

Genomic prediction of wheat quality traits in advanced breeding lines

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INTRODUCTION

Genomic prediction of wheat quality traits can be important in breeding programs to reduce the resources needed for phenotyping and enable selection of lines at early stages. Here, two types of genomic prediction models are compared, and their predictive abilities are evaluated using different cross-validation strategies.

MATERIALS AND METHODS

F₆ grain from single plots of 635 winter wheat (*Triticum aestivum* L.) lines from two breeding cycles of the Danish plant breeding company Nordic Seed A/S were phenotyped for five quality traits. A total of 10,802 informative SNPs were used for GWAS by single marker regression. Genomic predictions were done using GBLUP (Genomic Best Linear Unbiased Prediction) and Bayesian Power Lasso models with all SNPs.

RESULTS AND DISCUSSION

Phenotypic variation was observed for all five quality traits, and all traits had high narrow sense heritabilities (Table 1).

Table 1. Mean, range, coefficient of variation (CV), and narrow sense heritability (h²).

Phenotype	Mean	Range	CV (%)	h ²
Grain protein content (%)	8.7	7.5 – 10.9	6.4	0.56
Zeleny sedimentation (mL)	18.3	8.0 – 36.0	26.9	0.78
Test weight (kg/hL)	78.7	73.4 – 83.7	2.2	0.81
Thousand-kernel weight (g)	53.7	40.8-63.0	6.0	0.81
Falling number (s)	254.7	79.0-391.0	23.4	0.75

The correlations between observed phenotypes and GEBVs based on the GBLUP models ranged from 0.50 for grain protein content to 0.79 for Zeleny sedimentation using Leave-One-Out cross-validations (Fig. 1). The other types of cross-validations resulted in lower correlations due to a combination of smaller training sets, lower genetic relationship between lines in training and validation sets, and GxE interactions.

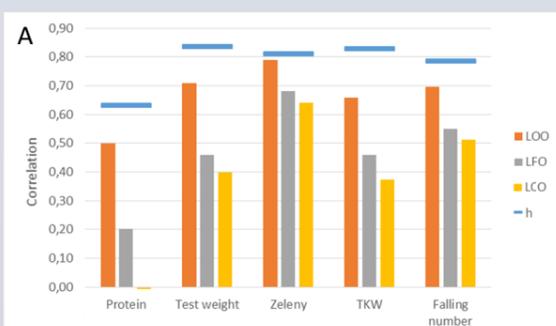


Figure 1. Correlations between observed phenotypes corrected for fixed effects and GEBVs based on GBLUP models.

Maximum correlation, h, is the square root of the narrow sense heritability and is shown as blue bars over the correlations. Correlations are based on different kinds of cross-validations:

A: LOO: Leave-One-Out, LFO: Leave-Family-Out, LCO: Leave-Cycle-Out.

B: 10-, 5-, and 2-fold cross-validations.



Grain protein content seems to be the most difficult of the traits to predict, especially across breeding cycles. It is strongly influenced by environmental effects and GxE interactions, and the GWAS indicated that grain protein content is controlled by many QTL with small effects, since no significant SNPs were found for this trait.

Zeleny sedimentation

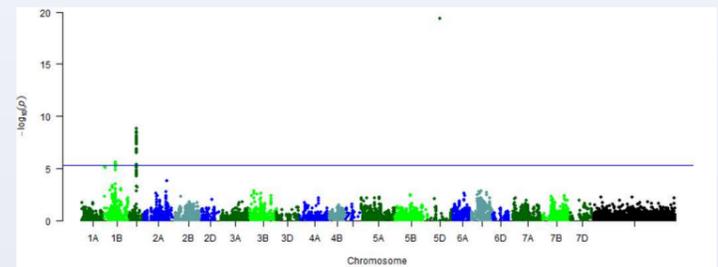


Figure 2. Manhattan plots of $-\log_{10}(p\text{-values})$. Last bin is unmapped SNPs.

SNPs significantly associated with Zeleny sedimentation were identified on chromosomes 1B, 1D, and 5D (Fig. 2). No SNPs were significantly associated with the other quality traits.

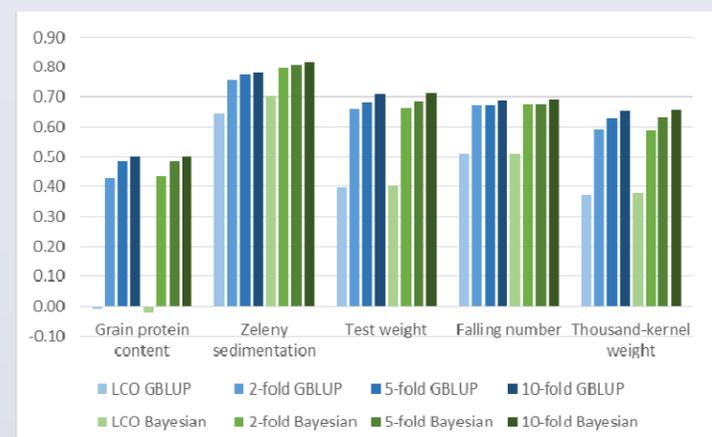


Figure 3. Comparison of predictive abilities based on GBLUP and Bayesian Power Lasso models. Predictive abilities are presented as correlations between phenotypes corrected for fixed effects and GEBVs. Cross-validations: LCO: Leave-Cycle-Out, and k-fold.

Bayesian Power Lasso models allow stronger shrinkage of small SNP effects and weaker shrinkage of large SNP effects than GBLUP models, so the genetic architecture might be modelled more realistically for some traits. Here, Bayesian Power Lasso and GBLUP models resulted in very similar predictive abilities (Fig. 3). Zeleny sedimentation was the only trait, where individual SNPs had a large effect, and for this trait, predictions improved slightly with the Bayesian Power Lasso.

CONCLUSIONS

Genomic prediction appears to be a promising strategy for improving wheat quality traits. Predictions were most accurate for Zeleny sedimentation and least for grain protein content. Bayesian Power Lasso models might improve predictive abilities compared to GBLUP models for traits controlled by SNPs with large effects.

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