Genomic prediction in a Finnish breeding programme of six-row barley

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Introduction

Genomic selection has the potential to accelerate genetic gain and to reduce phenotyping costs in commercial breeding programmes. Barley (*Hordeum vulgare* L.) is the most important field crop in Finland and accounts for about 50% of the country's grain harvest with a production of more than 1.5 million tons per year.

In this study, we evaluated accuracy of genomic prediction in field trial data of a commercial breeding programme of six-row barley.

Data

- In total, 1934 double-haploid and single-seed-descent lines representing 333 crosses (on average 5.8 lines/cross) phenotyped in 116 field trials across Finland 2007-2013
- 1124 lines in training population
- Two validation sets representing young crosses derived mainly from the training population:
  1. 429 early variety lines
  2. 381 late variety lines
- Genotype information for 5821 SNPs after editing

Prediction methods

- Two genomic evaluation models
  - multi-trait GBLUP
  - single-trait BayesB
- Non-genomic evaluation model
  - multi-trait BLUP with pedigree-based relationship matrix

Lines were evaluated for total yield, time to ripening and grain protein content. Total yield was subdivided into three traits according to three different types of environment based on growing zone (Fig. 1) and soil type.

Accuracy of genomic estimated breeding values (GEBV) and estimated breeding values (EBV) in validation lines was assessed by the correlation coefficient between GEBV/EBV and averaged phenotypic observations corrected for trial-specific effects.

Results

Heritabilities were between 0.30 and 0.45 for the three total yield traits, 0.57 for time to ripening and 0.64 for protein content. Pairwise genetic correlations were 0.82-0.91 among the three total yield traits, 0.48-0.71 between time to ripening and the total yield traits, and from -0.92 to -0.74 between protein content and the total yield traits.

Figure 1: Location of barley growing zones in Finland.

The validation correlations were calculated across lines from different crosses (r_{ac}) for genomic models and for pedigree-based BLUP (Table 1).

Model	Total yield*	Time to ripening	Protein content
GBLUP	0.31	0.52	0.62
BayesB	0.29	0.57	0.67
Pedigree BLUP	0.17	0.21	0.48

Table 1: Accuracy across lines from different crosses (r_{ac}) averaged across validation sets.
*Results for total yield averaged across growing zones and soil.

Correlations across lines within crosses (r_{wc}) were assessed only for the genomic models, as EBVs from pedigree-based BLUP are identical for lines from the same cross (Table 2).

Model	Total yield*	Time to ripening	Protein content
GBLUP	0.26	0.39	0.42
Bayes B	0.19	0.43	0.49

Table 2: Accuracy across lines within crosses (r_{wc}) averaged across validation sets and crosses. These correlations cannot be calculated for pedigree-based BLUP .
*Results for total yield averaged across growing zones and soil

Conclusions

The results indicate that genomic models predict future phenotypes better than pedigree-based BLUP. GBLUP performed slightly better than BayesB for total yield traits, whereas the opposite was found for the traits with higher heritabilities (protein content and time to ripening). As expected, there was some loss in accuracies, when the genomic breeding values were used to predict performance within crosses.

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