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Research Category: BAR-CP/VDHR

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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 set of promising sources of resistance through multiple years and locations of field screening. We are in the process of characterizing this core set of sources with DArT markers and SSR markers linked to previously identified FHB resistance QTL to determine which source(s) is most genetically different from those lines that have already been mapped. Our specific objective for this proposal is to determine the number, effect, and chromosomal position of FHB resistance loci in the newly identified source 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.

Prior to the start of the funding period, we will have genotyped potential parents with DArT markers. Based on this data, we will select parents to cross in January 2007. At the start of the funding period, we will have F₁ seed available. In the Summer (2007), we will backcross 40 of these F₁ progeny to M109 to obtain BC₁F₁ families with at least five progeny. Approximately 90 of these BC₁F₁ 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 an M109 background. These selected BC₁F₁ progeny will again be backcrossed to M109 to obtain BC₂F₁ progeny. Another round of genotyping will be made on ~190 BC₂F₁ progeny to again identify a subset having complete genome coverage of the introgressed resistant source barley chromosomes in an M109 background. This series of backcrossing and genotyping will allow us to accurately compile an introgression library of the resistant source chromosomal segments in an M109 background. Given that all of the DArT markers developed for cultivated and wild barley are positioned on the barley consensus map (A. Kilian, personal communication), we will have accurate information on the introgressions in each family. This scheme is patterned after the advanced backcross QTL method. BC₂F₂ progeny will be grown in the greenhouse to produce BC₂F₃ seed for FHB phenotyping in the field in summer 2009.