VARIETY DEVELOPMENT AND HOST PLANT RESISTANCE

GENOMIC SELECTION FOR FUSARIUM HEAD BLIGHT RESISTANCE IN A SOFT RED WINTER WHEAT (*TRITICUM AESTIVUM* L.) BREEDING PROGRAM

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ABSTRACT

Genomic Selection (GS) is breeding strategy aiming at selecting superior individuals based on their genomic estimated breeding values (GEBVs). The strategy is particularly promising for quantitative traits and requires dense, genome-wide marker data. Fusarium head blight (FHB), primarily caused by *Fusarium graminearum* in the US, has been shown to be quantitatively inherited. The aim of this work is to assess the effect of the training population size, level of genotypic missing data, imputation methods, and statistical models on GS accuracy. A total of 273 lines from the University of Illinois soft red winter wheat program, and from breeding programs around the Midwest and Eastern US were included in this study. Genotypic data were obtained using the Genotyping-by-Sequencing (GBS) protocol. Libraries were constructed using three two-enzyme combinations, where a rarer cutter (*PstI*) and three common cutters (*MspI*, *HinPI*, and *BfaI*) were combined. A different set of barcodes were used for each enzyme combination. Sequence data were obtained from 96-plex Illumina HiSeq2000 runs, and then analyzed with the UNEAK pipeline. Two data sets were obtained according to their maximum proportion of missing data per marker: 20%, and 50%. After applying the Fisher's exact test, the number of SNPs called for each data set was 5K and 16K. Four imputation methods were tested: mean imputation (MNI), singular value decomposition (SDVI), random forest regression (RFI), and expectation maximization (EMI). We also tested different sizes of the training population (96, 144, 192, and 218), as well as different proportions of the training population in relation to the validation population (0.5, 0.6, 0.7, 0.8, and 0.9). The phenotypic data were collected in a field nursery in Urbana, IL, in 2011, 2013, and 2014. Best unbiased linear predictors (BLUPs) were calculated for FHB severity, incidence, deoxynivalenol (DON) concentration, *Fusarium*-damaged kernels, the ISK and FHB indexes. Accuracy significantly increased for all traits when the largest training population (218) was used. Using eighty percent of individuals as the training set resulted in the best combination of mean accuracy and variance. No statistically significant differences were detected for accuracy when different genotypic data sets (5K and 16K SNPs) were compared. The imputation methods performed equally well, with a numerical advantage for EMI. Also, MNI and EMI were the least computationally intensive. For all traits except incidence, rr-BLUP outperformed LASSO and ELASTIC-NET. The highest five-fold cross-validated accuracies were recorded for incidence, ranging from 0.68 to 0.81, depending on the GS model. The lowest values were obtained for severity, ranging from 0.45 to 0.48. Other traits showed intermediate values. In conclusion, this study shows that measurements associated with FHB resistance can be predicted with GS models with moderate accuracy, even without a reference genome.

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USING MARKER-ASSISTED SELECTION TO IMPROVE HARD WINTER WHEAT FHB RESISTANCE

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ABSTRACT

Epidemics of wheat Fusarium head blight (FHB), incited by *Fusarium graminearum*, are more frequent and severe in hard winter wheat (HWW, *Triticum aestivum* L.) growing region due to reduced tillage and the continued expansion of corn (*Zeae mays* L.) into the region. Thus, improving FHB resistance becomes a major breeding objective in most HWW breeding programs. Although quantitative trait loci (QTL) for FHB resistance have been reported from different sources including some from HWW in the Great Plains, some resistant sources from China show the best resistance. To identify and validate QTL from Chinese landraces, we construct a consensus map of five mapping populations with Chinese landraces as resistant parents using genotyping-by-sequencing (GBS) generated single nucleotide polymorphism (SNP) markers. The consensus map was used for QTL meta-analysis to identify SNPs tightly linked to overlapping QTL across populations. Among QTL identified, *Fhb1* is the QTL with the largest effect across the populations. By screening recombinants in *Fhb1* region using a large segregation population derived from Ning7840/Clark through marker-assisted backcross, a small fragment co-segregating with *Fhb1* were identified. Markers from the region were developed for marker-assisted selection. Because *Fhb1* is not present in HWW cultivars in the Great Plains, we developed marker-assisted backcross project to transfer *Fhb1* to US adapted HWW backgrounds. The lines with *Fhb1* in different US winter wheat backgrounds showing a high level of type II FHB resistance were selected. To date, *Fhb1* has been transferred to17 adapted HWW cultivars. Some of the *Fhb1* lines have been used as resistant parents in different breeding programs, and others are in double haploid production and seed increasing stage and will be distributed to breeding programs for further yield testing.

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PHENOTYPIC ANALYSIS OF FHB RESISTANCE IN A SOFT WHEAT POPULATION FOR GENOME-WIDE ANALYSES

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ABSTRACT

Breeding for Fusarium Head Blight (FHB) resistance is vital to controlling this disease. In this study, a set of 649 soft winter wheat lines, termed the FHBGS population, were genotyped by GBS and phenotyped over three years in multiple uniform scab nurseries adapted to the Corn Belt (OH, NY, KY, MI, MO and IL). Traits assessed included incidence (INC), severity (SEV), index (IND, *Fusarium*-damaged kernel (FDK), INC+SEV+FDK (ISK), and concentration of deoxynivalenol (DON). Within each location the data was standardized for the mean and standard deviation of a set of 49 checks. Our results showed high heritability (0.88 to 0.94) for all traits. Best linear unbiased predictors (BLUPs) obtained from each trait were highly correlated to one another. Principal component (PC) analysis among all traits revealed high percentage of variance explained by the first PC (~81%). The most superior 5% of individuals performed better than the resistant check (Truman) for all traits except DON. Cluster analysis of marker data among all individuals showed clear differentiation of lines from New York from all others. The remaining lines were placed in two less differentiated clusters: one of these groups had a high proportion of parentage from Truman. On average the NY cluster was the most susceptible and the Truman cluster the most resistant. The results from this analysis will constitute the basis for subsequent association analysis and genomic selection study.

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PRELIMINARY ANALYSIS OF GENOMIC SELECTION FOR FHB RESISTANCE

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ABSTRACT

Resistance to FHB in soft winter wheat appears to be polygenic and phenotypic selection is slow and relatively inefficient. Genomic selection may be a useful alternative selection tool. A population of 649 soft winter wheat lines, termed the FHBGS population, was phenotyped for multiple FHB traits over multiple environments and genotyped with 4,643 GBS markers. FHB index (IND) was also evaluated in a population of 273 lines, termed the TCAP population, and genotyped with 3919 markers from the 90K SNP chip. The prediction accuracy of GS was assessed using cross-validation approach with ridge regression best linear unbiased prediction (RR-BLUP) model. In the FHBGS population GS accuracy across all individuals ranged from 0.43 to 0.55 (for SEV and FDK, respectively), while accuracy for IND in the TCAP population was 0.62. In both populations, genetic relatedness affected the accuracy of prediction. Higher accuracies were observed when individuals in training and predicting sets belonged to the same cluster: GS models developed in one cluster generally did not predict the observed phenotypes of the other clusters. The findings are directly applicable for breeders to implement GS schemes to improve FHB resistance in the Northern U.S. soft winter wheat breeding programs.

