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Project Title: Mapping FHB QTL in an IL97-1828 x Clark Derived RIL Population.

PROJECT 2 ABSTRACT

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Our objective in this research project is to identify molecular markers associated with loci for FHB resistance in a source that does not trace back to a Chinese source of FHB resistance (so called "native" resistance). The FHB resistant parent in this population, IL97-1828, has a very high level of FHB resistance. IL97-1828 has good plant type, good Type I and Type II resistance, low percentage of FDK and low DON levels. Clark was chosen as the recurrent parent primarily because it was used as a susceptible parent in the Ning 7840 RIL population that was studied previously. Also, Clark is an early, winter hardy, short, adapted soft red winter wheat variety. The RIL population was developed by single seed descent, and the 303 lines in the population are $F_{5:6}$. Phenotypic data will be collected in field nurseries at Urbana, IL in the 2008 and 2009 field seasons and at Wooster, OH in the 2008 field season (in cooperation with Clay Sneller). A misted, inoculated FHB field nursery will be used for evaluation of the RILs at both locations. Grain spawn (corn kernels cultured with a mixture of FHB isolates) will be used to inoculate the nursery at both locations. Two replications of the lines and checks will be evaluated each year at Urbana, and one replication of the lines will be evaluated at Wooster in 2008. Checks will be repeated more than once at the Wooster location. At Urbana data will be collected on incidence based on visual assessment of the percentage of heads in a row that show symptoms. Severity will be assessed by counting the number of infected spikelets per head on 7 to 10 heads per row. Grain samples will be harvested at both locations in 2008 and at Urbana in 2009, and percentage of FDK will be determined by visual assessment compared to standards with known FDK percentages. FHB and ISK indexes will be calculated. Grain samples will be sent to the lab at the University of Minnesota for DON evaluation.

Leaf tissue will be collected from $F_{5:6}$ seedlings, and DNA will be extracted using standard protocols. For molecular marker analysis we will select molecular markers dispersed across the genomes, but markers reported to be associated with scab resistance QTL will be high priority, including areas of chromosomes 2A, 2D, 3B, 5A and 6B. In addition to these regions, markers distributed over the entire wheat genome will also be selected. Markers will first be screened on the parents to ascertain which ones are polymorphic in this population. Because of time constraints, a subsample of the population may be used to first test markers, and markers with tentatively promising results will be evaluated on a larger number of RILs. The marker results will be combined with the phenotypic evaluation of FHB resistance to identify markers associated with QTL for FHB resistance in this population. All measures of disease (incidence, severity, FDK, and DON levels) will be treated separately in the QTL analysis in order to try to identify genes associated with the different types of FHB resistance. Mapmaker and JoinMap will be used for molecular marker analyses. Mapping information on "native" sources of resistance will be valuable in determining if these genes are different from Chinese sources, and from other "native" sources such as Ernie and Truman. This information will contribute to enhancing the efficiency of selection for FHB in the soft red winter wheat germplasm.