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PROJECT 3 ABSTRACT

(1 Page Limit)

Wheat varieties with greater resistance to *Fusarium* head blight (FHB) would make a substantial contribution to reducing the losses from this devastating disease. The objectives above relate directly to the U.S. Wheat and Barley Scab Initiative's overall goal of minimizing the threat of FHB.

Given the ongoing need for wheat varieties with greater FHB resistance than is currently available in released varieties, additional QTL are needed, along with associated DNA markers, to rapidly improve the resistance level. DNA markers for the 3BS QTL are used in almost every U.S. wheat breeding program working on FHB resistance and numerous other breeding programs worldwide. Therefore, breeders are willing to use DNA marker technology when a good gene and marker combination are available. We hope to identify at least one QTL from this population that can eventually impact breeding for FHB resistance.

PI 81791 appears to be a unique resistance source, does not contain the 3BS QTL, and provides a high level of resistance that has been confirmed by other researchers. Therefore, this genotype is a good target for a new QTL mapping effort and the QTLs are likely to be complementary to those already deployed.

The objectives of this research are to:

1) Characterize FHB resistance in RIL lines from the cross Wheaton/PI 81791 and identify highly resistant, agronomically adapted lines suitable for use as breeding parents.
2) Identify QTLs and associated DNA markers for FHB resistance in RIL from the cross Wheaton/PI 81791.

One hundred and fifty F_6-derived RIL from the cross Wheaton/PI 81791, parents, and checks will be evaluated in greenhouse and field environment for FHB resistance. Type II (resistance to fungal spread) characterization will be conducted in the greenhouse in the fall 2007 and spring 2008. Each line will be planted into 3 pots/season. Ten to fifteen heads/pot will be point-inoculated at full heading to early anthesis stage with l0µl of 10,000 conidia ml^{-1} from a single *F. graminearum* isolate. The inoculated heads will be incubated in a ziploc bag for 48 hr on a greenhouse bench. Disease severity will be recorded 21 days after inoculation. Field data will be collected from two inoculated, misted nurseries in 2007.

390 polymorphic SSR markers have already been identified between the two parents by the USDA-ARS Fargo Genotyping Lab. Polymorphic markers will be run on agarose gels or a LiCor DNA sequencer. The genetic map will initially be based on 94 randomly selected RIL. Markers in genomic regions suspected to be near FHB QTLs base in the analysis using 94 RILs will be assayed on the remaining 56 RILs to obtain a more accurate estimate of QTL effects.