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Analysis of training population effects on genomic selection in Brassica napus L.

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Canola is produced on 34.74 ha of land globally and is one of the most important oilseed crops in the world. As the world population grows, it is critical that plant breeders accelerate crop genetic gains using new breeding methods. Currently on the Western Prairies of Canada, more than 95% of the area sown to canola is composed of hybrid canola cultivars. Discovering an efficient method to identify the best parental combinations to produce superior hybrids is vital in canola breeding. Genomic selection (GS) has become a promising tool and has been used in maize, wheat, barley, rice, and canola breeding. In this study, GS was applied in predicting the best combinations of B line and R line as parents to produce superior hybrids.

The training population (TP) for GS consisted of 92 parents, including 31 B lines (maintainers) and 61 R lines (restorers) within the ogu INRA CMS pollination control system. The TP was phenotyped in the 2016-2018 field seasons at four locations across Southern Manitoba, Canada for both agronomic traits and seed quality traits. The TP was genotyped using the Brassica 60K Illumina Infinium™ SNP array, identifying 11,083 markers that were used to determine relatedness within the TP. Data analysis was conducted using rrBLUP and GAPIT in RStudio (v. 1.1.456) and Tassel 5.0 (v.20181219).

The results revealed large variation in the prediction accuracy depending upon the trait of interest. Mean accuracy could be manipulated with different marker filtration criteria as well as marker density. Mean accuracy improved from 0.49 to 0.58 for plant height (PHT), 0.34 to 0.43 for seed yield (YLD), 0.32 to 0.37 for oil content (OC), and 0.30 to 0.40 for glucosinolates content (GLUC) when appropriate marker filtration was applied (500 iterations of cross-validation). The assignment of training set and validation set within the TP could also affect mean accuracy, especially in a case when the training population has a limited number of individuals. In addition, association analysis results revealed certain markers located on chromosome 19 (C9) were tightly associated with PHT, YLD and GLUC, which requires further effort to confirm and validate.