

PI: James Anderson

PI's E-mail: ander319@umn.edu

Project ID: FY17-SP-004

ARS Agreement #: 59-0206-4-019

Research Category: VDHR-SPR

Duration of Award: 1 Year

Project Title: Using Targeted Sequencing to Breed for Fusarium Head Blight Resistant Wheat.

PROJECT 3 ABSTRACT

(1 Page Limit)

The availability of lower cost, high-throughput genotyping technologies in wheat has allowed breeders to include more marker-based technologies to increase the efficiency of selection. This technology has enabled the expansion of marker-assisted plant breeding from targeting a handful of traits under the control of genes/QTL with large effects to evaluating complex trait performance and G x E interactions by estimating genetic effects of many marker loci across the entire genomes, known as genome-wide or genomic selection (GS). To assist spring wheat breeding for improving disease resistance against Fusarium head blight (FHB) using genomic selection strategies, proper sequencing-based genotyping methods need to be evaluated and implemented. The main objective of this project is to explore and evaluate a targeted sequencing approach that is expected to reduce the genotyping cost to ~\$10/sample for spring wheat breeding efforts. The USDA-ARS Fargo genotyping lab will collaborate with the three public spring wheat breeding programs in MN, ND, and SD to carry out targeted sequencing by enriching several thousand genome-wide targets using a sequence capture method. The targeted regions will be selected based on previous results using wheat 9K and 90K SNP arrays, such as the spring wheat elite panels genotyped under Triticeae CAP, with an emphasis on those that were polymorphic among spring wheat germplasm. The evenness of marker distribution in the wheat genomes will also be taken into consideration. The D-genome SNPs under-represented in the SNP arrays will be supplemented with those discovered from Genotyping-By-Sequencing performed by the MN breeding program. In addition, markers tightly linked to the genes/QTLs that are routinely used for marker-assisted breeding, including resistance to FHB and other diseases, grain quality, plant height, and photoperiod/vernalization, will also be included in the final targeted set. The outcome of this research, when implemented, would allow spring wheat breeding programs to obtain genotype data from more breeding lines at an affordable cost, and benefit the breeding process for developing cultivars with better FHB resistance. A total of 1,685 U of MN F₅ lines (the same cohort used for USWBSI-funded GS) plus 65 parents will be subjected to this targeted sequencing approach. The NDSU and SDSU programs will each have 600 lines genotyped and subjected to Association Mapping analysis to discover FHB resistance QTLs. Genomic selection models using different combinations of lines from the 3 breeding programs will be evaluated for their ability to predict the FHB reaction of other lines. The efficiency and effectiveness of this targeted sequencing approach for GS will be based on its ability to predict line performance, cost in terms of consumables and personnel time versus the MAS/GS procedures we are currently investigating.