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

PROJECT 1 ABSTRACT

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Our primary and long-term goal is to reduce the losses caused by FHB, including quality discounts due to DON contamination. This can be best achieved by developing barley cultivars with the highest level of resistance possible. We have identified promising sources of resistance through multiple years and locations of field screening. We are in the process of characterizing these sources with DArT and SSR markers linked to previously identified FHB resistance QTL to identify those that are genetically distinct from previously reported resistance sources. Our specific objective for this proposal is to determine the number, effect, and chromosomal position of FHB resistance loci in the newly identified sources of resistance using the advanced backcross QTL method. At the same time, this research will lead to the development of advanced breeding lines with the major loci conferring resistance to FHB and the accumulation of DON. This information and germplasm will allow breeders to more rapidly develop FHB resistant barley cultivars for growers.

Molecular marker data for the new resistance sources will be available in April 2009. Based on this data, we will select parents for crossing in August 2009. However, one promising source of resistance already being advanced in the program is the accession PI466423, a wild barley from Israel. We already have BC_2 seed available in crosses with the new Minnesota cultivar Rasmusson. The BC_2 seeds will be increased in January 2009 and single seeds advanced again in August 2009. Then, approximately 70 BC_2F_3 progeny will be genotyped with Diversity Arrays Technology (DArT) markers to identify a subset having complete genome coverage of the introgressed wild barley chromosomes in a Rasmusson background. Given that all of the DArT markers developed for cultivated and wild barley are positioned on the barley concensus map, we will have accurate information on the introgressions in each family. This scheme is patterned after the advanced backcross QTL method. The first FHB phenotyping will be done on these advanced backcross lines at two locations in Minnesota during the summer of 2010. Subsequent phenotyping tests will be made in China in spring 2011 and again at two locations in Minnesota in summer 2011. The deliverables from this project will be to provide breeders with introgression lines for use in their crossing block; information on the introgressed wild barley segments contributing the highest level FHB resistance and lowest DON accumulation; and molecular markers useful for marker assisted selection of wild barley derived FHB resistance QTLs.