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META-ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE QTL IN CHINESE WHEAT LANDRACES

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ABSTRACT

Fusarium head blight (FHB) is one of the most devastating diseases in wheat. FHB not only causes significant losses in grain yield and quality, but also produces mycotoxins such as deoxynivalenol that are toxic to human and animal. FHB resistance has been reported from many sources, especially Chinese landraces, such as Sumai3, Wangshuibai. Among them, quantitative trait loci (QTLs) for FHB resistance in Sumai3 have been well characterized in multiple studies, however, QTLs in many other Chinese landraces are poorly characterized. Meta-analysis, a statistic method to combine QTL mapping results across independent studies, has been widely applied in human genetics research. In this study, five populations were developed from different Chinese wheat landraces Haiyanzhong (HYZ), Wangshuibai (WSB), Baishanyuehuang (BSYH), Huangfangzhu (HFZ) and Huangcandou (HCD). QTLs have been identified in each population using low-density maps constructed with a set of simple sequence repeats (SSR) and sequence tagged site (STS) markers. However, low density maps may not be able to cover all QTL regions in those populations and some QTLs may be missed. Genotyping-by-sequencing (GBS) is a novel approach that provides a rapid and robust tool for discovery of high-density SNPs for QTL mapping. In the current study, we analyzed the five populations with GBS SNP, developed high-density maps for the five populations and constructed a consensus map for meta-analysis of the QTLs. Using the new maps, 21 QTLs were remapped on 9 chromosomes (1AS, 3A, 5AS, 7AL, 3BS, 6BS, 2D, 3DL, 7DL) after adding GBS-SNP to original SSR maps, among which 10 QTLs are new QTL identified on 7 chromosomes (6A, 2B, 4B, 1D, 4D, 5D, 6D). QTLs were then projected onto the consensus maps by referring the original QTL confidence intervals (CIs) and QTL contributions (R^2). The FHB-resistance QTLs with the 95% CIs were shortened by using a clustering approach based on Gaussion mixture model in MetaQTL V1.0. Consistent QTLs among two or more populations were identified and tightly linked markers for these QTLs were identified. Thus, meta-analysis using GBS-SNP maps facilitate the validation of QTLs and identification of closely linked markers for marker-assisted selection.

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COMPARING OPTICAL SORTING, AIR SEPARATION AND DIGITAL IMAGE ANALYSIS ESTIMATIONS OF WHEAT *FUSARIUM* DAMAGED KERNELS

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ABSTRACT

One aspect of Fusarium head blight (FHB) of wheat (*Triticum aestivum* L.), caused by *Fusarium graminearum* Schwabe [teleomorph *Gibberella zeae* (Schwein.:Fr.) Petch], is grain mummification. The proportion of the characteristic resultant "tombstones", pale, shriveled grains, is quantified as percent *Fusarium*-damaged kernels (FDK). FDK is one of the most valuable measurements in the development of solutions to FHB. For instance, breeding programs can make thousands of FDK measurements each year. Because of the labor required, FDK is typically estimated visually rather than by hand separation and counting, the gold standard. We compare alternative methods for their accuracy and efficiency. Two methods are based on separating the *Fusarium*-damaged kernels, by optical sorting or air separation. FDK is then expressed as the proportion of the mass of the sample. We compare the results from these methods with a third method where estimates were obtained using an ImageJ program on digital images of grain samples.

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MAPPING OF QUANTITATIVE TRAIT LOCI FOR FHB AND DON RESISTANCE IN A DOUBLED HAPLOID POPULATION OF EVEREST X ART

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ABSTRACT

The current project is aimed at mapping and identifying quantitative trait loci for resistance in wheat to spread of Fusarium head blight (FHB) symptoms (type II resistance) and spread and accumulation of deoxynivalenol toxin (DON) (type III resistance) throughout the spike. The mapping population consists of 148 doubled haploid lines from an Everest x Art cross. The disease study was performed using a point inoculation technique in a greenhouse with a 14 hour 30°C day and 10 hour 18.9° C night. Inocula of *F. graminearum* consisted of a conidial suspension using field isolate GZ 3639 native to Kansas. The conidial suspension was adjusted to 100 μL^{-1} for inoculations. Pots were arranged in a completely randomized design on four greenhouse benches. Twenty to forty heads were randomly selected from each line and inoculated after the heads emerged from the leaf sheath. Selected spikes were injected with 10 μL^{-1} of conidial suspension, via a micropipette; into a central spikelet (approximately the tenth fully developed spikelet from the base). Spikes were rated for percent infection after 14 days. Kernels were harvested separately from each spikelet in order to determine how DON moves throughout the spike. DON spread and accumulation were measured using a single kernel near-infrared spectroscopy (SKINR) instrument. FHB resistance was significantly correlated with DON resistance ($r = 0.82$, $p = <0.001$). Genotyping-by-sequencing (GBS) was used to discover and genotype SNP markers. TASSEL software was then used to call and filter markers resulting in 7,311 SNPs that were bi-allelic between the parents. A linkage map was created with MSTMap® software using a LOD threshold of 8 and a no mapping distance threshold of 15 cM. The final linkage map consisted of 2,211 markers covering 31 linkage groups (LG) with an average of 71 markers per LG, average LG length of 93.6 cM, and average marker spacing of 1.3 cM. Standard interval mapping and composite interval mapping were performed separately for FHB and DON via the QTL package in RStudio v0.98.1080®. Four QTL for type II resistance were found on LGs 1, 2, 10, and 17. The QTL on LGs 1 and 2 were associated with alleles from Everest and explained 13.4% and 10.0% of the additive phenotypic variance, respectively. The QTL on LG 10 was associated with alleles from Art and explained 21.3% additive phenotypic variation. There were two LOD peaks on LG 17 at 52 cM using SIM (LOD = 3.12, $p = 0.0501$) and 79 cM using CIM (LOD = 3.36, $p = 0.032$). The more significant peak obtained from CIM was used as the location of the QTL and explained 11% of the additive phenotypic variation. The narrow-sense heritability estimate for type II resistance was slightly low at 0.13. There were no significant QTL observed for type III resistance to spread of DON toxin. This experiment is being repeated and the results will be useful in determining if the sources of type II and type III resistance in the cultivars Art and Everest evolved independent of each other. This will allow for the potential to combine QTL for the release of germplasm with high resistance.

'PARSHALL': AN INDIGENOUS AND NOVEL FHB RESISTANCE SOURCE FOR FUSARIUM HEAD BLIGHT WITH HIGH QUALITY AND ADAPTED HARD RED SPRING WHEAT CULTIVAR

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ABSTRACT

Fusarium head blight (FHB) is a devastating disease affecting wheat growing regions worldwide. Economically, FHB epidemics have resulted in losses of hundreds of millions in the US alone since the 1990s. Developing wheat cultivars with FHB resistance that meet the producers and processors needs is critical. 'Parshall' is a NDSU released cultivar with good FHB resistance. However, the genetics underlying Parshall's FHB resistance have yet to be characterized. A RIL population was generated from the cross Parshall × 'Reeder' (PR) and tested in several locations across three states (ND, MN, and SD). Five FHB traits {severity, incidence, disease index, level of deoxynivalenol (DON), and *Fusarium* damaged kernels (FDK)} and one agronomic trait (heading date) were evaluated in field and greenhouse experiments over three years (2010-2012). The PR population was genotyped using DArT and SNP markers. A genetic map consisting of 504 markers was used for composite interval mapping to identify corresponding FHB QTL traits. In total, 81 (genome A=41; B=38 and D=2) QTL were identified on 15 different chromosomes, across locations and years. In total five QTL for resistance type I, 17 for type II, 13 for type III, 11 for type IV, 12 for FHB-NDX and 23 for heading dates (HD) were identified. Among these, 3, 8, 2, 3, 5, and 13 were identified as stable QTL for resistances type I, II, III, and IV; and NDX and HD, respectively. Similarly, the number of major QTL detected for resistance type I, II, III, IV, NDX, and HD were 3, 13, 9, 9, 8, and 14, respectively. Most importantly, major and stable QTL were identified on 2A2 and 4B regions and explained respectively, 16-50% and 7-40% of the FHB traits phenotypic variation. . Some of the FHB resistance regions identified in this study were previously reported to be associated with loci for salinity tolerance, defense response genes, high yield, and quality traits. Since the pedigree of Parshall does not include Sumai3 background; we conclude that Parshall is a new source of FHB resistance with specific adaptation to the Northern American Central Plains region. As such, Parshall may be especially useful in wheat improvement and marker-based wheat breeding.

