Genomic prediction of flowering time and yield through SNP and metabolite analysis in the barley NAM population HEB-25

Mathias R. Gemmer[1], Chris Richter[2], Yong Jiang[3], Thomas Schmutzer[1], Manish L. Raorane[2], Andreas Maurer[1], Björn Junker[2], Klaus Pillen[1]

[1]Institute of Agricultural and Nutritional Sciences, Martin Luther University Halle-Wittenberg, Betty-Heimann-Str. 3, 06120 Halle, Germany; [2]Institute of Pharmacy, Martin Luther University Halle-Wittenberg, Hoher Weg 8, 06120 Halle, Germany;
[3]Department of Breeding Research, Quantitative Genetics, Leibniz Institute of Plant Genetics and Crop Plant Research, 06466 Gatersleben, Germany.
E-Mail: klaus.pillen@landw.uni-halle.de;

Introduction

Breeding for yield performance in elite barley (*Hordeum vulgare* ssp. *vulgare*) led to a reduction of biodiversity through allele erosion, the so-called genetic bottleneck effect. Consequently, future improvement of the performance of barley becomes increasingly difficult. Moreover, classical selection methods with several years of field trials are expensive.

To accelerate the breeding progress, indirect selection methods are of increasing importance. A promising method is the SNP-based estimation of breeding values through genomic prediction (Heffner et al. 2009). A study in maize confirmed that a reliable estimation of performance with metabolite data is also possible (Riedelsheimer et al. 2012). The advantage of genomic prediction is the early estimation of traits already in seedling stage of the plant which accelerates the selection of the best plants during the breeding process.

Materials and Methods

The population HEB-25 is the worldwide first nested association mapping population of barley. It was generated by crossing and subsequent backcrossing of 25 wild barleys with the elite cultivar Barke (Fig. 1). The population comprises 1,420 BC_1S_3 lines, which were phenotyped from 2011 to 2018, were characterized with SNPs (50K SNP chip) and through metabolic profiling of 128 or 122 metabolites of one early and one late sampling date. Sampling took place (May: BBCH 30-31 and June: BBCH 59-69) in 2017. For this, the middle of the youngest fully developed leaf was harvested and instantly stored in liquid nitrogen (Fig. 2). The plant material was analyzed by GC-MS (gas chromatography + mass spectrometry). For genomic prediction, the BayesB model with a fivefold cross-validation (CV) and 100 cross validation runs was applied. The prediction ability is the correlation between observed and predicted values (average of all 100 CV runs). Prediction accuracy is defined as the quotient of prediction ability and the square root of heritability.

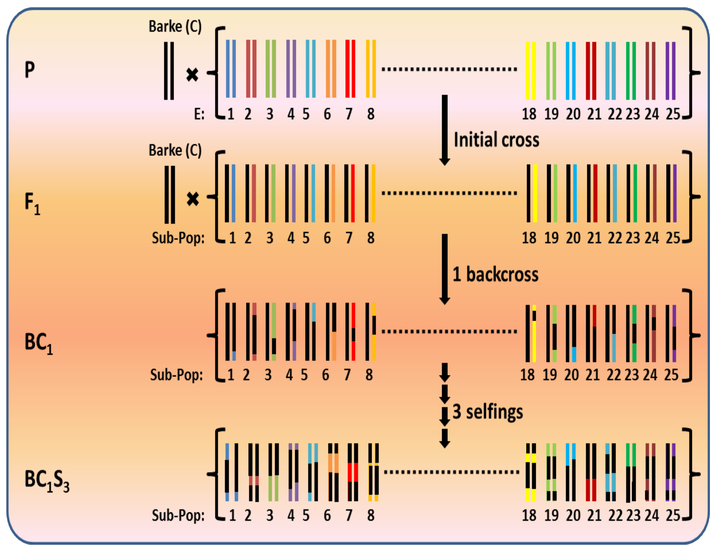

Fig. 1: Crossing scheme of HEB-25, taken from Maurer et al. (2015)

Tab. 1: Summary of SNP and metabolic prediction

		SNPs			Metabolites 1st date			Metabolites 2nd date		
Trait	**h^2**	**r_{ab}**	**r_{ac}**	**SD**	**r_{ab}**	**r_{ac}**	**SD**	**r_{ab}**	**r_{ac}**	**SD**
Shooting	0.91	0.88	0.93	0.02	0.57	0.59	0.05	0.47	0.50	0.05
Heading	0.93	0.87	0.91	0.02	0.59	0.61	0.05	0.50	0.52	0.05
Maturity	0.83	0.87	0.95	0.02	0.56	0.61	0.06	0.54	0.59	0.05
Plant height	0.91	0.93	0.97	0.01	0.37	0.38	0.06	0.27	0.28	0.05
Grains per ear	0.84	0.88	0.96	0.04	0.27	0.29	0.07	0.29	0.32	0.06
Thousand grain weight	0.83	0.86	0.94	0.02	0.26	0.28	0.05	0.19	0.21	0.06

Prediction abilities (r_{ab}) and prediction accuracies (r_{ac}) of traits, averaged over 100 cross-validation runs and their standard deviation (SD) are shown. BayesB model was applied using SNP or metabolite data. Metabolite data from the first and second sampling was used, respectively. Heritabilities (h^2) for the traits are given (eight years of phenotypic data).

Results and Outlook

Results for genomic prediction with SNP and metabolite data are shown in Table 1. Metabolites collected at the early sampling date performed better than those taken from the late sampling date. Combination of SNP and metabolite data did not lead to an enhancement in prediction accuracy. The estimated effects of SNPs and metabolites in the model were highly concordant, indicating metabolites as an interesting alternative to SNPs.

In addition, first GWAS results located QTLs controlling sugar-like metabolites. Sugars play a key role in signalling, plant growth and plant development.

Fig. 2: Sampling of leaf material for metabolite analysis

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