Statistics Improves Effectiveness of Genomic Selection in Plant Breeding

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Abstract: The genomic revolution opened up the possibility for predicting un-tested phenotypes in schemes commonly referred as genomic selection (GS). Considering the practicality of applying GS in the line development stage of a hard red winter (HRW) wheat variety development program (VDP), effectiveness of GS was evaluated by prediction accuracy, as well as by the response to selection across field seasons that demonstrated challenges for crop improvement under significant climate variability. Important breeding targets for HRW wheat improvement in the southern Great Plains of USA, including Grain Yield, Kernel Weight, Wheat Protein content, and Sodium Dodecyl Sulfate (SDS) Sedimentation Volume as a rapid test for predicting breadmaking quality, were used to estimate GS's effectiveness across harvest years from 2014 (drought) to 2016 (normal). In general, nonparametric algorithms RKHS and RF produced higher accuracies in both same-year/environment cross validations and cross-year/environment predictions, for the purpose of line selection in this bi-parental doubled haploid (DH) population. Further, the stability of GS performance was greatest for SDS Sedimentation Volume but least for Wheat Protein content. To ensure long-term genetic gain, our study on selection response suggested that across this sample of environmental variability, and though there are cases where phenotypic selection (PS) might be still preferential, training conducted under drought stress or in suboptimal conditions could still provide an encouraging prediction outcome, when selection decisions were made in normal conditions. However, it is not advisable to use training information collected from a normal field season to predict trait performance under drought conditions. Further, the superiority of response to selection was most evident if the training population can be optimized.