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GENETIC MAPPING OF QUANTITATIVE TRAIT LOCI FOR FUSARIUM HEAD BLIGHT RESISTANCE IN SPRING BARLEY 'KUTAHYA' AND WILD BARLEY 'W-365'

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ABSTRACT

The deployment of resistant cultivars is one of the best methods for controlling Fusarium head blight (FHB) in barley and reducing the impact of mycotoxin contamination in harvested grain. Here, we report on the identification of quantitative trait loci (QTL) for FHB resistance in two advanced backcross populations. The resistant donor parents are Kutahya, a two-rowed Dutch cultivar, and W-365, a wild barley from Iraq. The recurrent parent of both populations, Quest, is a six-rowed Minnesota barley with a moderate level of FHB resistance. From 2012-2014, the Kutahya/Quest population was screened for FHB resistance and accumulation of deoxynivalenol (DON) in 6-7 environments and the W-365/Quest population in 4-5 environments. Agronomic traits affecting disease development (i.e. plant height, heading date, row type, spike density, and spike angle) were also measured in multiple environments. The populations were genotyped using the Illumina Infinium Assay. Single nucleotide polymorphism (SNP) markers were used to construct the Kutahya/Quest (2,983 markers in total) and W-365/Quest (2,162 markers) maps. QTLs for FHB resistance were identified on every chromosome in the Kutahya/Quest population, explaining from 3.25-7.58% of the phenotypic variation for FHB severity. Of the 6 QTLs identified, those on chromosomes 1H, 2H, and 5H were consistently detected in most environments. In the W-365/Quest population, QTLs were identified on chromosomes 1H, 2H, 3H, 4H, and 5H and explained from 4.60-23.76% of the phenotypic variation for FHB severity. Previously described QTL contributed by Quest were confirmed on chromosomes 1H, 2H, 3H, 4H, 5H, and 6H. Resistance QTLs contributed by the Kutahya and W-365 identified on chromosome 2H, 3H, and 2H, 4H, respectively. In addition to identifying these resistance QTLs, putative transgressive segregants were identified.

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USING ASSOCIATION ANALYSIS AND GENOMIC SELECTION TO IMPROVE FUSARIUM HEAD BLIGHT RESISTANCE IN SOFT RED WINTER WHEAT

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ABSTRACT

With new marker platforms continuing to become available for crop species and the cost of genotyping reducing, breeders are now able to use this technology for crop improvement. Association analysis aims to identify marker trait relationships and is based on linkage disequilibrium between the quantitative trait loci (QTL) and markers: these associations can be used in marker-assisted selection (MAS). However, most quantitative traits are controlled by many small effect QTL making MAS ineffective. An alternative approach is to use genomic selection (GS) to estimate all marker effects simultaneously and determine the breeding value of the individuals. The first objective of this research was to identify, locate, and determine the magnitude of QTL effects for Fusarium head blight (FHB) resistance. The second objective was to determine the accuracy of GS models for predicting FHB resistance. We used a population of 470 elite breeding lines genotyped using genotyping-by-sequencing. Lines were phenotyped for FHB index for two years. The heritability of FHB Index was 0.59. We identified four significant QTL with R^2 values ranging from 2.6 to 2.8% and allele effects ranging from 1.07 to 1.76%. No QTLs were found in common between FHB and heading date (HD) or height. The relative efficiencies of GS models for FHB prediction ranged from 0.22 to 0.5. Based on these results we believe these technologies will be useful for improving FHB resistance in this soft red winter wheat population.

FUSARIUM HEAD BLIGHT RESISTANCE IN SOFT RED WINTER WHEAT

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ABSTRACT

Development of resistant wheat cultivars is the most efficient approach to control Fusarium Head Blight. Local broadly adaptive cultivars have been crossed with *Fhb1* derived lines, Truman, Neuse, Jamestown, Oakes, and derived lines with *Fhb1* to introduce FHB resistant QTL into adaptive genetic backgrounds. Elite lines with resistance from Truman, Neuse, GAMD08-27-E9 and Jamestown, were evaluated in the field during 2014 for FHB resistance and agronomic performances. Several elite lines have been identified with good FHB resistant derived from Jamestown. GA051477-13ES4 from the cross of AGS 2020 / Jamestown had similar ratings as Jamestown for incidence, index and ISK. Lines with moderate levels of FHB resistance from either Jamestown or Neuse were identified with high yield potential. In addition, GA04151-10E29 was evaluated in the 2012 Uniform Southern Wheat Nursery and also showed moderate level of FHB resistance with high grain yield was released in 2014. Several other lines with Jamestown, Truman, Oakes, and IN 97397 as source of resistance were identified with moderate level for FHB index and ISK and high grain yield when compared to the checks "SS 8641" and "AGS 2035". These lines will be further evaluated for FHB and grain yield. Double haploid lines, NC 10014-38 (NC 06-198-96/NC 08-140) and NC 10435-11 (NC 05-21937 / Oakes // Jamestown) showed a high level of FHB resistance and high yield performance.

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IDENTIFICATION OF FHB RESISTANCE QTL IN NATIVE SRW WHEAT CULTIVAR TRIBUTE

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ABSTRACT

Deployment of native sources of resistance to Fusarium head blight (FHB), caused by *Fusarium graminearum*, has been a priority in wheat (*Triticum aestivum*) breeding programs because of local adaptation and minimum yield drag. Pyramiding different sources of resistance would be an effective approach to enhance FHB resistance. The objectives of the study were to identify the FHB resistance QTL in the native soft red winter (SRW) wheat cultivar Tribute and develop diagnostic markers for use in marker-assisted breeding. A total of 115 double haploid (DH) lines, developed at NCSU, were evaluated for FHB incidence and FHB severity by cooperators in AR, KY, MD, NC, and VA during 2013 and 2014 (except MD). Grain samples from each location were visually assessed for *Fusarium* Damaged Kernels (FDK) and analyzed for deoxynivalenol (DON) toxin content. The population was also evaluated for type II resistance to disease spread in the greenhouse at Virginia Tech. A set of SSR markers were used to genotype the mapping population. Genotype-by-location interaction was significant for the population. Composite interval mapping identified seven putative QTL on chromosomes 1A, 1B, 2A, 2D, 3BS, 5A, and 7D for FHB incidence, FHB severity, FDK, and DON content. Putative QTL for FHB resistance were detected on 1A, 1B, 2A, 3BS, and 5A, whereas putative QTL for FHB susceptibility were detected on 7D. The putative QTL on 2D was associated with both resistance and susceptibility to FHB. The putative QTL for FHB on 2A and 2D were linked to loci governing heading date and flowering date across locations, whereas the putative QTL for FHB on 1B was linked to plant height but only in MD. The variation explained by putative QTL on 1A, 1B, 2A, 2D, 3BS, 5A, and 7D was 14% to 17% (Additive = -3.8 to -8.6), 8% to 20.6% (Additive = -1.1), 8% to 26% (Additive = -0.1 to -9.0), 40% to 42% (Additive = -8.4 and 9.0), 11% to 17% (Additive = -4.0 to -8.9), 12.5% to 15.7% (Additive = -5.3 to -8.6), and 11% to 15.7% (Additive = 5.2 to 10.4), respectively. The population is being genotyped for 90K SNP and diagnostic markers for the putative QTL on 1A, 3BS, and 5A will be identified for utilization in marker-assisted breeding.

A BREEDING TOOL FOR ESTIMATING GENETIC VARIANCE AND CORRELATED RESPONSE IN BI-PARENTAL CROSSES: TARGETING HIGH-YIELD AND LOW-DEOXYNIVALENOL (DON)

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ABSTRACT

Breeding programs of self-pollinated crops usually focus on crosses between the most elite germplasm. While elite × elite crosses ensure a desired population mean, they do not guarantee any level of genetic variation (V_G). Unlike population mean, which is simply predicted by the mid-parent value, prediction of genetic variance relies on the knowledge of population parameters that are not readily known. The purpose of this research was to use genome-wide markers to predict V_G of DON and yield of simulated bi-parental RIL populations resulting from pairwise crosses among parent candidates using a procedure that combines genomic simulation and genome-wide prediction. In our example, we demonstrate the utility of the procedure to evaluate the 435 possible crosses resulting from a half-diallel of 30 parents through simulation to identify a manageable number of crosses that could then be potentially advanced to field-based trials. We show that the procedure can be used to screen among high × high crosses for yield and among low × low crosses for DON based on the expected progeny variances across crosses. Since yield and DON are unfavorably correlated, we also demonstrate how equally yielding crosses may differ in their correlated response for DON. Finally, we propose a genome-wide equation to quantify the "coefficient of gene distribution" theoretically outlined in classical quantitative genetics texts as a measure of genetic distance in the context of a given trait. This computational resource will be provided in a package in the R environment and should be useful to breeders who are designing crosses to develop improved FHB resistant varieties.

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THE 2013-14 SOUTHERN UNIFORM SOFT RED WINTER WHEAT SCAB NURSERY

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ABSTRACT

The Southern Uniform Winter Wheat Scab Nursery provides breeders in the public and private sectors with an opportunity for multi-environment, independent evaluations of FHB resistance in advanced generation breeding lines compared with the current most resistant check varieties Ernie, Bess and Jamestown. Valuable data are provided on resistance to other important fungal and viral diseases, milling and baking quality and agronomic characteristics. In addition, genotypic analyses identify alleles present at numerous important loci. The nursery is the primary method to facilitate the sharing of the best resistant materials throughout the breeding community.

