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PROJECT 5 ABSTRACT
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Genomic selection (GS) is a new technology that uses genome wide marker selection to select nearly all the genes that affect FHB resistance, including those with small effects. Genomic selection uses a training population of lines that is phenotyped and genotyped. A prediction model is built using the phenotypic and genotypic data from the training population. That model can then be used to predict the value of other genotyped individuals that are related to the training population even without phenotyping those individuals.

Objectives:
1. To implement GS for FHB resistance in soft winter wheat by completing two cycles of GS.
2. Initiate evaluation of the effectiveness of GS for FHB.

Over the past three years we have phenotyped a training population of 649 lines. This includes 600 RILs (100 from each of six breeding programs, each phenotyped at the breeder's location only) and 49 checks (phenotyped by all six breeders at all locations and years). We have planted the best lines from the training population, have made crosses among them and planted F2 seed in August of 2014. We genotyped 940 F2s using genotyping-by-sequencing (GBS) at the Institute for Genomic Diversity (Cornell University). The best F2 plants at each location were crossed to generate F1s in December/January of 2014/2015. That will complete the first cycle of GS. The 10 best, 10 worst, and 10 random F2 plants will also be selfed to produce 30 F2:3 populations. This was repeated for two cycles and are now being evaluated in the 2015-16 FHB nursery.