Multiple-trait breeding goals – Does genomic selection offer new opportunities?

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Summary

Multiple-trait genetic evaluations commonly assume a constant genetic correlation between traits across the genome. In a genomic evaluation, it is possible to estimate breeding values for each chromosome an individual carries, and relax the assumption of constant genetic correlation between traits. This study reports on a comparison of two approaches for multiple-trait genomic prediction and the effect on response to selection for a total merit index. A multiple-trait model with an effect per chromosome that allowed for different genetic correlations between traits by chromosome was compared with a conventional multiple-trait genomic-BLUP model. When correlations differed considerably between chromosomes, or when heritabilities differed between traits, the model with an effect per chromosome resulted in greater response to selection.

Keywords: genetic progress, genomic selection, chromosomal breeding values, multiple-trait models

Introduction

Genomic selection has revolutionized animal breeding and increases in genetic progress due to implementation of genomic selection have been documented (Garcia-Riuz et al., 2016). Research-wise, many efforts have been directed toward investigating improvements in genomic prediction of breeding values but many possibilities to optimize breeding plans that utilize genomic information remain to be explored.

Cole and VanRaden (2010) presented the concept of chromosomal estimated breeding values and discussed how displaying an individual’s genetic merit in this way could be used in mating decisions. Their approach assumed that, a priori, the amount of genetic variation per chromosome is proportional to the number of genetic markers per chromosome. In studies where the amount of genetic variation per chromosome has been estimated, this assumption has been found to hold for some traits but not for others (e.g. Jensen et al., 2012). Likewise, in a multiple-trait context, it is conceivable that the genetic correlation between traits is not constant across the genome, which can have implications for multiple-trait breeding goals.

The aim of this study was to investigate the effect of genetic correlations that vary across the genome on the rate of genetic progress for a multiple-trait breeding goal.

Material and methods

A breeding program of 25 discrete generations was simulated. Each generation, 50 males (out of 500) and all (=500) females were selected as parents of the next generation using genomic breeding values. Mating was at random, and each mating resulted in two offspring: one male
and one female.

The simulated genome consisted of three chromosomes, each one Morgan of length. Sequence information for base generation animals were generated using the MaCS software (Chen et al., 2009), parameterized according the historical effective populations size of the Holstein breed (Villa-Angulo et al., 2009). Recombination events for successive generations were simulated in proportion to chromosome length; no mutations were generated.

For each chromosome, 1000 randomly chosen markers were assigned as QTL. Two traits were simulated, and the QTL effects for each trait were drawn from a bivariate distribution with a variance-covariance matrix that differed between chromosomes. The amount of genetic variation was assumed to be the same for each chromosome and for each trait. Three values genetic correlations between traits were considered (-0.5, 0, +0.5); the genetic correlation between traits differed between chromosomes and several combinations of the three values were evaluated (Table 1).

Phenotypes were generated for both sexes and each trait as the sum of the true breeding value and a random residual effect. The heritability for the first trait was set to 0.5 and either to 0.5 or 0.1 for the second trait.

Genomic breeding values were estimated using two approaches: 1) a genomic BLUP with one genetic effect per individual and trait, using a genomic relationship matrix built using markers of all three chromosomes (denoted GBLUP), and 2) a genomic BLUP with three genetic effects per individual and trait, each having its own genomic relationship matrix built using the markers on that chromosome (denoted CBLUP). Genomic relationship matrices were constructed following VanRaden (2008). For every generation, only the two previous generations of individuals were included in the reference population for genomic prediction. Phenotypes for both traits were included for individuals in the reference population. Genomic breeding values for both traits were estimated simultaneously with a multiple-trait model. Simulated variances and genetic correlations were used in the genomic breeding value estimation.

Both traits were included in the breeding objective with equal weight. With CBLUP, each individual received three breeding values per trait (one for each chromosome). An overall breeding value per trait was calculated as the sum of the three chromosomtal breeding values before combining the traits in an index. Note that the genetic variance for the breeding objective was not the same for all scenarios considered, due to the difference genetic correlations considered.

Genetic progress per generation was calculated by a regression of true breeding values for the breeding objective on generation number, using information from generations 11 to 25. Each scenario was replicated 20 times.

**Results and discussion**

The difference in response to selection from GBLUP and CBLUP was influenced by two factors. Assuming one genetic correlation across the genome (as in GBLUP), if the genetic correlations differ between chromosomes the accuracy of estimated breeding values reduced. On the other hand, with CBLUP, three chromosome breeding values (per trait) were predicted for each individual, and there is a cost (i.e. lower precision) associated with predicting more effects.

Response to selection was slightly higher for GBLUP compared to CBLUP when the heritability was 0.5 for both traits and the genetic correlations between traits were positive for two chromosome, but negative for the third (Table 1). All animals in the reference population
had information on both traits, and since heritabilities were high, information on correlated traits added relatively little accuracy to the estimated breeding values. Ignoring small differences in genetic correlations between traits for different chromosomes in GBLUP had a small impact and seemed to outweigh the costs of predicting three breeding values with CBLUP.

When the genetic correlation was 0.5, 0 and -0.5 for chromosome 1, 2 and 3, respectively, the differences between GBLUP and CBLUP were larger and in favour of CBLUP. For this scenario, the genetic correlation across the genome was zero, and the bivariate GBLUP evaluation essentially boils down to two univariate GBLUP evaluations. For CBLUP, however, information from the correlated trait is utilized. Regarding the pattern of response, there was higher response for the second and lower response for the third chromosome in CBLUP compared to GBLUP.

The rate of progress was also higher with CBLUP when the heritability for the second trait was 0.1. For this scenario, the first trait adds considerably to the accuracy of estimated breeding values for the second trait, more so when differences in genetic correlations between chromosomes were considered in CBLUP.

Table 1. Response to selection for various combinations of heritabilities and genetic correlations between traits, using either GBLUP or CBLUP for genomic prediction.

<table>
<thead>
<tr>
<th>Heritability</th>
<th>Genetic correlation between traits</th>
<th>Response to selection&lt;sup&gt;1&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trait 1</td>
<td>Trait 2</td>
<td>Chr1 Chr2 Chr3 GBLUP CBLUP Sign</td>
</tr>
<tr>
<td>0.5</td>
<td>0.5</td>
<td>0.5 0.5 -0.5 1.18 1.17 Ns</td>
</tr>
<tr>
<td>0.5</td>
<td>0.5</td>
<td>0.5 0 0 -0.5 1.06 1.12 *</td>
</tr>
<tr>
<td>0.5</td>
<td>0.1</td>
<td>0.5 0.5 -0.5 1.04 1.07 *</td>
</tr>
</tbody>
</table>

<sup>1</sup>Response per generation; mean of 20 replicates; SEM < 0.004; Ns = non-significant difference between GBLUP and CBLUP and * = P < 0.05; genetic SD for the breeding objective ≈ 6.

<sup>2</sup>Chr1 = Chromosome 1

**Conclusions**

If genetic correlation between traits differ between chromosomes, considering these differences in genomic prediction can increase genetic progress for a multiple-trait breeding objective.

**List of References**


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