The 2013-14 nursery comprised 58 advanced generation breeding lines and four check cultivars, 'Ernie', 'Bess', 'Jamestown' (partially resistant) and 'Coker 9835' (susceptible). Seven U.S. public programs (Univ. of Arkansas, Univ. of Georgia, Louisiana State University, Univ. of Maryland, N.C. State Univ., VA Tech., and USDA-ARS), and three private companies (Agripro-Coker, KWS, and Limagrain) submitted entries. The nursery was distributed to 11 U.S., one Romanian, and one Hungarian cooperator for field, and/or greenhouse evaluations. In addition, three USDA-ARS laboratories conducted evaluations for Hessian fly resistance, milling and baking quality and marker genotypes based on established diagnostic markers.

The mean level of FHB resistance in the nursery was high. Between 83 and 97 percent of entries had significantly better means than the susceptible check for Severity, Index and ISK. DON data are still being reported. Sources of resistance included Chinese, South and North American germplasms.

Copies of the full report will be available at the 2014 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org/.

ACKNOWLEDGEMENT AND DISCLAIMER

This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 58-6645-3-030. This is a cooperative project with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

Table 1. Means across locations and genotypic content of regions associated with FHB resistance.

	Cultivar/ Designation	FHB Incidence	RANK	FHB Severity	RANK	FHB Index	RANK	FDK	RANK	ISK	RANK	DON	RANK
1	ERNIE	54	15	23	10	14	10	22	14	26	16		
2	COKER9835	88	62	62	62	56	62	51	61	63	62		
3	BESS	48	7	23	10	13	8	18	6	21	6		
4	JAMESTOWN	52	12	22	8	14	10	18	6	22	7		
5	M10-1615	51	9	21	6	12	4	22	14	26	16		
6	AR00179-2-2	60	27	26	16	19	21	16	4	29	24		
7	AR00334-5-2	66	44	27	18	21	27	22	14	31	29		
8	AR01136-3-2	62	33	32	29	24	37	29	30	31	29		
9	AR04001-3	54	15	29	23	16	17	25	21	24	12		
10	AR04084-1-3	59	26	34	34	20	25	27	24	29	24		
11	ARGE07-1347-6-7-9	43	2	20	2	12	4	19	9	18	2		
12	ARGE07-1354-2-6-1	55	19	27	18	19	21	21	13	24	12		
13	ARGE07-1355-16-6-6	54	15	28	22	19	21	18	6	23	8		
14	ARS09-228	63	37	33	32	23	34	32	39	31	29		
15	ARS10-028	74	57	29	23	24	37	30	34	36	43		
16	ARS10-038	68	48	59	61	41	60	55	62	57	61		
17	ARS10-043	81	61	40	48	34	57	39	51	49	58		
18	ARS10-172	78	59	52	59	44	61	43	56	51	59		
19	ARS10-389	40	1	20	2	9	2	20	11	15	1		
20	B09-0002	46	6	20	2	13	8	14	2	19	4		
21	B09*900256	65	42	43	53	30	53	46	58	45	56		
22	B08-91993	58	24	36	39	24	37	32	39	33	35		
23	GA04494-13ES1	61	29	49	57	31	54	48	59	41	52		
24	GA051477-13ES2	61	29	40	48	26	44	30	34	35	40		
25	GA051477-13ES4	45	5	32	31	15	15	28	27	24	12		
26	GA051207-13ES11	64	39	41	52	27	47	32	39	33	35		
27	GA061050-13ES18	62	33	40	48	23	34	37	49	34	38		
28	GA06586-13ES21	76	58	51	58	36	58	48	59	51	59		
29	GA06390-13ES24	62	33	38	43	27	47	43	56	34	38		
30	GA061050-13ES17	61	29	39	46	26	44	32	39	35	40		
31	KWS 013	65	42	39	46	28	49	34	46	38	46		
32	KWS 026	55	19	26	16	14	10	15	3	27	20		
33	KWS 027	68	48	36	39	26	44	41	55	38	46		
34	LA06149C-P7	71	53	34	34	24	37	29	30	38	46		
35	LA08201C-57	54	15	34	34	18	20	23	19	29	24		
36	LANC8170-41-1	64	39	43	53	24	37	32	39	38	46		
37	LA07085CW-P4	56	22	30	25	20	25	29	30	27	20		
38	LANC8170-41-2	55	19	31	27	16	17	23	19	26	16		
39	LCS 08577-4	73	55	52	59	36	58	39	51	48	57		
40	LCS 229	68	48	44	56	31	54	33	45	39	50		
41	M09-9547	60	27	34	34	21	27	32	39	33	35		
42	M11-1027#	64	39	31	27	21	27	28	27	35	40		
43	M11-2298	51	9	24	12	12	4	22	14	23	8		
44	MD08-22-22-13-4	56	22	25	14	19	21	13	1	23	8		
45	MD26-H2-23-13-1	66	44	25	14	22	30	20	11	29	24		
46	MD09W272-8-4-13-3	58	24	24	12	15	15	26	23	28	23		
47	MDC07026-F2-19-13-4	68	48	30	25	22	30	30	34	31	29		
48	NC11-21401	52	12	22	8	12	4	25	21	23	8		
49	NC11-22289	43	2	19	1	8	1	19	9	20	5		
50	NC11-22291	44	4	20	2	11	3	16	4	18	2		
51	NC8170-45-17	50	8	21	6	14	10	22	14	24	12		
52	NC8170-86-2	53	14	27	18	17	19	28	27	27	20		
53	NC9305-7	51	9	27	18	14	10	27	24	26	16		
54	NC09-21916	61	29	36	39	24	37	27	24	30	28		
55	VA10W-96	63	37	36	39	24	37	31	37	32	33		
56	VA11W-108†	73	55	40	48	32	56	38	50	44	54		
57	VA11W-230	62	33	32	29	22	30	31	37	32	33		
58	VA11W-278	66	44	43	53	28	49	40	53	39	50		
59	VA12W-102	69	52	38	43	29	52	34	46	41	52		
60	VA12W-150	66	44	38	43	23	34	29	30	37	45		
61	VA12FHB-37	78	59	34	34	28	49	40	53	44	54		
62	VA12FHB-85	71	53	33	32	22	30	36	48	36	43		
	Mean	61		33		22		29		32			
	LSD (0.05)	24		20		19		21		15			
	CV%	20.1		31.4		43.4		37.2		23.7			

