Generating test-day methane emissions as a basis for genetic studies with random regressions

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Background

- Greenhaus gas (GHG) emissions
  - CO₂, N₂O, and CH₄
  - global climate change
  - inefficient use of dietary energy

- The dairy cattle sector (FAO, 2010)
  - 4% of GHG emissions
  - 52% contribution of methane emissions (ME)

- Methods to measure ME
  - respiration chamber
  - sulfur hexafluoride tracer
  - mobile laser methane detector
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**Aims of this study**

- simulate and predict test-day ME using indicator traits
- estimate heritabilities for ME by DIM
- genetic correlations: test-day ME and test-day production traits by DIM
- genetic correlations: test-day ME and fertility traits by DIM
- genetic correlations: test-day ME and clinical mastitis by DIM
- evaluate breeding program designs
  - progeny testing program
  - genomic breeding programs

1. Simulation and prediction of test-day ME
Data

• Real data
  – 7804 test-day records
  – 916 first lactation Brown Swiss cows
  – 41 low input farms in mountainous regions in Switzerland

• Test-day production traits
  – Milk yield (MY), fat percentage (Fat%), protein percentage (Pro%), milk urea nitrogen (MUN)

• Conformation traits
  – Wither height (WH), hip width (HW), body condition score (BCS)

• Fertility traits
  – Calving interval (CI), days open (DO), stillbirth (SB)

• Health trait: clinical mastitis (CM)
Predict methane emissions - equation 1

\[ MEI = (10.0 + 4.9 \times \text{MY} + 1.5 \times \text{BW}^{0.75}) \times 0.0132 \]

(Kirchgeßner et al., 1995)

Test-day MY

\[ BW = 439 + 0.2 \times \text{DIM} + 4.2 \times \text{HH} + 29.2 \times \text{HW} + 0.3 \times \text{HW}^2 + 33.5 \times \text{BCS} \]

(Enevoldsen et al., 1997)
Predict methane emissions - equation 2

\[ ME2 = \frac{F_1 \times 18.4}{0.005565 \times 0.006} \times [1 + (2.38 - L_1) \times 0.04] \]

(de Haas et al., 2011)
Predict methane emissions - equation 2

\[ ME2 = \text{FI} \times 18.4 / 0.005565 \times 0.006 \times \left[ 1 + \left( 2.38 - \text{LI} \right) \times 0.04 \right] \]

\[
\begin{align*}
\text{FI} &= 15.28 + 0.008 \times (\text{BW} - 603) \\
&+ 0.2389 \times (\text{ECM} - 20) - 0.005874 \times (\text{ECM} - 20)^2 \\
&+ 0.305 \times (\text{Con} - 2.88) \\
&+ 0.959 \times (\text{ECR} - 5.41) \\
&- 0.0028 \times (\text{DIM} - 112) + 1.142 \times (\ln(\text{DIM}) - 4.33) \\
&+ 0.0443 \times (\text{Mon} - 6.36) - 0.019776 \times (\text{Mon} - 6.36)^2
\end{align*}
\]

(Schwarz and Gruber, 1999)

(de Haas et al., 2011)
**Predict methane emissions - equation 2**

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ME2 = \frac{FI \times 18.4}{0.005565 \times 0.006 \times [1 + (2.38 - LI) \times 0.04]}
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\]

### Milk urea nitrogen (in mg/dl)

<table>
<thead>
<tr>
<th>Protein %</th>
<th>&lt; 25.14</th>
<th>&gt; 25.14</th>
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<tbody>
<tr>
<td>&lt; 3.418</td>
<td>No concentrate 4.5 MJ NEL/kg DM</td>
<td>No concentrate 6 MJ NEL/kg DM</td>
</tr>
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<td>&gt; 3.418</td>
<td>10% concentrate ( N(1.78, 0.41) ) 4.5 MJ NEL/kg DM</td>
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Predict methane emissions - equation 2

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\[ + 0.0443 \times (Mon - 6.36) - 0.019776 \times (Mon - 6.36)^2 \]

Level of intake: can be calculated based on FI and BW

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(de Haas et al., 2011)
Predicted ME1 (in Mcal) and ME2 (in g)

- Phenotypic correlation between ME1 and ME2: 0.63
2. Heritabilities for test-day ME

http://www.brownswiss.org/thebrownswissbreed.html
Bivariate random regression models
DMU package (Madsen and Jensen, 2012)

\[ y = Xb + Qu + Zp + e \]

- **Fixed effects**
  - Farm
  - Test-year-season
  - Fixed regression with Legendre polynomials 3 (LP 3)

- **Time dependent covariate**
  - DIM 1-305

- **LP 2 for additive genetic and permanent environment effects**

**Fixed effects**

**PE**

Vector of the test-day methane ME1 and ME2

**Ad**
Daily heritabilities for methane emissions

![Graph showing heritability over days in milk for ME1 and ME2 with peak heritability at around 200 days for ME1 and 150 days for ME2.](image-url)
3. Genetic correlations:

• test-day ME and test-day production traits
Genetic correlations

Days in milk

Genetic correlation

-1 -0.8 -0.6 -0.4 -0.2 0 0.2 0.4 0.6 0.8 1

ME2-MY

ME1-MUN

ME2-MUN
4. Genetic correlations:

