

DETERMINING THE RELATIONSHIPS BETWEEN GENOMIC AND PHENOTYPIC BREEDING VALUES

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Abstract

The main aim of the animal breeding is to increase the yields of economic traits in future generations and increase the obtained production per animal. Genomic selection studies have become applicable as a result of rapid increase of both genetic and computer sciences. In this study, Bayes A, Bayes B, Bayes C, Bayes Cpi which are used in genomic selection and BLUP (best linear unbiased prediction) methods which are used traditional selection will be compared. For this aim genomic breeding value and phenotypic breeding value has been estimated for lactation milk yield of Holstein cows breeding in a private company in USA. Holstein cows (400 individuals) were genotyped with 54k SNPs. The marker input file was coded as -10, 0, and 10 for marker genotypes AA, AB, and BB, respectively. A total of 50,000 iterations were used, with the first 5000 excluded as the burn-in. Bayes A, Bayes B, Bayes C and Bayes Cpi were performed using the software GenSel 4.55 and phenotypic breeding values for lactation milk yield in Holstein cows were estimated by restricted error maximum likelihood (REML), BLUP procedures using an MTDFREML (multiple trait derivative free restricted maximum likelihood) program employing an animal model. Correlations were examined between phenotypic and genomic breeding values with Spearman correlation. As a result, for estimating breeding values, while the highest correlation was found between BLUP with Bayes Cpi, the lowest correlation were found between BLUP with Bayes A.

Key words: Bayes, BLUP, Genomic Selection, Breeding Value.

INTRODUCTION

The main aim of the animal breeding is to increase the yields of economic traits in future generations and increase the obtained production per animal. Genetic improvement of breeding stock has been the goal of livestock producers for centuries (Verbyla, 2010).

During the first decade of the 21st century, there has been a rapid development of genomic selection tools. Through the application of genomic selection (Meuwissen et al., 2001), marker information from high-density SNP genotyping can increase prediction accuracies at a young age, shorten generation intervals and improve control of inbreeding (Daetwyler et al., 2007), which should lead to higher genetic gain per year.

Whole genome prediction (WGP) using commercially available medium to high density (50,000) single nucleotide polymorphism (SNP) panels have transformed livestock and plant breeding. Typically, the allelic substitution effects of all SNP markers are jointly estimated in WGP evaluation models

assuming additive inheritance and summed to predict breeding values of each individual animal on the basis of its SNP genotypes (Yang and Tempelman, 2012).

The availability of high-density single nucleotide polymorphism (SNP) genotypes across the whole genome has enabled more accurate prediction of breeding values than conventional pedigree-based methods, as well as the mapping of QTL across the genome. Current routine genomic evaluations of cattle populations are performed using selected genotypes that are obtained from the ~54,000 SNPs that are included in the BovineSNP50 or so-called 50 K array. However, high-density Affymetrix (648,874 SNPs) and Illumina (777,962 SNPs, referred to as the 770 K array) genotyping arrays are now available (Hassani et al., 2015).

Another approach is to develop genomic predictions that are accurate in multiple breeds through training on multibreed populations of purebred or crossbred animals. This has the advantage of allowing small populations to be pooled to create reference populations of the

scale required to derive accurate genomic predictions (Weber et al., 2012). Many simulation studies have shown the benefits of this technology, depending on heritability, number and distribution of effects of QTL, population structure, size of training data set used to estimate SNP effects, and other factors. However, studies on real data are still scarce (Wolc et al., 2011).

In this study, we aimed to compare Bayes A, Bayes B, Bayes C, Bayes Cpi which are used in genomic selection and BLUP (best linear unbiased prediction) methods which are used traditional selection.

MATERIALS AND METHODS

Genomic breeding value and phenotypic breeding value has been estimated for lactation milk yield of Holstein cows breeding in a private company in USA. Holstein cows (400 individuals) were genotyped with 54k SNPs.

The marker input file was coded as -10, 0, and 10 for marker genotypes AA, AB, and BB, respectively. A total of 50.000 iterations were used, with the first 5000 excluded as the burn-in. Bayes A, Bayes B, Bayes C and Bayes Cpi were performed using the software GenSel 4.55 and phenotypic breeding values for lactation milk yield in Holstein cows were estimated by restricted error maximum likelihood (REML), BLUP procedures using an MTDFREML (multiple trait derivative free restricted maximum likelihood) program employing an animal model.

RESULTS AND DISCUSSIONS

Estimated Spearman rank correlation among breeding values obtained from Bayes A, Bayes B, Bayes C, Bayes Cpi and BLUP were given in Table 1.

Table 1. Spearman rank correlations for BV

Specification	BLUP	Bayes A	Bayes B	Bayes C
Bayes A	-0.519			
Bayes B	-0.518	0.999		
Bayes C	-0.613	0.941	0.942	
Bayes Cpi	-0.387	0.642	0.653	0.654

All the obtained correlation coefficients were found statistically significant ($P < 0.01$). In analysis 6414 markers was removed because was monomorphic. Estimated parameters were given in Table 2 and Table 3.

Table 2. Genetic parameters estimated from Bayes methods

Specification	Bayes A	Bayes B	Bayes C	Bayes Cpi
Genetic Variance	0.000506953	0.000514429	0.00708704	0.00239004
Residual Variance	0.0254734	0.0254589	0.0190007	0.0238036
Total Variance	0.0259804	0.0259733	0.0260877	0.0261936
h ²	0.019	0.019	0.272	0.091
Pi	-	-	-	0.999
Compute Time (sn)	4300	5908	1071	7669

Table 3. Genetic parameters estimated from BLUP method

Variance Components	Value
σ_a^2	264879.6
σ_c^2	643304.2
σ_e^2	1161231.1
σ_p^2	2069414.9
h ²	0.13
r	0.44

Estimated heritability from BLUP was found as expected. Mall heritability values observed from Bayes methods except Bayes C which was relatively high than other methods. Negative correlations were estimated BLUP versus Bayes methods as expected for less heritable traits such as milk yield (Dekkers, 2007).

CONCLUSIONS

Bayes methods produced similar results for studied data. Negative Spearman rank correlations were observed between BLUP and Bayes methods and the case of these results attributed to less heritable trait of studied milk yield. Further studies should be conducted with larger sample sizes.

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