Table 1. Continued

	Cultivar/ Designation	Heading Date	RANK	Plant Height	RANK	Flour Yield %	RANK	Softness Equivalent %	RANK	Hessian Fly Biotype L	Fhb1	Fhb Massey 3BL	Fhb 5A	Fhb 2DL-Wuhan1/W14
1	ERNIE	131	7	33	12	66	46	55	36	0-14	_	Het	Ernie	_
2	COKER9835	135	51	31	3	65	59	63	1	0-15	_	_	no data	_
3	BESS	134	39	38	57	67	31	63	1	0-15	_	_	_	_
4	JAMESTOWN	130	2	34	25	68	18	60	13	0-20	_	_	_	_
5	M10-1615	131	7	35	38	69	10	57	26	0-16	_	_	_	_
6	AR00179-2-2	133	26	39	59	67	31	61	7	0-15	_	_	_	_
7	AR00334-5-2	133	26	39	58	67	31	58	21	0-20	_	Het	_	_
8	AR01136-3-2	134	39	37	51	67	31	58	21	0-16	_	_	_	_
9	AR04001-3	132	15	40	62	69	10	58	21	0-14	_	_	_	_
10	AR04084-1-3	135	51	36	46	70	6	59	17	0-11	_	_	_	_
11	ARGE07-1347-6-7-9	133	26	37	53	66	46	55	36	0-11	Het	Het	_	Het
12	ARGE07-1354-2-6-1	135	51	37	48	66	46	61	7	0-12	_	_	_	_
13	ARGE07-1355-16-6-6	133	26	40	61	67	31	59	17	0-11	_	_	_	_
14	ARS09-228	134	39	35	30	72	4	35	62	0-13	_	_	_	_
15	ARS10-028	134	39	34	18	73	2	44	58	0-12	_	_	_	_
16	ARS10-038	135	51	36	44	72	4	43	59	0-15	_	_	Ernie	_
17	ARS10-043	136	58	33	13	73	2	39	61	0-9	_	_	Ernie	_
18	ARS10-172	135	51	32	7	70	6	51	51	0-12	_	_	_	_
19	ARS10-389	130	2	34	23	74	1	41	60	0-13	_	_	_	_
20	B09-0002	132	15	36	45	68	18	53	45	0-10	_	_	_	_
21	B09*900256	133	26	34	20	65	59	60	13	0-14	_	_	Ernie	_
22	B08-91993	131	7	38	56	66	46	60	13	0-15	_	Yes	_	_
23	GA04494-13ES1	131	7	31	4	69	10	52	48	0-16	_	_	Ernie	_
24	GA051477-13ES2	131	7	36	41	68	18	62	6	0-14	_	_	_	_
25	GA051477-13ES4	131	7	35	31	67	31	63	1	0-14	_	_	_	_
26	GA051207-13ES11	132	15	36	39	70	6	58	21	0-14	_	_	_	_
27	GA061050-13ES18	132	15	32	6	66	46	58	21	0-15	_	_	_	_
28	GA06586-13ES21	132	15	36	42	69	10	50	54	0-7	_	_	_	_
29	GA06390-13ES24	132	15	31	2	68	18	55	36	0-12	_	_	_	_
30	GA061050-13ES17	132	15	35	26	66	46	59	17	0-15	_	_	_	_
31	KWS 013	129	1	35	36	67	31	57	26	0-16	_	_	Ernie	_
32	KWS 026	132	15	36	40	68	18	57	26	0-15	_	Het	_	_
33	KWS 027	137	61	38	54	70	6	53	45	0-18	_	_	_	_
34	LA06149C-P7	135	51	37	50	66	46	61	7	0-19	_	_	_	_
35	LA08201C-57	134	39	39	60	68	18	56	33	0-17	_	_	_	_
36	LANC8170-41-1	134	39	35	27	67	31	49	56	0-13	Yes	_	_	_
37	LA07085CW-P4	131	7	34	19	68	18	60	13	0-15	_	_	_	_
38	LANC8170-41-2	133	26	32	8	68	18	51	51	0-13	Yes	_	_	_
39	LCS 08577-4	133	26	35	33	69	10	63	1	0-15	_	_	_	_
40	LCS 229	132	15	35	35	67	31	63	1	0-15	_	Yes	_	_
41	M09-9547	134	39	37	47	68	18	54	43	0-15	_	_	_	_
42	M11-1027#	134	39	34	24	66	46	61	7	0-14	_	Het	_	_
43	M11-2298	132	15	37	52	67	31	55	36	0-12	_	Het	_	_
44	MD08-22-22-13-4	134	39	33	9	66	46	54	43	0-14	Yes	_	Ning	Yes
45	MD26-H2-23-13-1	136	58	34	17	67	31	51	51	0-13	Yes	_	Ning	Yes
46	MD09W272-8-4-13-3	133	26	33	14	66	46	56	33	0-14	Yes	_	_	_
47	MDC07026-F2-19-13-4	133	26	34	16	69	10	55	36	0-19	Yes	_	_	_
48	NC11-21401	133	26	32	5	65	59	56	33	0-15	Yes	_	_	Yes
49	NC11-22289	130	2	34	21	66	46	50	54	0-16	_	_	_	_
50	NC11-22291	130	2	35	29	67	31	52	48	0-13	_	_	_	_
51	NC8170-45-17	134	39	36	43	67	31	52	48	0-14	Yes	_	Ning	_
52	NC8170-86-2	133	26	35	32	65	59	55	36	0-17	Yes	_	_	_
53	NC9305-7	134	39	38	55	66	46	55	36	0-12	_	_	_	_
54	NC09-21916	133	26	35	34	68	18	61	7	0-17	_	_	_	_
55	VA10W-96	130	2	35	37	68	18	53	45	0-15	_	_	_	_
56	VA11W-108†	133	26	35	28	67	31	61	7	0-12	_	_	_	_
57	VA11W-230	132	15	33	10	68	18	57	26	0-12	_	_	_	_
58	VA11W-278	131	7	33	15	67	31	57	26	0-14	_	Yes	_	_
59	VA12W-102	135	51	31	1	69	10	59	17	0-15	_	_	_	_
60	VA12W-150	134	39	34	22	66	46	57	26	0-10	_	_	_	_
61	VA12FHB-37	137	61	33	11	68	18	57	26	0-15	_	_	_	_
62	VA12FHB-85	136	58	37	49	69	10	49	56	0-15	_	Het	_	_
	Mean	133		35		68		55						
	LSD (0.05)	4		3		.		.						
	CV%	1.4		5.0		.		.						

QTL CONFERRING TYPE II RESISTANCE TO FUSARIUM HEAD BLIGHT IN ADAPTED WHEAT CULTIVAR 'UI STONE' AND ITS EFFECT ON YIELD

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ABSTRACT

Fusarium head blight (FHB) is an emerging wheat disease in Southeastern Idaho. Most cultivars grown in this region are susceptible to FHB. Several exotic sources of resistance are available to fill this hole, however, lack of adaptation and often complication arises due to "linkage drag" limit their direct utilization. Therefore, identification and development of adapted FHB resistant cultivars is one of major objectives in the University of Idaho wheat breeding program. The objectives of this study were to map QTL associate with type II FHB resistance in the adapted soft white spring (SWS) wheat cultivar 'UI Stone' and evaluate side effect of identified QTL on yield. A total of 151($F_{4:6}$) recombinant inbred lines (RILs) derived from the cross between resistant cultivar 'UI Stone' and a moderately susceptible cultivar 'Alturas' were evaluated for type II FHB resistance by measuring disease severity expressed as a percentage of infected spikelets (PIS) in four greenhouse experiments over three years. The RILs were genotyped with 154 markers (77 SSR and 77 SNP). A Linkage map was constructed using MapMaker 3.0b and QTL analysis was performed using WinQTL Cartographer Ver. 2.5. Two major QTL for type II FHB resistance, *QFhbuis.ab-2B* and *QFhbuis.ab-3B*, were identified by both single marker analysis and composite interval mapping (CIM) methods and the two QTL together explained 23.6 to 24.8% of phenotypic variation. These QTL had no significant effect on yield based on the regression analyses. This study also identified 4 lines with better FHB resistance and higher grain yield than UI Stone. These four lines could be used as germplasm and/or released as new resistant cultivars after further evaluation. More phenotypic evaluation for FHB severity by cooperators in 2015 and 90K SNP marker data will be utilized to validate the effect of these two QTL for potential application in marker-assisted breeding.

FT-NIR OPTICAL CHARACTERISTICS OF SOUND AND *FUSARIUM* DAMAGED WHEAT AT TWO MOISTURE CONTENT LEVELS

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ABSTRACT

In prior research, we developed near-infrared spectrometric methods to detect *Fusarium*-damaged kernels (FDK) of wheat and their deoxynivalenol (DON) levels using the Single Kernel Near-Infrared (SKNIR) system which is operated in the 950-1650 nm spectral range. Those studies showed that DON has NIR absorption bands with peaks around 1408, 1904 and 1919 nm. These DON absorption bands may be interfered by the broad water absorption bands around 1450 and 1940 nm. Water and DON bands may be shifted to lower or higher wavelengths depending on the moisture content and *Fusarium* damage levels of the grain matrix and this may affect the performance of calibrations for detection and quantification of DON levels in FDK, especially when kernels with different moisture content levels are evaluated. Therefore, it is useful to study the NIR absorption patterns of sound and FDK at different moisture content levels to identify specific NIR absorption bands associated with moisture and *Fusarium* damage in kernels independent from each other. That information may be useful to improve NIR calibrations and also may help improve FDK sorting by the new rapid LED-based grain sorters. To study the FDK and moisture absorption bands, sound and FDK of cultivar 'Art' harvested from a FHB screening nursery were selected. Half of the kernels (~5-6 g) were partly dried at 80C for one hour (dry) and the rest were at equilibrium moisture level (wet) at room temperature. The kernels were scanned with two repacks in glass vials (14mm x 45mm) using the PerkinElmer Spectrum 400 FT-NIR spectrometer in the 1000-2500 nm spectral range. The spectrometer conditions used were data interval = 2nm; resolution = 16nm, number of scans = 25 with 0.2 cm/s scan mirror speed. The second derivatives of the spectra were constructed with 25 data points for slope calculation using PerkinElmer Spectrum software. Spectral subtractions were performed between wet and dry kernels of sound and FDK groups, and between sound and FDK of dry and wet kernel groups to identify peak NIR absorptions due to water and *Fusarium* damage, respectively. *Fusarium* damage related peak absorptions were observed at 1013 nm, 1198nm, 1274 nm, 1355-1362 nm, 1418-1428 nm, 1585nm, 1698nm, 1744nm, 1782nm, 1826nm, 2276nm, 2328 nm and 2371 nm regions. Moisture content related peak absorptions were detected at 1162 nm, 1337 nm, 1405-1408nm and 2002 nm regions. These absorption peaks which are isolated and independent from the influence of absorptions due either to moisture or *Fusarium* damage may be useful for improving performance of NIR calibrations for scab sorting and DON estimation and for modifications in LED-based high speed sorting instruments by incorporating LEDs for those wavelengths.

