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Project Title: Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.

PROJECT 1 ABSTRACT

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Our overall goal is to reduce the losses caused by Fusarium head blight (FHB), especially quality discounts due to the accumulation of mycotoxins such as deoxynivalenol (DON). This can be best achieved by identifying and incorporating into barley cultivars genes that confer a high level of resistance to FHB and the accumulation of mycotoxins. The focus of this proposal is to develop populations and map loci conferring resistance to FHB and the accumulation of DON in two *Hordeum* accessions (both *Hordeum vulgare* subsp. *vulgare* and subsp. *spontaneum*) with moderate FHB resistance. Over the past decade, we have evaluated over 20,000 accessions of *Hordeum* for FHB reaction and have identified a subset of about 100 that possess a level of resistance comparable to the six-rowed control Chevron. Diversity analyses based on Diversity Arrays Technology (DArT) markers have been completed on this subset and were used to identify accessions that likely possess alleles for FHB resistance that have not yet been exploited in breeding programs. Nine of these accessions have been included in the fall crossing block to produce the initial F_1's. Two sources with highest level of partial resistance have been backcrossed twice to cultivar 'Quest' to create advanced backcross mapping populations. These lines are being advanced to the BC_2F_4 generation for phenotyping and genotyping. This research addresses Objective #2 (Map novel QTL for resistance to FHB in barley) of the USWBSI Research Area "Variety Development and Host Resistance" (VDHR), but is also a step toward Objective #4 (Develop new barley varieties with enhanced resistance to FHB and lower DON). The outputs from this work will fulfill the USWBSI research priority to "develop germplasm to further enhance short term and long term improvement of FHB resistance and to efficiently introgress effective resistance genes into breeding germplasm."