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ARS Agreement #: *New (59-0206-4-020 is in 5th year)*

Research Category: BAR-CP

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Project Title: Developing and Testing Genome-Wide Marker Methods to Optimize Prediction Accuracy

PROJECT 2 ABSTRACT

(1 Page Limit)

Genomic selection is becoming a routine way to use markers in breeding programs. It takes advantage of the ability to genotype many markers across the genome and use them to predict performance for quantitative traits. Genetic mapping studies in barley indicate that FHB resistance is controlled by many loci of which most have small effects and thus is amenable to genomic selection. The overall goal of this research is to continue to improve and optimize the ways that we use genome-wide markers in breeding for FHB resistance. To date, we have evaluated different approaches to using and optimizing various aspects of genomic selection (Sallam et al., 2014; Sallam and Smith, 2015, Tiede et al., 2016). In particular, we have demonstrated the importance of using training populations that are genetically related to selection candidates (Lorenz and Smith, 2015). Simulation studies conducted by our group have shown that updating the training population with recent high performing breeding lines should be an effective way to maintain genetic gain over subsequent cycles of selection (Neyhart et al., 2017). These and other studies have provided important insights to designing breeding strategies that utilize genomic selection. We are now interested in ways to use genome-wide markers to improve FHB resistance in wide crosses designed to exploit FHB resistance in six-rows to improve resistance in two-rows. Since (1) we have made progress in improving resistance in six-rows, (2) FHB resistance appears to be controlled by different loci in six- and two-row barley, and (3) the industry is increasingly interested in two-row, we would like to efficiently exploit resistance in six-rows to improve resistance in two-row barley. Our specific objectives are continue our work to: 1. Evaluate parent selection based on genome-wide marker effects to increase genetic variance and reduce unfavorable trait correlations; and initiate new work to 2. Map FHB resistance and DON accumulation in elite two-row by six-row crosses and 3. Introgress six-row resistance into two-row barley using genome-wide markers. We will utilize marker and trait data sets from historical and current breeding germplasm to develop and test different approaches to design parent combinations and select among progeny to improve disease resistance and reduce unfavorable linkages. We will generate data on new populations to validate our prediction models. This work will consist of an iterative process of selecting parent combinations and generating progeny populations informed by genome-wide markers, evaluating selected germplasm in the field, and assessing the effectiveness of the selection methodology. We will carry out this iterative process over a five year period drawing conclusions about the effectiveness of selection methodologies annually. Results of this work should accelerate the development of new varieties and provide information about breeding methods that could be adopted by other wheat and/or barley breeders.