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Project Title: Genomic Selection for Fusarium Head Blight Resistance in Spring Wheat.

PROJECT 2 ABSTRACT

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The objectives of this research are to evaluate the effectiveness of a FHB Genomic Selection model developed using 350 University of Minnesota spring wheat breeding lines to 1) identify susceptible F_5 lines; and 2) predict FHB reaction of NDSU and SDSU germplasm using similar numbers of breeding lines.

In the U of MN breeding program, we initiated a Genomic Selection (GS) experiment in 2013 using the Illumina wheat 90K SNP chip to genotype 288 U of MN advanced yield trial lines in a training population and 96 lines in a validation population. The lines were evaluated for FHB traits in four to six inoculated, misted nurseries (2 to 3 locations in 2011, 2012, and 2013). Because the U of MN spring wheat breeding program has a large proportion of its pedigrees containing NDSU and SDSU breeding lines and varieties, and many FHB resistance sources (e.g. Chinese material) are common across the germplasm in the region, we expect that this GS model will be effective across the breeding programs in the spring wheat region.

Objective 1) Separate genomic selection models will be developed for FHB resistance traits Severity, Visual Scabby Kernels, and DON. A model using a combination of all traits and models with and without major QTL such as *Fhb1* and 5AS also will be explored. A random sample of 384 F_5 lines from the U of MN breeding program (192 from each of our 2012 and 2013 cohorts) will be utilized. We will evaluate the 384 lines as single rows with 4 replications of checks in two FHB misted/inoculated nurseries in 2014 and 2015. Genotyping – By – Sequencing (GBS) will be used to genotype the 384 F_5 lines. The GS model will be applied to the F_5 lines to assess its effectiveness in identifying the susceptible F_5's.

Objective 2) A total of 384 breeding lines, all will previous FHB data, from each of the NDSU and SDSU spring wheat breeding programs will be genotyped using GBS. A minimum of 4 environments of FHB phenotypes is required. For those lines not having sufficient phenotyping data, the respective breeding program will collect additional FHB data as needed in 2014 and 2015. The GS model developed in Objective 1 will be used to predict FHB reaction of these breeding lines.