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## The Prediction Ability of Genomic Selection in the Wheat Core Collection

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### [Abstract]

Genome selection is a promising tool for plant and animal breeding, which uses genome-wide molecular marker data to capture large and small effect quantitative trait loci and predict the genetic value of selection candidates. Genomic selection has been shown previously to have higher prediction accuracies than conventional marker-assisted selection (MAS) for quantitative traits. In this study, the prediction accuracy of 10 agricultural traits in the wheat core group with 567 points was compared. We used a cross-validation approach to train and validate prediction accuracy to evaluate the effects of training population size and training model. As for the prediction accuracy according to the model, the prediction accuracy of 0.4 or more was evaluated except for the SVN model among the 6 models (GBLUP, LASSO, BayseA, RKHS, SVN, RF) used in most all traits. For traits such as days to heading and days to maturity, the prediction accuracy was very high, over 0.8. As for the prediction accuracy according to the training group, the prediction accuracy increased as the number of training groups increased in all traits. It was confirmed that the prediction accuracy was different in the training population according to the genetic composition regardless of the number. All training models were verified through 5-fold cross-validation. To verify the prediction ability of the training population of the wheat core collection, we compared the actual phenotype and genomic estimated breeding value using 35 breeding population. In fact, out of 10 individuals with the fastest days to heading, 5 individuals were selected through genomic selection, and 6 individuals were selected through genomic selection out of the 10 individuals with the slowest days to heading. Therefore, we confirmed the possibility of selecting individuals according to traits with only the genotype for a shorter period of time through genomic selection.

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