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Project Title: Optimization of Training Population Content and Size for Genomic Selection for FHB

PROJECT 2 ABSTRACT

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Genomic (or Genomewide) selection is showing good potential to reduce phenotyping costs and improve efficiency of selection for Fusarium head blight resistance (FHB) in wheat. This proposal represents the 3rd iteration of our genomic selection investigations to select for FHB resistance in spring wheat. Following the results from our previous USWBSI-funded research, we have implemented GS at the F₅ (pre-yield trial) stage in our breeding program. The goal at this stage of selection is to identify and eliminate lines that are highly susceptible to FHB prior to entering them in yield trials. Any lines advanced to the preliminary yield trial stage or later will continue to undergo phenotypic assessment of FHB reaction in two misted, inoculated nurseries on an annual basis. The next frontier of this research is to further optimize training population content and size. New algorithms are being developed to select the best, smallest set of training population members by using their genotypic profiles instead of only pedigree information. Our hypothesis is that a training population of 200 (or fewer) lines, selected based on genotypic relationships, will be as effective as our current training population of 500 F₅ lines, selected based on pedigree relationships.

We will genotype our entire 2018 cohort of ~2,500 F₅'s using high-throughput sequencing. A training population of 200 lines will be selected based on genotypic information alone and supplemented with an additional 300 lines selected to complement the pedigrees of the selected lines. The 500 F₅ lines will be phenotyped for FHB traits in two inoculated, misted nurseries. Two replications of the subset of 200 genotypically chosen lines and one replication of the 300 lines chosen by pedigree will be phenotyped at each location. Known QTLs segregating in our germplasm, including *Fhb1* and *Fhb5* (5AS) will be included as fixed effects in the evaluation of various genomic selection models.

Comparison of the prediction accuracy of models based on 100, 150 (subsets of the 200 chosen based on genotype), 200, and 500 lines will be calculated following phenotyping of ~500 selected preliminary yield trial lines that are selected from the set of F₅'s. This process will be repeated with the 2019 and 2020 F₅ cohorts. In addition to prediction accuracy, minimizing the proportion of highly susceptible lines selected for advancement to preliminary yield trials is an important metric in comparing the efficacy of the different training populations.