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PROJECT 2 ABSTRACT

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Funded in part by USWBSI, we are currently training a genomic selection (GS) model using our advanced breeding lines to predict FHB reaction of other breeding lines, including F₅ lines – the generation in which we typically screen 2,000 lines in two FHB field nurseries and discard 30-50% based on their FHB reaction. However, the advanced lines and the F₅ lines, our targets for implementation of GS, differ in several aspects, most notably their genetic relatedness to a particular cohort of F₅ lines.

In this proposal we aim to explore alternative genomic selection training populations that may perform better. Specifically, we aim to test the hypotheses that 1) GS models trained using a subset of F₅ lines will have a higher prediction accuracy in predicting F₅ FHB resistance compared to models trained using advanced lines; 2) optimal selection of training populations and marker compositions will increase our FHB GS prediction accuracies and help achieve desired training population sizes. Our expected outcomes are:

1. The GS accuracies using F₅ lines to predict F₅ lines are higher compared to using advanced lines.
2. The GS accuracies could be improved by incorporating training population design methods; the required training population sizes could also be reduced.
3. The combined use of target markers and genome wide markers will further improve prediction accuracies.

We will collect genotypic and phenotypic data on 500 lines, a representative subset of our F₅ lines, in each of 2015, 2016, and 2017. GBS will be used as the genotyping platform. The 500 F₅ lines will be phenotyped for FHB traits in two inoculated, misted nurseries. Comparison of the prediction accuracy of this model and the model from our current project will help to optimize the size and composition of the training population. In addition to testing the efficacy of different training models, we will also investigate the predictive ability of selection models that use 1) only targeted QTL (*Fhb1*, 5AS, plus other QTL detected using Association Mapping from our 384-member training population); 2) genome wide markers; or 3) some combination of the two methodologies. The results of this research will determine the genomic selection procedure to be utilized in our breeding program and should inform other breeding programs considering implementing genomic selection for FHB resistance.