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Project ID: FY14-BA-007   **ARS Agreement #:** 59-0206-4-020

Research Category: BAR-CP   **Duration of Award:** 1 Year

Project Title: Genomic Selection for FHB Resistance in Midwest Barley.

PROJECT 2 ABSTRACT
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Genomic selection (GS) is a promising new approach to marker assisted selection that uses large DNA marker and trait data sets to calibrate models that are used to predict the performance of breeding lines that have not undergone phenotypic evaluation. GS predicted genetic values of breeding lines can be used to select parents in early generations substantially shortening the breeding cycle from the four years that it typically takes with phenotypic selection to a single year. Given the relatively low heritability of FHB severity and DON concentration and the high cost of phenotyping these and other important traits, GS should be useful to accelerate efforts to breed resistance to FHB. The overall goal of this project will be to conduct two cycles of GS within the two year funding cycle to generate breeding lines that will be available for testing in the springs of 2015 and 2016. The major tasks to be carried out will be crossing of selected parents, advancing populations to the F2 and F3 generations, and GS prediction of breeding values. In the prior funding periods, we have carried out four cycles of genomic selection in spring six-row breeding germplasm. In this funding period we will carry out cycles 5 and 6 in our spring six-row program and initiate GS in our new spring two-row program. Approximately 3,000 F3 plants will be grown in the greenhouse in the fall of 2014, genotyped using genotyping-by-sequencing to generate marker that will be used to make GS model predictions to select parents. The GS model will be developed using previously collected marker and phenotypic data from breeding lines that were part of the Barley Coordinated Agricultural Project (CAP) as well as data from previous cycles of selection in our breeding program. Predicted values for DON, yield, height, heading date, and major malting quality traits (malt extract, grain protein, ratio of soluble to total protein, diastatic power, alpha amylase activity, and wort beta-glucan) will be used to select superior parents for crossing. Crosses among these F2 plants will be made in the 2014 fall greenhouse. These populations will be advanced to the F1 in the winter 2013 greenhouse, F2 in the summer of 2015, and F3 in the fall of 2015 where the model prediction and parent selection will be carried out for the sixth and second cycles of selection for six-row and two-row, respectively. Since parents and training data sets are being collected in collaboration with the NDSU breeding program, lines developed from this project will be shared with NDSU for evaluation. In addition, a set of 50 randomly selected and GS selected breeding lines in each cycle of selection will be advanced and evaluated to measure the effectiveness of this GS project and gain from selection over time. The specific objectives for this project are to (1) generate data sets to be used in GS model training; (2) make selections based on GS predictions; and (3) carry out experiments to assess prediction accuracy and gain from selection. Making crosses, advancing lines after selection and all subsequent evaluation of breeding lines is covered by our breeding project (see Developing Malting Barley Varieties with FHB Resistance and Low DON). This research should generate elite breeding lines that combine favorable alleles for disease resistance, agronomic performance, and malting quality as well as describe the effectiveness of genomic selection to improve FHB resistance in malting barley.