

GWAS and genomic prediction of baking quality in winter wheat

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INTRODUCTION

The aim of this study was to identify SNP markers associated with wheat baking quality traits, and to develop models for genomic prediction of the traits.

MATERIALS AND METHODS

A total of 635 F₆ winter wheat (*Triticum aestivum* L.) lines from two breeding cycles of the Danish plant breeding company Nordic Seed A/S were phenotyped for four quality traits at CIMMYT, Mexico. GWAS and genomic predictions were performed using 10,802 informative SNPs. Single marker regression was done for each of the SNPs using a G-matrix (genetic relationship matrix) to correct for family structure. GBLUP (Genomic Best Linear Unbiased Prediction) models were used for predictions based on all SNPs, and the predictive abilities were determined using different kinds of cross-validations.

RESULTS AND DISCUSSION

Phenotypic variation was observed for all four quality traits, especially for Alveograph W, P, and L (dough strength, tenacity, and extensibility) (Table 1).

A principal component analysis of the G-matrix showed that the wheat lines were genetically related both within and across the two breeding cycles (Fig. 1).

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

Phenotype	Mean	Range	CV (%)	h ²
Flour yield (%)	69.6	60.7-77.3	4.5	0.38
Alveograph W (10 ⁻⁴ J)	138.4	40-325	34.5	0.72
Alveograph P (mm)	75.1	31-201	32.3	0.69
Alveograph L (mm)	56.4	21-114	27.7	0.60

One SNP on chromosome 5D was significantly associated with flour yield, Alveograph W, and Alveograph P (Fig. 2). For Alveograph W, significant SNPs were also identified on chromosomes 1B and 1D. No significant SNPs were identified for Alveograph L.

Wheat quality is to a large extent determined by gluten content, gluten composition, and grain hardness, so the identified SNPs are likely linked to genes encoding gluten proteins (glutenins and gliadins) on chromosomes 1B and 1D, or to the *Hardness* locus on chromosome 5D, containing the *Pina-D1* and *Pinb-D1* genes.

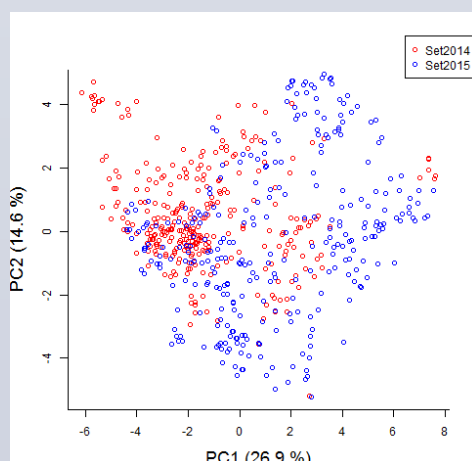


Figure 1. Principal component analysis of the G-matrix. Wheat lines from the two breeding cycles are displayed in red and blue, respectively.

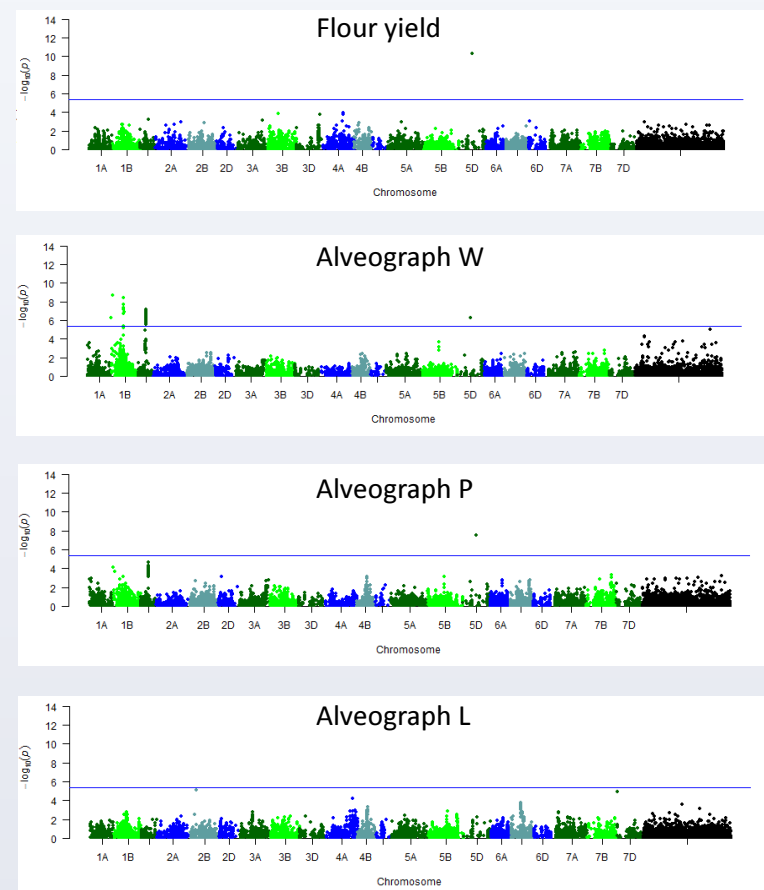


Figure 2. Manhattan plots of $-\log_{10}(p\text{-values})$. Last bin is unmapped SNPs.

Predictive abilities based on GBLUP models with all SNPs ranged from 0.50 for flour yield to 0.79 for Alveograph W using Leave-One-Out cross-validations (Fig. 3). Comparing the different cross-validation strategies showed that GxE interactions and the genetic relationship between lines of the training and validation set had a larger impact on the predictive abilities than the size of the training set.

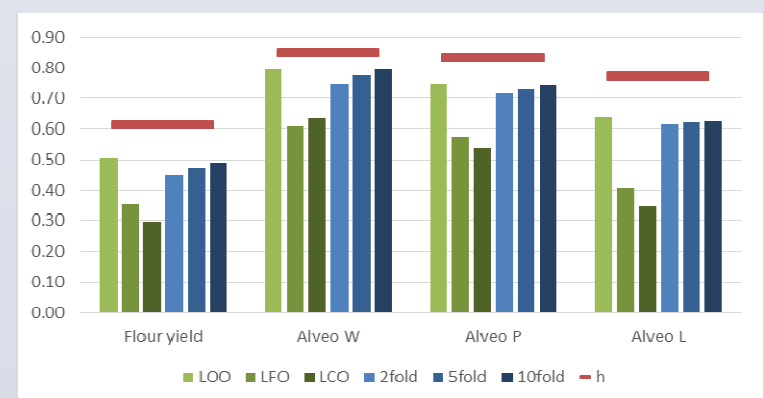


Figure 3. Correlations between observed phenotypes corrected for fixed effects and GEBVs. Maximum correlation, h, is the square root of the narrow sense heritability and is shown as red bars over the correlations. Correlations are based on different kinds of cross-validations: LOO: Leave-One-Out, LFO: Leave-Family-Out, LCO: Leave-Cycle-Out, and k-folds (2, 5, and 10).

CONCLUSIONS

SNPs significantly associated with Alveograph W were identified on chromosome 1B, 1D, and 5D. The SNP on 5D was also significantly associated with flour yield and Alveograph P. Genomic predictions showed good potential for all traits, so implementation of genomic prediction in breeding programs could be useful for improving wheat baking quality.

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