overexpressing *HvUGT13248*.

My laboratory, in collaboration with Kevin Smith, mapped QTL associated with FHB resistance derived from the cv. Chevron. In this mapping study a QTL on chromosome 6H bin 7 was identified. The chromosome 6H bin 7 QTL is also associated with grain protein content such that FHB resistance is associated with high grain protein content. Unfortunately, high grain protein content is unacceptable in the malting and brewing industry. In this proposal, we aim to identify genetic markers linked to the QTL that can be used in breeding programs. We also plan to identify genetic recombinants between the loci that control FHB resistance and grain protein content. If these recombinants are identified, the genetic stocks carrying the FHB resistance allele and not carrying the high grain protein allele will be used directly in breeding programs.

In a prior study, in collaboration with Brian Steffenson, we characterized a highly susceptible barley genotype (PI383933). Most QTL mapping studies are focused on mapping 'large effect' QTL from highly resistant genotypes. We developed a recombinant inbred line population via a cross between PI383933 and the moderately susceptible cv. Rasmusson and genotyped the population with the 9K iSelect SNP assay. Due to the population design (a highly susceptible genotype crossed to a moderately susceptible genotype), it is likely 'major effect' QTL will not be segregating and masking 'smaller effect' QTL. Therefore, our objective is to map novel QTL that are not masked by 'major effect' QTL.

In collaboration with Jochen Kumlehn (IPK-Gaterslaben, Germany), we developed transgenic barley overexpressing *HvUGT13248*. We have introgressed the *HvUGT13248* transgene into the cv. Rasmusson and have derived lines for field testing. In this proposal, we will characterize these barley transgenics for resistance to FHB and trichothecenes.

Stakeholders (breeders and geneticists) will benefit from our work through new genetic tools (markers, lines and transgenics) that can be used to increase FHB resistance in barley.