Increase in accuracy using multi-trait genomic breeding value estimation

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Introduction Genomic selection is becoming common practice in animal breeding. It uses genome-wide dense marker maps, to accurately predict the genetic ability of animals, without the need to record phenotypic performance from the animal itself or from close relatives. Presented applications of genomic selection have mainly been limited to implementations where genomic breeding values are estimated using single trait models. A major breakthrough in traditional breeding value estimation was the application of multi-trait breeding value estimation, for instance to combine mastitis and somatic cell count information. Therefore, our objective was to develop multi-trait genomic breeding value estimation methods.

Materials and methods Four different multi-trait models were considered: 1) a model with a traditional pedigree based relationship matrix (A-BLUP), 2) a model where the traditional pedigree based relationship matrix is replaced by a genomic relationship matrix based on markers (G-BLUP) (e.g. VanRaden, 2008), 3) a model that includes SNP effects drawn from a single distribution (BayesA), and 4) a model that includes SNP effects drawn from two distributions to distinguish between SNPs that are (not) associated with QTL (BayesC) (a single trait implementation is presented by Calus *et al.*, (2008)). The second model assumes equal contribution of each SNP to the total additive genetic (co)variance. Model 3 and 4 explicitly estimate the (co)variance of the SNP effects, per sampled distribution of SNP effects. The additive genetic (co)variance matrix was used as prior information for the SNP variances. The four models were applied to two simulated traits with heritabilities of 0.9 and 0.6, to reflect e.g. de-regressed proofs, having a genetic correlation of 0.2, 0.5 or 0.8 between them. In the simulated data, 2 generations of 500 animals each were available with phenotypes for both traits, and thus formed the reference population. Two additional generations of 500 animals were used as validation data, e.g. their breeding values were predicted while they had no phenotypic information of their own or from offspring in the model.

Results Increases in accuracy, due to applying multi-trait instead of single trait genomic breeding value estimation, depended on the genetic correlation between the traits. At a genetic correlation of 0.8, the accuracy of the breeding values of animals without phenotypes for the second trait increased by 0.03 to 0.07 (see Table 1). At a genetic correlation of 0.5, this increase ranged from 0.01 to 0.04. The highest increase was found using model BayesC, followed by BayesA, G-BLUP, and A-BLUP respectively. Regression of the simulated on the estimated breeding values showed that the estimated breeding values were generally unbiased.

Table 1 Increase in accuracies for breeding values of the first generation of animals without phenotypes, obtained from multitrait versus single trait models.

	Genetic correlation	
Model	0.5	0.8
A-BLUP	0.009	0.034
G-BLUP	0.017	0.052
BayesA	0.024	0.056
BayesC	0.040	0.071

Conclusions In a scenario where all animals in the reference population have phenotypes for all traits, multi-trait genomic breeding value estimation showed an increase of up to 0.07 in accuracy for juvenile animals, compared to single trait analysis. Thus, the application of multi-trait genomic selection in this scenario proved to be more accurate than single trait genomic selection. In practice, higher accuracy increases are expected when one of the traits is measured on some of the animals only.

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References

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