FUSARIUM HEAD BLIGHT RESISTANCE QTL IN THE NC-NEUSE / AGS2000 RECOMBINANT INBRED LINE POPULATION

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ABSTRACT

Breeding for resistance to Fusarium Head Blight is of major importance as the disease can have serious negative impacts on wheat production in warm and humid regions of the world, including the state of North Carolina. Fusarium Head Blight can cause significant grain yield reduction, but also severely affect the grain quality due to accumulation of mycotoxins produced by the pathogen. The importance of finding native sources of resistance in U.S. soft red winter wheat lines has been emphasized in recent years. The North Carolina cultivar NC-Neuse is a moderately FHB resistant soft red winter wheat, released in 2003.

A population of 170 random F_5-derived recombinant inbred lines derived from a cross between 'NC-Neuse' and the FHB susceptible line 'AGS 2000' was evaluated for FHB resistance over several years and locations. Suitable data for at least some FHB traits were collected from a total of seven environments (2-3 reps/env). These included Kinston, NC in 2011, 2012, 2013, and 2014; Salisbury, MD in 2012; and Lake Wheeler, NC in 2013 and 2014. The FHB related traits evaluated were disease incidence (INC), severity (SEV), *Fusarium* damaged kernels (FDK), and accumulation of the mycotoxin deoxynivalenol (DON).

Least squares means (lsmeans) were calculated from the phenotypic data within and across environments. In environments where heading date (HD) was significant, this was used as covariate in the data analysis and calculations of lsmeans.

A linkage map containing a total of 1839 polymorphic SSR, DArT and SNP markers across 27 linkage groups was developed and utilized for mapping of QTL in this population. QTL analysis was conducted using Composite Interval Mapping (CIM) and then Multiple Interval Mapping (MIM) with WinQTLCart 2.5. The critical LOD value to declare QTL significance was 3.0, based on 1000 permutations.

We identified QTL associated with FHB resistance (from several environments and/or several resistance traits) on chromosomes 1A, 1B, 2A, 4A, 5B, and 6A. Their LOD scores ranged from 3.0 to 5.4 with effects between 5.5-11.5%. At all QTL except the one on chromosome 5B, the NC-Neuse allele contributed resistance. The QTL on 5B (co-localized with the *Vrn-B1* locus) showed up only in 2012 environments, probably due to an usually mild winter. QTL for HD and plant height were mapped to chromosomes 2B, 4A, 5B, 6A, and 7D. The resistance QTL on chromosomes 4A and 6A did not co-localize with QTL controlling HD and/or plant height.

In the coming months, markers associated with the identified resistance QTL will be run on a broader set of wheat lines to test their usefulness and to test frequencies of resistance alleles.

ACKNOWLEDGEMENT AND DISCLAIMER

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VALIDATION OF FUSARIUM HEAD BLIGHT RESISTANCE QTL USING THE NC-NEUSE / BESS DOUBLED HAPLOID POPULATION

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ABSTRACT

Fusarium Head Blight (FHB) is one of the most damaging diseases of wheat. It lowers the grain yield and quality, and contaminates grain with the mycotoxin deoxynivalenol (DON). Genetic resistance is a critical control measure and breeding objective. Many studies have focused on the genetic basis of FHB resistance in Asian wheat sources, while resistance in native sources has not been characterized as well yet. In addition, the need for validation of mapped QTL remains an important research objective in order to use markers more efficiently in marker-assisted selection (MAS).

The two cultivars 'NC-Neuse' and 'Bess' display moderate resistance to FHB. NC-Neuse was developed and released from North Carolina State University. Bess is one of the most FHB resistant lines in the Southeast, and is a full-sib of the cultivar 'Truman'. Bess and Truman were both developed and released from the University of Missouri, and have similar resistance levels.

Quantitative trait loci (QTL) associated with FHB resistance in NC-Neuse were very recently identified and mapped to chromosomes 1A, 1B, 2A, 4A, 5B, and 6A (Abstract presented at this Forum also).

The wheat breeding group at University of Missouri recently identified and mapped QTL associated with resistance in Truman (*in press*). The QTL were mapped to chromosomes 1B, 2A, 2B, 2D, 3B, 4B, 6B, and 7B.

The objective of this study was to map QTL for FHB resistance in the NC-Neuse / Bess DH population, and use these results to validate FHB resistance QTL found in previous studies including NC-Neuse and Truman.

A population of 100 doubled haploid (DH) lines derived from a cross between NC-Neuse and Bess was evaluated for FHB resistance over several years and locations. Suitable data for at least some FHB traits was collected from a total of seven environments (2-3 reps/env). These included Kinston, NC in 2012, 2013, and 2014; Columbia, MO in 2012 and 2013; and Lake Wheeler, NC in 2013 and 2014. The FHB related traits evaluated were disease incidence (INC), severity (SEV), *Fusarium* damaged kernels (FDK), and accumulation of DON.

Least squares means (lsmeans) were calculated from the phenotypic data within and across environments. In environments where heading date (HD) was significant, it was used as covariate in the data analysis and calculations of lsmeans.

A linkage map containing a total of 4013 polymorphic SSR and SNP markers across 51 linkage groups was developed and utilized for mapping of QTL associated with FHB resistance in this population. QTL analysis using lsmeans from the phenotypic data (across and within individual environments) was conducted using Composite Interval Mapping (CIM) and then Multiple Interval Mapping (MIM) with WinQTLCart 2.5. The critical LOD value to declare QTL significance was 3.0, based on 1000 permutations.

Preliminary results showed QTL associated with one or more FHB resistance traits on chromosomes 1A, 1B, 2A, 2B, 3A, 3B, 4A, 4B, 5A, and 6A. At the QTL on chromosomes 1A, 2A, 3A, 4A, 4B, and 6A the NC-Neuse allele conferred resistance. At the QTL on chromosomes 1B, 2B, 3B, and 5A the Bess allele conferred resistance. Their LOD scores ranged from 3.13 to 10.33 with effects between 4.4-23.6%.

An update on pertinent results and map comparisons will be presented at the Forum.

ACKNOWLEDGEMENT AND DISCLAIMER

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CHANGES IN THE WHEAT PRIMARY METABOLISM DURING DEFENSE AGAINST *FUSARIUM GRAMINEARUM*

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ABSTRACT

Wheat is commonly infected by *Fusarium graminearum*, causing Fusarium head blight, which leads to severe losses in grain yield and quality. A decisive factor in the mounted defense response is how plants counteract the effects of the *F. graminearum* toxin deoxynivalenol, which elicits oxidative stress and inhibits protein biosynthesis. In response plants generate secondary metabolites, inactivate the toxin by metabolization and try to compensate for the reduced levels of protein biosynthesis. All these incur at significant cost and require restructuring of the primary metabolism to meet the elevated needs in energy, carbon and nitrogen equivalents. We have investigated changes to the primary metabolism in response to the pathogen in transcriptomic and metabolomic datasets and additionally to the toxin in metabolomic datasets. These data have been generated by RNAseq and GC-MS from wheat near-isogenic lines segregating for the resistance QTL *Fhb1* and *Qfhs.ifa-5A* in a series of time points after inoculation with the fungus or deoxynivalenol. We observed increased levels in the respiration including the pentose phosphate pathway, which produces also erythrose-4-phosphate, required as a precursor in the shikimate pathway, which ultimatively leads to the production of defense-associated phenylpropanoids. The detrimental effects on translation by the toxin are met by the increased synthesis of amino acids and tRNA ligases. Significant differences for *Fhb1* were observed in metabolite levels after DON treatment and to a lesser extent for lines lacking *Qfhs.ifa-5A* after *Fusarium graminearum* treatment.

