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Research Area: **HGR**	**Duration of Award:** **1 Year**
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PROJECT 2 ABSTRACT

(1 Page Limit)

Extensive efforts have been directed at identifying novel sources of Fusarium head blight (FHB) resistance that may be used to develop new wheat cultivars with enhanced resistance to this disease. In many instances presumptive unique scab resistance quantitative trait loci (QTLs) have been mapped in a diverse range of common wheat (*Triticum aestivum*) genotypes and related species, but have not yet been introgressed into U.S. hard red spring wheat (HRSW). In 2001, we initiated a program to use marker-assisted backcrossing to individually introgress five scab resistance QTLs from diverse germplasm sources into three different FHB-susceptible HRSW backgrounds (Norm, Wheaton, Apogee). The initial QTLs selected included two from Sumai 3 to serve as reference QTLs (on chromosome arms 3BS and 5AS), one from the soft red winter wheat Freedom (chromosome arm 2AS), one from the Brazilian wheat Frontana (chromosome arm 3AL), and one from wild emmer, *T. dicoccoides* (chromosome arm 3AS). Our goal has been to develop BC_4-derived near-isogenic lines (NILs) that are essentially HRS in genome composition, but differ by which FHB resistance QTL is present. These NILs will be subjected to comparative FHB resistance evaluations to determine which of the new introgressed QTLs confer resistance and what level of resistance each QTL confers in the HRS genetic backgrounds. This program is intended to be an ongoing endeavor to incorporate diverse new FHB resistance QTL into HRSW as they are reported. The NILs harboring new and validated FHB resistance QTLs will be released to HRSW breeding programs for use as sources of unique genes for crossing. These NILs will be far more attractive as parents for crosses within HRSW breeding programs than the original sources of the QTLs, because their genomes will be primarily HRSW in derivation and thus adapted to the HRSW production region. **In this continuing proposal, we request funding to accomplish the following goals: 1) greenhouse and field evaluations of FHB resistance in the QTL NILs developed during the FY 05 funding cycle; and 2) initiate development of FHB resistance QTL pyramids by crossing between NIL sets within each genetic background, in preparation for future evaluations of different unique FHB resistance QTL combinations in HRSW.** This research project development is precisely aligned with the HGR Research Priority "generation of unique and adapted parental germplasm (pre-breeding)".