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Project Title: QTL Mapping of Wheat Fusarium Head Blight Resistance in the Japanese Landrace PI 81791.

PROJECT 3 ABSTRACT

(1 Page Limit)

Although genetic resistance to FHB has increased in the past 15 years in the spring wheat region of the U.S., there are still susceptible varieties in production and the 2005 FHB epidemic in the spring wheat region showed us that even the varieties with enhanced FHB resistance available today can suffer significant damage due to FHB in environments favorable for disease development. Therefore, the overall level of FHB resistance of regional varieties must be improved. The outcomes of this research will provide wheat breeders in the spring wheat and other regions affected by FHB additional markers for QTLs that they can incorporate into improved germplasm. PI 81791 appears to be a unique resistance source that does not contain *Fhb1*, and provides a high level of resistance that has been confirmed by other researchers. Therefore, this genotype is a good target QTL mapping efforts and the QTLs are likely to be complementary to those already deployed.

Objectives:
1) Characterize FHB resistance in RIL lines from the cross Wheaton/PI 81971 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 81971.
Validate identified QTLs using QTL-NILs.

One hundred and fifty F_6-derived RIL from the cross Wheaton/PI 81971, parents, and the checks ND2710 (R), BacUp (MR), Alsen (MR), Roblin (S), and MN00269 (S) will be evaluated in two field environments for FHB resistance in 2008.

520 polymorphic SSR markers have already been identified between the two parents by the USDA-ARS Fargo Genotyping Lab, courtesy of Shiaoman Chao. We have fragment sizes of both parents from the Genotyping Center. This will allow us to group markers into different categories based on their expected band sizes to facilitate multiple loading of gels. Markers with large size differences will be run on agarose gels. The map will initially be based on 94 randomly selected RIL. This increases our efficiency of mapping because PCR will include 94 RILs + two parents. Markers in genomic regions suspected to be near FHB QTLs based on the analysis using 94 RILs will be assayed on the remaining 56 RILs to obtain a more accurate estimate of QTL effects.

We developed a unique approach to QTL validation that is amenable to direct incorporation into breeding activities (Pumphrey et al., 2007). Currently, 11 F_3 populations from cross combinations involving four highly resistant RILs from the Wheaton/PI 81971 population and three adapted spring wheat lines are available and will be advanced to the F_4 generation for field screening in 2008 for agronomic screening before extracting QTL-NILs using markers. Homozygous QTL NILs will be developed from selected lines in summer/fall 2008, and increased in 2009 in anticipation of phenotyping in the field and greenhouse.