PYRAMIDING *FHB1* WITH USEFUL RUST RESISTANCE GENES IN A WINTER-HARDY WHEAT GENETIC BACKGROUND

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ABSTRACT

A winter wheat breeding program was initiated at North Dakota State University in 2011. The first objective of the new program is to develop a productive breeding population with adequate variation for cold-hardiness, yield, disease resistance and processing quality.

This study is part of a larger pre-breeding effort to develop new parental materials carrying useful genes for disease resistance and adaptation. Norstar is an old Canadian variety with exceptional cold-hardiness, yet is lacking in disease resistance and is too tall under North Dakota growing conditions. In view of the difficulty to pyramid cold-hardiness (low heritability) with disease resistance through regular crosses, it was decided to upgrade Norstar for its future use as a breeding parent. Marker-assisted backcrosses were therefore employed to transfer and pyramid combinations of resistance genes into the Norstar background.

The targeted genes included a Fusarium head blight resistance gene (*Fhb1*), two leaf rust resistance genes (*Lr34, Lr53*) and four stem rust resistance genes (*Sr2, Sr26, Sr39, Sr50*). An attempt was also made to co-transfer the reduced height gene, *Rht-B1b*, with the disease resistance genes. Following the third backcross to Norstar, the various near-isogenic progenies were inter-mated to derive progeny having combinations of *Fhb1* and *Rht-B1b* plus targeted leaf and/or stem rust resistance genes. Five different near-isogenic lines (each carrying *Fhb1* and *Rht-B1b*) that differ for the leaf and stem rust resistance genes they possess, were recovered following selfing of the intercrossed F_1 progenies.

With respect to their utility as cross parents, the set of NILs: (i) will be used in direct crosses with other breeding parents; (ii) will first be inter-crossed to derive more complex F_1 parents that are homozygous *Fhb1*, *RhtB1b*, but simultaneously heterozygous for two or more rust resistance genes.

DEVELOP SNP MARKERS FOR *FHB1* THROUGH FINE MAPPING USING WHEAT 90K SNP ARRAYS

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ABSTRACT

Wheat Fusarium head blight (FHB) is one of the most destructive diseases limiting wheat production worldwide. *Fhb1*, located on chromosome 3BS, is the most stable quantitative trait locus (QTL) with the largest effect on wheat resistance to spread of diseases in a spike (type II). *Fhb1* has been widely used in breeding to improve FHB resistance in wheat, but the gene underlying *Fhb1* has not been cloned. This study used single nucleotide polymorphism (SNP) from wheat 90K SNP arrays to saturate the *Fhb1* region. A high-density linkage map was constructed by adding 25 SNP markers to the region using a recombinant inbred population and a backcross-derived near isogenic line (NIL) population derived from Ning7840 x Clark BC_7F_2. *Fhb1* was delimited to a 0.88 cM interval between SNP3026 and SNP241 containing 11 SNPs. The SNP markers in the *Fhb1* region were converted to competitive allele-specific PCR (KASP) markers for further fine mapping. SNP79259 and SNP77323 co-segregated with *Fhb1* in the 376 NILs that have recombination between *Xgwm533* and *Xgwm493*. The physical distance of the two SNP markers is about 300 kb on the reference sequences of chromosome 3B contig 0954 of Chinese Spring. The two KASP SNPs can be used for marker-assisted pyramiding of *Fhb1* with other resistance QTLs. This result demonstrated that wheat 90K SNP array is a useful tool for increasing the marker density in the candidate gene region to facilitate fine mapping in wheat.

ACKNOWLEDGEMENT AND DISCLAIMERS

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VALIDATION OF FUSARIUM HEAD BLIGHT RESISTANCE QTLS IN WHEAT USING DOUBLE HAPLOIDS DERIVED FROM FOUR-WAY CROSSES

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ABSTRACT

Fusarium head blight (FHB), caused primarily by *Fusarium graminearum*, is one of the most devastating plant diseases in the world. Specifically in wheat, FHB has become responsible for significant economic and health concerns worldwide due to mycotoxin accumulation in infected grain, as well as yield and quality losses. To date, sources of resistance conferring complete resistance to FHB have not been identified in wheat. Thus, extensive research efforts worldwide has focused on development and use of resistant cereal cultivars for the control of FHB. QTLs for FHB resistance have been mapped to almost all wheat chromosomes when different mapping populations were investigated. In our research, we are using double haploid (DH) wheat lines derived from selected four-way crosses combining several sources of resistance to validate putative QTLs (Xmc758. Gwm33, xbacr176, Xgm120, Xwmc317, Xwmc332, Xwmc522 and Xwmc296) that could minimize the threat of FHB including the reduction of mycotoxins, to the producers, processors, and consumers of wheat. We use molecular techniques to validate DH lines and their corresponding parents. In this study, we report on our work on the DH derived lines screen for FHB in three northern plains location. Our finding will assist ongoing efforts aimed to develop resistance wheat varieties, minimize the impact of the disease, and provide resources that can possibly assist in the advancement of wheat germplasm research.

CHANGES IN FUSARIUM HEAD BLIGHT AND GRAIN YIELD TRAITS OVER THREE CYCLES OF GENOMIC SELECTION IN A BARLEY BREEDING POPULATION

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ABSTRACT

To date, the potential of genomic selection (GS) has been documented largely by theoretical and simulation-based research. While not entirely absent, empirical evidence of genomic selection's efficacy, principally gain from selection, is lacking in the literature. The barley program at the University of Minnesota has implemented GS and has so far completed five cycles of advanced cycle breeding. The first three breeding cycles, each comprised of 50 selected individuals accompanied by 50 randomly selected individuals, along with the "cycle 0" parents have been grown as a single experiment in multiple Minnesota environments and phenotyped for multiple traits, including Fusarium head blight, grain deoxynivalenol concentration, and grain yield. This study will assess gain from selection over the first three breeding cycles and provide part of the empirical evidence for the effectiveness of GS in plant breeding.

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GENETIC AND MOLECULAR ANALYSIS OF NOVEL FHB RESISTANCE

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ABSTRACT

Fusarium head blight (FHB) caused by *Fusarium graminuearum* (*Fg*) is one of the most prevalent diseases of wheat (*Triticum aestivum* L.) and other small grain cereals. It has proven difficult to move existing sources of FHB resistance into adapted Canadian varieties due to poor agronomics and low yield. Recently, a novel source of FHB resistance, FL62R1, which has high FHB resistance and high agronomics and yield, was created by germplasm developers at Agriculture and Agri-Food Canada. In this study, we will use genetic and molecular approaches to characterize this new FHB resistance and with the goal of eventually introgressing desirable alleles into Canadian elite wheat varieties. The spread of *Fg* in heads of FL62R1 was considerably reduced compared to susceptible varieties, and the high level of type II resistance observed was similar to the well-known FHB resistant variety, Sumai 3. Fungal progression was monitored by using a GFP-tagged *Fg* strain. Microscopic data showed that *Fg* was effectively blocked in the rachis and did not spread to uninoculated spikelets of FL62R1. Double haploid mapping populations of FL62R1 crossed with two Canadian elite wheat varieties have been generated for genetic analysis.

