Different estimations of heritabilities in dependence of major gene effects (Brief Report)

Unterschiedliche Schätzung von Heritabilitäten in Abhängigkeit von Hauptgeneffekten (Brief Report)

BERND BUSKE and NICOLAS GENGLER

Gembloux Agricultural University, Gembloux, Belgium

Background

Knowledge of major gene effects for quantitative traits (e.g. milk performance traits) and the consequent selection of animals with desirable genotypes can accelerate breeding progress and can therefore equal large gain in profits. It is generally accepted that in most cases, the total breeding value for quantitative traits of any animal can be divided in one or some major gene effects and a pure random polygenic component, in which the latter results from a finite number of remaining loci (FERNANDO et al. 1994). Thus, the aim of this study was to investigate, how the estimation of heritability is influenced by the application of two different models, one of them containing a major single gene effect. The myostatin gene (MSTN) was chosen because the knowledge of this gene effect is used for selection decisions in the Dual Purpose Belgian Blue Breed (DP-BBB) in the Walloon Region of Belgium.

Procedures

A field dataset including 1,455 genotyped DP-BBB cows with 40,269 test-day (TD) records was available. All cows were genotyped for the 11 bp-deletion in the coding sequence of MSTN using a method adapted from FAHRENKRUG et al. (1999). Genotype and allele frequencies were 0.181 (+/+), 0.371 (mh/+) and 0.447 (mh/mh) as well as 0.37 (+) and 0.63 (mh), respectively.

TD records per lactation were sampled between 1991 and 2008. For all traits, the following linear single trait mixed inheritance test-day model was used

$$y = \mu + X\beta + Hh + Wi + Zp + Zu + ZQg + e$$

whereas \( y \) is a vector of TD records representing the phenotype of the animal, \( \mu \) is the overall mean, \( \beta \) represents a vector of fixed effects, \( h \) is a vector for a random herd \( \times \) test-day effect, \( i \) for a random intra lactation effect, \( p \) for a random permanent environment effect, and \( e \) represents the residual. The vector \( u \) stands for the random polygenic animal effect, and \( g \) represents the myostatin genotype effect. Genotype effect was considered as fix including an additive and a dominance effect. The incidence matrices \( X, H, W \) and \( Z \) link the records to the fixed effects, herd \( \times \) test-day, animal \( \times \) lactation number and animals, respectively, whereas \( Q \) is a matrix linking animals to their myostatin genotype. The second model was the same model as described above, except that the component for the major gene effect
**Results**

Results showed that heritabilities were higher for all traits when the major gene effect was removed from the model except for protein content (Table 1). This was expected because it is well known that the presence of the »+« allele of MSTN leads to increases for milk, fat and protein yield to a considerable amount but not for protein content. Therefore, the variability of the major gene effect was transferred into the random polygenic additive genetic variance. This should be the case when it is assumed that the myostatin gene is responsible for variability for these traits. Furthermore, convergence between permanent environment and random polygenic animal effect was less stable for fat content, when the myostatin gene effect was not included in the model indicating that fixed or systematic effects should be modelled adequately as it is also mentioned by MISZTAL (2008). The results clearly show that estimation of heritability depends strongly on the knowledge and inclusion of major gene effects and therefore, such gene effects should be considered when heritability should be estimated reliably.

Table 1

<table>
<thead>
<tr>
<th>Trait</th>
<th>Model without mstn</th>
<th>Model with mstn</th>
<th>Milk yield $\sigma^2$</th>
<th>Protein yield $\sigma^2$</th>
<th>Protein content $\sigma^2$</th>
<th>Fat yield $\sigma^2$</th>
<th>Fat content $\sigma^2$</th>
<th>$h^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>2.905</td>
<td>0.261</td>
<td>2.129</td>
<td>0.545</td>
<td>0.212</td>
<td>0.208</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>13.679</td>
<td>1.401</td>
<td>8.193</td>
<td>2.375</td>
<td>31.451</td>
<td>0.195</td>
</tr>
</tbody>
</table>

$\sigma^2_g$ additive genetic variance, $\sigma^2_t$ total variance, All variances except for milk yield were multiplied by 100
References


Received 20 July 2009, accepted 4 October 2010.

Corresponding author:

BERND BUSKE
email: buske.b@fsagx.ac.be

Gembloux Agricultural University, Passage des Déportés, 2, 5030 Gembloux, Belgium