

Incorporation of environmental variables in genomic selection models for oat grain yield

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This study examined environmental and genomic factors, along with their interactions, that contributed to variation in yield data measured in an unbalanced set of 305 Western Canadian oat lines grown from 2002-2014.

Firstly, influential environmental variables and correlated agronomic traits affecting oat grain yield were investigated. Using environmental variables, days to heading, days to maturity and plant height, a structural equation model was built to explain the phenotypic variation (55%-75%) for grain yield among three oat varieties grown at multi-locations over 12 years.

Secondly, genomic selection was performed for yield using GBS genotypic data and best linear unbiased predictor (BLUP) calculated phenotypes. Various models, including RR-BLUP, Bayes B, BGLR, SVM, Random Forest and neural network, were evaluated for yield, as were the influence of marker density, training population size and trait heritability.

In the final set of analyses, genotype and environment interaction were used to conduct genomic selection for yield using the R package BGLR. Three mega-environments were identified from Ward's hierarchical clustering using the significant environmental variables identified in the first study. Using mega-environments (280 lines and 3 mega-environments with balanced data in each environment) offered better prediction accuracy than using individual locations (161 lines and 5 locations with balanced data in each environment). The reaction norm model (161 lines and 58 environments with unbalanced data in each environment) was also tested so significant environmental variables could be incorporated as a covariance matrix in the model. It was found that including an environmental covariance matrix and interaction terms increased prediction accuracy compared to models with only main effects for lines and environment.