IDENTIFICATION OF NEW QTL FOR NATIVE RESISTANCE TO FHB IN SRW WHEAT

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ABSTRACT

Fusarium Head Blight (FHB), caused by *Fusarium graminearum* Schwabe, is a major disease of wheat (*Triticum aestivum* L.). Frequently FHB results in severe yield loss, reduced seed quality, and accumulation of mycotoxins such as deoxynivalenol (DON) and nivalenol (NIV). Control of FHB can be achieved via pyramiding multiple genes conferring resistance to initial infection, disease spread, kernel damage, and toxin accumulation and in turn provide for broad and effective cumulative resistance. The objective of this study was to identify quantitative trait loci (QTL) associated with FHB in the native soft red winter (SRW) wheat cultivar Jamestown. A total of 186 $F_{5:7}$ recombinant inbred lines (RILs) derived from a cross of Pioneer 25R47 / Jamestown (P47/JT) were evaluated for FHB incidence, FHB severity, FHB index, *Fusarium* damaged kernels (FDK) and DON concentration for two years in three environments (MD, NC, and VA). Both public and proprietary single nucleotide polymorphism (SNP) markers were used at Monsanto Company to initially genotype 42 of the P47/JT RILs having contrasting phenotypes for FHB. Subsequently, a set of 142 RILs were genotyped with public 90K SNP. Bulk segregant analysis was used to select microsatellite markers (SSRs) associated with FHB. Linkage maps were constructed using JoinMap. Windows Cartographer (WinQTLCart version 2.5) was used to identify possible QTLs. Six consistent QTL identified in P47/JT and located on chromosomes 1B, 3B, 5A, 5B, and 6A were associated with FHB incidence, FHB severity, FDK and DON content. The putative QTL on 1B and 6A were associated with resistance to FHB, whereas the putative QTL on 3B, 5A, and 5B were associated with susceptibility to FHB. The variation explained by putative FHB resistance QTL on 1B and 6A was 7% to 19.5% (Additive = -0.3 to -7.4) and 7.2% to 14.7% (Additive = -0.8 to -6.0). The most diagnostic marker for the QTL on 1B was *WMC500*; flanked by *GWM18* and *GWM273* (12.2 cM interval). The QTL on 6A was flanked by *Barc146* and *D_GBUVHFX01CSU22_382* (10.3 cM interval). These QTL are being validated in FG95195 / Jamestown and Jamestown / LA97113UC-124 mapping populations. Diagnostic markers for FHB resistance QTL in Jamestown would facilitate marker-assisted breeding.

IDENTIFICATION AND MAPPING OF QUANTITATIVE TRAIT LOCI FOR FUSARIUM HEAD BLIGHT RESISTANCE IN EMMER AND DURUM WHEAT

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ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum*, presently threatens durum wheat (*Triticum turgidum* subsp. *durum*) production in many durum-growing regions. It is critical to identify useful sources of FHB resistance for durum wheat. A domesticated emmer wheat (*T. turgidum* subsp. *dicoccum*) accession, PI 41025, was previously shown to be moderately resistant to FHB. This study was undertaken to identify quantitative trait loci (QTL) associated with FHB resistance in PI 41025. A population of 200 recombinant inbred lines developed from a cross between the durum variety 'Ben' and PI 41025 was evaluated for reaction to *F. graminearum* in one field and three greenhouse environments. The disease severity data and a single nucleotide polymorphism marker-based linkage map from this population were used for QTL analysis. The results showed that a QTL on chromosome 2A derived from Ben and two QTL on 3A and 5A derived from PI 41025 were associated with FHB resistance. The 2A and 3A QTL were detected only in the greenhouse experiments and they each explained 8% of the phenotypic variation. The QTL on 5A, which mapped very close to the domestication gene *Q*, explained 11% and 35% of phenotypic variation in greenhouse and field evaluations, respectively. The identification of the 2A QTL from Ben confirmed the presence of FHB resistance in North Dakota durum cultivars, which have been successfully used for developing new varieties with improved FHB tolerance. This study indicates that combining the QTL from related tetraploid species with native durum QTL will be useful for improving FHB resistance in durum wheat.

ACKNOWLEDGEMENT AND DISCLAIMER

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MOLECULAR MAPPING OF FUSARIUM HEAD BLIGHT RESISTANCE IN ND2710

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ABSTRACT

ND2710 is a hard red spring wheat line developed by NDSU wheat breeding program with a very high level of resistance to Fusarium head blight (FHB). It was selected from the progeny of a cross between ND2603 (an advanced breeding line derived from the Sumai 3/Wheaton cross) and Grandin. Therefore, the FHB resistance of ND2710 is presumably derived from Sumai 3 since both Grandin and Wheaton are very susceptible to FHB. To identify and map the quantitative trait loci (QTL) for FHB resistance in ND2710, we developed a mapping population consisting of 233 recombinant inbred lines (RILs) from a cross between ND2710 and the CIMMYT spring wheat 'Bobwhite'. These RILs along with their parents and checks were evaluated for reactions to FHB in four greenhouse seasons and two field locations in 2013 and 2014. A linkage map was developed for this population using 747 SNP markers, which were distributed on 19 of the 21 wheat chromosomes spanning 1,716 cM of genetic distance. Further analyses using both phenotype and genotype data identified one major QTL on chromosome 3BS, explaining up to 27.3% of FHB severity variation in all experiments, and minor QTLs on 2A, 2B, 6A, and 6B explaining up to 10% phenotypic variation in at least two experiments. The QTL on 3BS and 6B were mapped to the same genomic regions as those harboring *Fhb1* and *Fhb2* in Sumai 3 or its derivatives. Plant maturity was not associated with FHB resistance. Three SSR markers (*Xgwm533*, *Xgwm493*, and UMN10) were also mapped to the 3BS QTL region saturated with SNP markers. These SNP markers will be further validated and used for marker-assisted selection of *Fhb1* in wheat breeding programs.

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EFFECTS OF DURUM WHEAT BACKGROUND ON THE EXPRESSION OF HEXAPLOID WHEAT-DERIVED FUSARIUM HEAD BLIGHT RESISTANCE GENES

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ABSTRACT

Multiple Fusarium head blight (FHB) resistance sources have been identified in common wheat, but an effective source of resistance to FHB has not been found in durum wheat. Significant efforts have been made toward introgression of FHB resistance from hexaploid wheat to durum wheat. However, progress has been limited due to complex inheritance patterns of the hexaploid wheat-derived FHB resistance in durum background. Here we report preliminary results on the effects of durum background on the expression of hexaploid wheat-derived FHB resistance genes. Two highly FHB-resistant hexaploid spring wheat accessions, Sumai 3 and PI 277012, were crossed to the durum cultivars 'Langdon' (LDN), 'Divide', 'Grenora', 'Alkabo', and LDN-Chinese Spring (CS) D genome substitution lines where a pair of homologous LDN A- or B-genome chromosomes were substituted by their homoeologous counterparts in CS D genome. Also, Sumai 3 was crossed to four FHB-susceptible hexaploid wheat accessions ('2398', 'Choteau', 'AC Vista', and 'AC Lillian'). All F_1's of Sumai 3 with durum exhibited a resistance level similar as or lower than their durum parents, whereas F_1's of Sumai 3 with hexaploids exhibited a resistance level intermediate to their parents. Apparently, FHB resistance genes in Sumai 3, including *Fhb1*, were normally expressed in the F_1's with hexaploids, but not in the F_1's with durum. The F_1's of PI 277012 with durum all exhibited a resistance level comparable to PI 277012, indicating complete dominance of the resistance genes in PI 277012 over the susceptible alleles in durum. Individual homoeologous substitution of D-genome chromosomes for LDN durum chromosomes 2B, 3A, 3B, 4A, 4B, 5B, 6A, 6B, and 7A all augmented resistance levels of the F_1's between Sumai 3 and the LDN D genome substitution lines, suggesting these durum chromosomes may contain genes that suppress expression of the Sumai 3-derived FHB resistance genes in the F_1's. Individual substitution of LDN durum chromosomes 4A, 6A, and 6B by their D-genome homoeologs lowered resistance levels in the F_1's of PI 277012 with the LDN D genome substitution lines, whereas individual substitution of other LDN durum chromosomes did not significantly change resistance levels of their F_1's. This suggests that LDN chromosomes 4A, 6A, and 6B may contain genetic factors required for the expression of the PI 277012-derived FHB resistance genes in the F_1's. A wide range of segregation on FHB severity (10-90%) was observed in the F_2 generation from the crosses of Sumai 3 with durum LDN and Divide. The F_3 families derived from the most resistant F_2 segregants segregated toward more susceptible end. A similar segregation trend as the F_3 families was observed in the F_4 generation. We hardly found individuals with significantly higher levels of resistance than their durum parents in the F_4 generation. In the crosses of PI 277012 with durum, resistance also seemed to be slightly diluting over generations, but multiple resistant segregants were recovered in each generation of these crosses. Thereby, durum wheat contains multiple genetic factors on different chromosomes that positively and/or negatively

regulate expression of hexaploid wheat-derived FHB resistance genes. This has made FHB resistance introgression from hexaploids into durum a challenging task.

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