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Comparison of genomic prediction models for different heritable traits in soybean

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Genomic Selection (GS) is an important plant breeding tool that utilizes genome-wide markers to predict the breeding value (BV) of complex traits. Efficiency of GS depends on the prediction accuracy (PA) of model to predict performance of individuals. In this study, we compared a number of statistical models for PA and computational time using three different soybean traits that differed in heritability (H) including oxygen isotope ratio ($\delta18O$) (H = 20%), carbon isotope ratio ($\delta13C$) (H = 60%), and canopy wilting (CW) (H = 80%). We also compared the PA of models using three sets of markers including a complete set and two subsets of markers consisting of significant markers at P-values of < 0.1 and < 0.05. Correlation between observed and the cross-validated BVs (10-fold, 30-fold, and 50-fold cross-validations) was used to assess the predictive ability of the models. We observed similar accuracies for all models, but BayesA, BayesB, and BayesC had higher accuracies than most other models, and some models had very short computational times. Prediction accuracy was high for traits with high (CW) and moderate ($\delta13C$) heritability and was extremely low or negative for a trait with low heritability ($\delta18O$). Accuracy of all models for all traits was increased when a subset of significant markers was used compared with the accuracy obtained when all markers were used. For example, PA increased from -0.17 to 0.40 for $\delta18O$ when a subset of significant markers ($P < 0.05$) were used compared to PA when the full marker set was used.