- test-day ME and fertility traits
- test-day ME and clinical mastitis

http://www.brownswiss.org/thebrownswissbred.html
http://lankavet.blogspot.dk/2013/01/mastitis-in-cows.html
**Bivariate random regression and single trait models**

(***DMU package***)

\[
\begin{bmatrix}
  y_1 \\
  y_2
\end{bmatrix} = \begin{bmatrix}
  X_1 b_1 + Z_1 a_1 + W_p + e_1 \\
  X_2 b_2 + Z_2 a_2 + Q_s + e_2
\end{bmatrix}
\]

- **Dependent variables**
  - \(y_1\): test-day ME1 or ME2
  - \(y_2\): fertility traits or clinical mastitis

- **Fixed effects**
  - \(b_1\): farm, test-year-season, LP 3
  - \(b_2\): farm, calving-year-season, sex of the calf for SB

- **Random effects**
  - \(a_1\): additive genetic effect with LP 2
  - \(p\): permanent environment effect with LP 2
  - \(a_2\): additive genetic effect
  - \(s\): service sire effect for CI and SB
Genetic correlations

Days in milk

Genetic correlation

-0.2
0
0.2
0.4
0.6
0.8
1

0 50 100 150 200 250 300

ME1-DO
ME2-DO
ME1-CI
ME2-CI
5. Breeding program

- progeny testing
- genomic breeding programs
Evaluation of breeding programs
ZPLAN+ (Täubert et al., 2010)

Economic weight for milk yield was five times higher than for other traits

Progeny testing and genomic breeding program with different accuracy
Conclusions

• Methane emissions can be predicted when combining real data with deterministic equations and stochastic simulations
• Moderateheritabilities for methane emissions
• Genetic correlation between methane emissions and
  – milk yield: antagonistic
  – fertility traits: positive
• Genomic breeding program is better
  – response to selection
  – discounted return per animal
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Thank you for your attention!
## Characteristics of breeding programs

<table>
<thead>
<tr>
<th></th>
<th>Progeny testing</th>
<th>Genomic selection</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milking cow</td>
<td>25’000</td>
<td>25’000</td>
</tr>
<tr>
<td>Bull dam</td>
<td>250</td>
<td>250</td>
</tr>
<tr>
<td>Bull calves</td>
<td>125</td>
<td>125</td>
</tr>
<tr>
<td>Test bull</td>
<td>50</td>
<td>--</td>
</tr>
<tr>
<td>Proven bull</td>
<td>5</td>
<td>10</td>
</tr>
<tr>
<td>Elite bull</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Bull sire</td>
<td>80% proven bull</td>
<td>97% proven bull</td>
</tr>
<tr>
<td></td>
<td>20% elite bull</td>
<td>3% elite bull</td>
</tr>
<tr>
<td>Cow sire</td>
<td>40% test bull</td>
<td>--</td>
</tr>
<tr>
<td></td>
<td>50% proven bull</td>
<td>67% proven bull</td>
</tr>
<tr>
<td></td>
<td>10% elite bull</td>
<td>33% elite bull</td>
</tr>
</tbody>
</table>
Heritabilities and correlations among the traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>ME</th>
<th>MY</th>
<th>DO</th>
<th>CM</th>
<th>BCS</th>
<th>MT</th>
<th>Economic value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Methane emission (ME)</td>
<td>0.44</td>
<td>0.89</td>
<td>0.86</td>
<td>0.03</td>
<td>0.35</td>
<td>x</td>
<td>-6.84</td>
</tr>
<tr>
<td>Milk yield (MY)</td>
<td>0.92</td>
<td>0.34</td>
<td>0.93</td>
<td>0.04</td>
<td>-0.4</td>
<td>0</td>
<td>0.60 / 3.00</td>
</tr>
<tr>
<td>Days open (DO)</td>
<td>0.10</td>
<td>0.12</td>
<td>0.03</td>
<td>-0.18</td>
<td>-0.4</td>
<td>-0.03</td>
<td>-0.10</td>
</tr>
<tr>
<td>Clinical mastitis (CM)</td>
<td>0.02</td>
<td>0.01</td>
<td>0.02</td>
<td>0.10</td>
<td>-0.26</td>
<td>0.19</td>
<td>-1.66</td>
</tr>
<tr>
<td>Body condition score (BCS)</td>
<td>0.25</td>
<td>-0.01</td>
<td>-0.08</td>
<td>-0.01</td>
<td>0.15</td>
<td>x</td>
<td>6.11</td>
</tr>
<tr>
<td>Milking temperament (MT)</td>
<td>x</td>
<td>0</td>
<td>x</td>
<td>-0.67</td>
<td>x</td>
<td>0.04</td>
<td>8.01</td>
</tr>
<tr>
<td>Phenotypic SD</td>
<td>0.22</td>
<td>2.88</td>
<td>60.57</td>
<td>1.91</td>
<td>0.42</td>
<td>0.62</td>
<td></td>
</tr>
</tbody>
</table>
Equal economic weight was assumed for the six traits

Response to selection / genetic standard deviation

Accuracies of genomic selection

0.2  |  0.4  |  0.6  |  0.8

Progeny testing

Total discounted return per animal unit

Progeny testing and genomic breeding program with different accuracy
Total genetic gain of a bull per generation

Number of daughters for ME1 (x100) in scenario I / Accuracy in scenarios II and III