

Use of Predictive Models Based on Genomic Information to Estimate Fusarium Head Blight Traits in Soft Red Winter Wheat

Virginia L. Verges and David A. Van Sanford—Department of Plant and Soil Sciences
University of Kentucky, Lexington, KY 40546
PH: (859) 338-2409; Email: dvs@uky.edu

Fusarium head blight (FHB) or head scab is a devastating disease of wheat and barley in Kentucky and around the world. Resistance is based on many genes and the disease can be technically difficult to reproduce, so breeding for resistance in wheat is costly and slow. You need 2-3 cycles of evaluation under the right conditions, so we have to reproduce an epidemic every year in the field. In recent years, many predictive models have been developed by researchers to estimate the value of different traits. These models give us Genomic Estimated Breeding Values (GEBVs). Numerous studies demonstrate the value of genomic selection in breeding for disease resistance in crops. In our recent study, 4-5 years of data from the Uniform Northern and Uniform Southern soft red winter wheat scab nurseries were used as training populations to predict scab traits in breeding lines of the UK wheat breeding program. DON (vomitoxin) content was best predicted by the southern nursery; FDK (Fusarium damaged kernels), and FHB rating, were best predicted by the northern. Prediction accuracy is estimated by the correlation between the actual data we take annually in the field, and the predicted values generated by the model. The highest prediction accuracies were obtained when the northern and southern nurseries were combined, reaching a correlation of 0.5 for most traits. Now we are trying to reduce the number of DNA markers used, to reduce genotyping costs. So far, our results are promising, with accuracies of 60 to 80% in the correlations between field results and predicted values. The use of historical data from regional nurseries, as our results confirm, offers breeders an excellent tool to estimate GEBVs for lines that have not yet been evaluated in the field. This reduces field costs tremendously because the training population data set is generated by a collaborative effort among many breeders. This allows us to discard susceptible lines in early generations and reallocate the budget for DON analysis of more advanced breeding lines. Our study shows with a prediction accuracy of 0.5, 50 to 70% of the lines are correctly selected using genomic predictions. In early stages of field-testing, when the breeder has thousands of lines for yield evaluation, the ability to select based on predictions for DON is a valuable tool when scab resistance is a critical objective in the breeding program. This means that we only take lines with an acceptable level of scab resistance to the field for yield testing.

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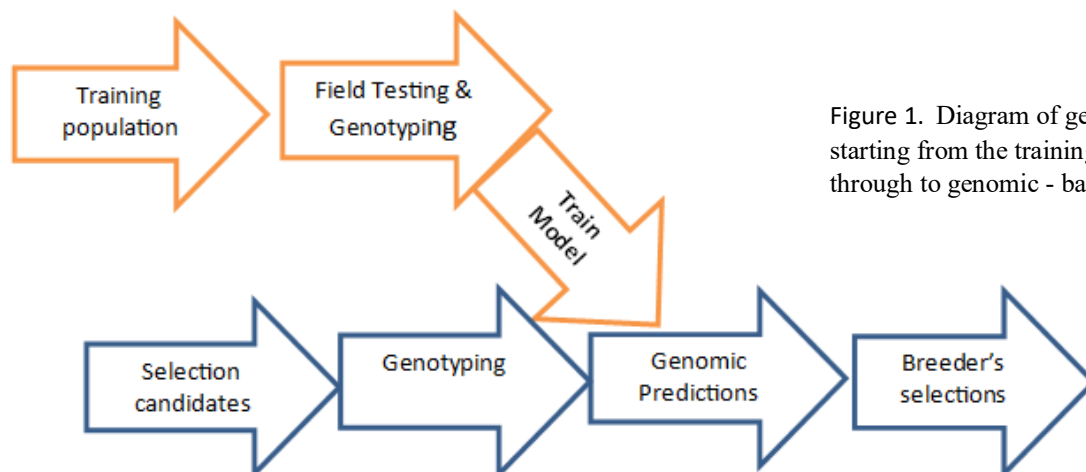


Figure 1. Diagram of genomic selection processes starting from the training population continuing through to genomic - based selection.