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PROJECT 1 ABSTRACT
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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. Two objectives will be addressed including: (1) characterize transgenic barley overexpressing *HvUGT13248*; and (2) fine map and characterize the chromosome 2H bin8 and 6H bin 7 FHB resistance QTL.

In collaboration with Jochen Kumlehn (IPK-Gaterslaben, Germany), we developed transgenic barley overexpressing *HvUGT13248*. We showed that these plants exhibit high levels of DON resistance in a root assay. The transgenic plants were developed in the Golden Promise genetic background, which precludes FHB screening in the field due to the inability for the spike to emerge from the boot in Upper Midwestern climates. Therefore, we introgressed the *HvUGT13248* transgene into the cv. Rasmusson and derived lines that are homozygous for the transgene and the spike emerges properly from the boot. These lines are ready for field testing and assessing DON detoxification. In this proposal, we will characterize these barley transgenics for resistance to FHB and trichothecenes.

My laboratory, in collaboration with Kevin Smith, mapped QTL associated with FHB resistance derived from the cv. Chevron. In this mapping study, QTL on chromosomes 2H bin8 and 6H bin 7 were identified. The chromosome 2H bin8 and 6H bin 7 resistant QTL are associated with late heading date and high grain protein content, respectively. Late heading plants and high grain protein content are deleterious traits for growers and brewers, respectively. In this proposal, we aim to identify genetic markers linked to both QTL that can be used in breeding programs. We also plan to identify genetic recombinants between the loci that control FHB resistance and the deleterious loci that control late heading date and high grain protein content. If these recombinants are identified, the genetic stocks carrying the FHB resistance allele and not carrying the deleterious allele will be used directly in breeding programs.

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.