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Phenomic selection: predicting quantitative traits in canola with NIRS-profiles

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Background:

Phenomic selection is a promising potential alternative to genomic selection in plant breeding. Phenomic selection uses non-destructive, high-throughput phenotyping methods like near-infrared reflectance spectroscopy (NIRS) to obtain predictors for various traits, making it considerably more cost-effective than genomic selection, particularly in canola/rapeseed breeding where NIRS data is already routinely generated for seed quality analysis. Potentially it can be used as a universally applicable tool in a wide range of different crops. However, since this is a very young field of breeding research, most publications to date were limited to cereals.

Objective:

Here, we applied phenomic prediction to canola test-hybrids generated by crossings of a microNAM-population with two different male-sterile inbred lines. The objective was to evaluate the prediction performance for different quantitative traits collected at five different locations over two years. Different phenomic prediction scenarios were compared to SNP-based genomic selection. Additionally, the predictive ability of a multi-omics approach using a combination of both SNP and NIRS profiles was tested.

Methods:

Genomic and phenomic predictions were conducted with linear and machine learning models including ridge regression BLUP, Bayesian LASSO, RKHS regression, random forest and support vector machine. NIRS profiles used for prediction of hybrid yield, plant height and flowering time were obtained from F2 seeds harvested from open-pollinated F1 hybrids. In a family-wise cross validation, the impact of population structure on prediction accuracy was assessed. Furthermore, NIRS profiles of seeds from parental lines were used to predict hybrid traits.

Results:

Predictive ability of NIRS profiles obtained from F2 seeds exceeded the accuracy of SNP-based genomic predictions for seed yield and plant height. Combining SNP and NIRS predictors in a multi-omics approach resulted in even higher accuracies. In the family-wise prediction scenario, phenomic prediction outperformed genomic prediction for all tested traits. Phenomic prediction from NIRS spectra of parental seed samples showed a similar level of accuracy to SNP-based predictions.

Conclusions:

Phenomic selection based on NIRS profiles could serve as a low-cost and high-throughput alternative to genomic selection. Moreover, it seems to be less influenced by population structure than SNP-based predictions. For canola breeding the required NIRS data is often already routinely collected in order to determine qualitative seed characteristics. Hence, phenomic selection has a high potential to improve ongoing genomic selection programs without additional cost or effort.