

PI: Ruth Dill-Macky

PI's E-mail: ruthdm@umn.edu

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Research Area: VDUN

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Project Title: FHB Resistance QTLs in Hard Red Spring Wheat Near-Isogenic Lines.

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 scab resistance. In many instances presumptive unique scab resistance quantitative trait loci (QTL) 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 (HRS). In 2001, we initiated a program to use marker-assisted backcrossing to individually introgress five scab resistance QTL from diverse germplasm sources into three FHB-susceptible HRS backgrounds (Norm, Wheaton, Apogee). The initial QTL selected included two from Sumai 3 (on chromosome arms 3BS and 5AS) to serve as reference QTLs, 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 is to develop BC₄-derived lines that are principally HRS in genome composition, but are near-isogenic for the different QTL (NILs); to date many of the lines being developed have reached the BC₄ generation. These lines will be subjected to comparative FHB resistance evaluations to determine which of the new introgressed QTL confer resistance in HRS backgrounds, and what level of resistance each QTL confers. This program is intended to be an ongoing endeavor to incorporate diverse new FHB resistance QTL into HRS over time as they are identified. For this proposal, we are seeking funding to help accomplish the following goals:

- 1) finish NIL development for the FHB resistance QTL initially selected for introgression; and
- 2) initiate greenhouse and field evaluations of FHB resistance in the NILs.

The development of the NILs as described above directly relates to the FY 05 VDUN Research Priority "Validation of molecular markers reportedly linked to FHB resistance". The NILs that harbor new validated FHB resistance QTLs will be released to HRS breeding programs as sources of new genes with which to increase FHB resistance. These NILs will be far more attractive as parents for crosses than the original sources of the QTLs because their genomes will be primarily HRS in derivation.