Genetic Parameters Of Predicted Methane Production In Holstein Friesian Cows

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Introduction

Methane emissions contribute significantly to the greenhouse effect having many times the global warming potential of carbon dioxide (IPCC, 2001; Kebreab et al., 2008). Among human activities, agriculture is responsible for about 50% of overall anthropogenic methane production (IPCC, 2001), and the largest biogenic source of this gas is enteric fermentation from ruminants. Methane produced within the rumen is a by-product of normal anaerobic fermentations of the organic matter, and represents a loss in productive energy for the animal. Typically, 2 to 12% of the gross energy intake in cattle is lost through eructation of methane (Johnson and Johnson, 1995). Because methane concentration in the atmosphere is increasing, there is a strong interest in developing strategies to reduce its emissions, particularly from the livestock sector, which accounts for 37% of worldwide methane production (McCann-Thies, 2006). This can be achieved working on the diet, but also on genetics of animals. Aim of this study was to estimate heritability for predicted methane production in dairy cattle, and to assess genetic correlations between predicted methane production and milk yield traits.

Material and methods

Data. A total of 670 test day records of milk yield (MY, kg/d), fat content (FC, %), protein content (PC, %), and somatic cell count (SCC), with a pedigree file of more than 2000 individuals, were provided by the Breeders Association of Treviso province (Treviso, Italy). Data were recorded on lactating Holstein Friesian cows reared in 10 commercial dairy herds. Each cow was sampled once, i.e., no repeated records were available. Somatic cell count was log-transformed to obtain somatic cell score (SCS, units), as proposed by Schutz (1994). Methane production (PMP, MJ/d) was predicted using predicted dry matter intake through the best equation for dairy cattle, in term of $R^2$ (0.65) and error due to bias, as a percentage of total root mean square prediction error (5.19) (Ellis et al., 2007). Predicted dry matter intake was derived by MY, FC, and estimated body weight of cows, as reported by Chase and Sniffen (1985) and Cassandro et al. (1997). Average predicted dry matter intake was 18.67±1.88 with a Pearson’s correlation of 0.90 ($P<0.001$), 0.27 ($P<0.001$) and 0.01 (NS) with MY, estimated body weight and FC, respectively.

Statistical analyses. (Co)variance components and related parameters for MY, FC, PC, SCS, and PMP were assessed through bivariate animal models in which PMP was analysed

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simultaneously with one of the other traits. A Bayesian approach and Monte Carlo Markov-Chain methods (Sorensen and Gianola, 2002) were used. Models accounted for systematic effects of herd, year-season of milk testing, days in milk, and age at calving, and for the additive genetic effect. Flat prior distributions were assigned to all the effects. Parameters were drawn from the posterior distributions using Gibbs sampling as implemented in TM program (available at: http://cat.toulouse.inra.fr/~alegarra/). A single chain of 1,000,000 iterations was obtained for each analyses, with a burn-in of 50,000. Samples were saved every 200 iterations. The posterior median was used as a point estimate of heritability and genetic correlations. Lower and upper bounds of the highest 95% confidence region for genetic parameters were obtained from the estimated marginal densities, as well as the posterior probability for values of heritability greater than 0.10.

Results and discussion

Descriptive statistics and features of the marginal posterior distribution of heritability for the studied traits are reported in Table 1. Predicted methane production was estimated to be 15.33±1.52 MJ/d in dairy cows with 23.53±6.81 kg/d of MY and 3.57±0.68% of FC. Heritability of MY was 0.09 with a posterior probability for values of $h^2$ greater than 0.10 of 44%. Estimates of heritability for FC and PC were 0.17 and 0.34, respectively, with a posterior probability for values of $h^2$ greater than 0.10 of 77% and 99%. For SCS, heritability was 0.13 with a posterior probability for values of $h^2$ greater than 0.10 of 67%. Similar results were found by Cassandro et al. (2008) using REML procedure, except to FC and SCS, where heritability values were higher for FC (0.40) and lower for SCS (0.07). Heritability for the new trait PMP was moderate to low (0.12); however, posterior probability for values of $h^2$ greater than 0.10 was 60%.

Table 1: Basic statistics and features of the marginal posterior distribution of heritability for milk yield (MY, kg/d), fat content (FC, %), protein content (PC, %), somatic cell score (SCS, units), and methane production (PMP, MJ/d)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean</th>
<th>SD</th>
<th>CV, %</th>
<th>PM$^1$</th>
<th>LB95%$^2$</th>
<th>UB95%$^2$</th>
<th>P$^3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>MY, kg/d</td>
<td>23.53</td>
<td>6.81</td>
<td>28.9</td>
<td>0.09</td>
<td>0.01</td>
<td>0.24</td>
<td>44</td>
</tr>
<tr>
<td>FC, %</td>
<td>3.57</td>
<td>0.68</td>
<td>19.0</td>
<td>0.17</td>
<td>0.03</td>
<td>0.36</td>
<td>77</td>
</tr>
<tr>
<td>PC, %</td>
<td>3.25</td>
<td>0.31</td>
<td>9.7</td>
<td>0.34</td>
<td>0.13</td>
<td>0.56</td>
<td>99</td>
</tr>
<tr>
<td>SCS</td>
<td>2.90</td>
<td>1.71</td>
<td>59.2</td>
<td>0.13</td>
<td>0.02</td>
<td>0.31</td>
<td>67</td>
</tr>
<tr>
<td>PMP, MJ/d</td>
<td>15.33</td>
<td>1.52</td>
<td>9.9</td>
<td>0.12</td>
<td>0.03</td>
<td>0.28</td>
<td>60</td>
</tr>
</tbody>
</table>

$^1$PM = median of the posterior density; $^2$LB95% = lower bound of 95% probability density region; $^3$UB95% = upper bound of 95% probability density region; $^4$P ($h^2 > 0.10$) = posterior probability for values of $h^2$ greater than 0.10

Marginal posterior densities of genetic correlations between PMP and milk production traits are displayed in Figure 1. Medians of the posterior distributions were 0.92, 0.67, 0.14, and 0.14 between PMP and MY, PMP and FC, PMP and PC, and PMP and SCS, respectively. Reduction of PMP seems to be viable through selection strategies without affecting udder health and PC. Recent advances for measuring methane emission from individual animals showed that it is possible using a tracer technique (Johnson et al., 1994; Lassey et al., 1994;
Hegarty et al., 2007). For further research studies, direct measurement of methane emission, based on SF6 tracer, seem to be available and validated with chamber methods (Boadi et al., 2002) and with micrometeorological methods (Judd et al., 1999; Leuning et al., 1999). Further studies on genetic aspects, should be done using direct estimation of methane emission although the predicted measurement of this greenhouse gas in the present study provided the first estimation of (co)variance genetic components with routinely recorded milk traits.

\[ a) \text{MeP-MY} \]
\[ \text{b) PMP-FC} \]
\[ c) \text{PMP-PC} \]
\[ d) \text{PMP-SCS} \]

**Figure 1:** Estimated marginal posterior density of genetic correlations between (a) PMP and MY, (b) PMP and FC, (c) PMP and PC, and (d) PMP and SCS.

**Conclusion**

The new rules of livestock sector should account for environment safeguard and climate changes, as limitation of greenhouse gasses. Results of this explorative study suggest that PMP can be successfully selected for reduced gas emissions. Recent advances in the direct measurements of methane production at individual level using a methane collection apparatus seem to be very helpful for more efficient selection strategies and a better genetic control on daily methane emission. A more large dataset should be considered to confirm these results.
References


