Genetic relationship between environmental impact traits and milk composition in dairy cows

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Outline of Presentation

• **Part I** – Genetic parameters for methane indicators obtained from Mid-infrared spectroscopy (MIR) of milk fatty acids (Year 2011-2012 ~ short)

• **Part II** – Development of calibration equation from direct MIR spectra of milk samples (Belgium + Ireland)

• **Part III** – Genetic parameters for methane indicator traits (predicted from part II)
Introduction

- Methane (CH$_4$) is the largest contributor to total greenhouse gas emitted by the dairy sector.
- CH$_4$ is 21 times more potent than CO$_2$ in greenhouse effect.
- Respiration chamber or Sulphur hexafluoride (SF$_6$) method are commonly used to measure CH4.
- Phenotype gap for direct methane measurement leads to indirect indicators to estimate genetic parameters:
  - Milk fatty acids (FA) in milk
  - Direct MIR prediction from milk
  - Other proxies

Why genetics?

• Genetic selection of animal having low CH$_4$ emissions
  ✓ Additive
  ✓ Permanent

Objectives

• Predictions of CH$_4$ emissions (indicators)
• Estimation of genetic parameters
• Correlations with other economic traits
Part I

Genetic parameters for CH₄ indicators obtained from MIR of milk fatty acids in dairy cows (2011-12)

Kandel, P. B.¹, N. Gengler¹, and H. Soyeurt¹,²

¹ Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium
² National Fund for Scientific Research, Brussels, Belgium
Highlights of this study

• Previously published 5 CH\textsubscript{4} prediction equations developed from gas chromatographic analysis of milk fatty acids were selected

• These equations were calibrated with MIR spectroscopy to predict methane emissions from Walloon dairy cows

• The predicted methane was in general in range of published measurements

• Heritabilities for these five CH\textsubscript{4} indicator traits were estimated from 0.19 to 0.35

Chiliard et al. 2009; Dijkstra et al. 2011
Part II

Prediction of individual enteric methane emission of dairy cows from milk mid-infrared spectra

A. Vanlierde¹, F. Dehareng¹, E. Froidmont¹, P. Dardenne¹, P. B. Kandel², N. Gengler², E. Lewis³, F. Buckley³, M. Deighton³, S. McParland³, D. Berry³ and H. Soyeurt¹

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²Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium
³Animal & Grassland Research and Innovation Center, Teagasc, Moorepark, Co. Cork, Ireland
Introduction

• Previous studies have shown that mid-infrared spectrometry can be used to predict milk FA
• FA are related to methane emissions.
• Therefore, direct prediction of methane from mid-infrared is a logical step.

Chiliard et al., 2009; Dijkstra et al., 2011, Dehareng et al., 2012
CH$_4$ was measured using SF$_6$ method and milk spectra was collected for same animal (some animals had multiple measurements)

<table>
<thead>
<tr>
<th></th>
<th>Ireland</th>
<th>Belgium</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of SF$_6$ measurements Animals</td>
<td>285</td>
<td>196</td>
</tr>
<tr>
<td></td>
<td>119</td>
<td>27</td>
</tr>
<tr>
<td>CH$_4$/day (Mean ±SD)</td>
<td>356.99±101.64</td>
<td>466.13±101.87</td>
</tr>
</tbody>
</table>
Calibration for CH$_4$ equation

- After removing potential outliers in MIR spectra and CH$_4$
- Final calibration equation

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td><strong>N</strong></td>
<td>452</td>
</tr>
<tr>
<td><strong>Mean (Reference value)</strong></td>
<td>394.58 g/day</td>
</tr>
<tr>
<td><strong>SD</strong></td>
<td>126.39 g/day</td>
</tr>
<tr>
<td><strong>SEC (standard error of calibration)</strong></td>
<td>61.97 g/day</td>
</tr>
<tr>
<td><strong>SECV (standard error of cross validation)</strong></td>
<td>68.68 g/day</td>
</tr>
<tr>
<td><strong>$R^2_{cv}$ (cross validation coefficient of determination)</strong></td>
<td>0.70</td>
</tr>
<tr>
<td><strong>RPD (residual predictive deviation)</strong></td>
<td>2.03</td>
</tr>
</tbody>
</table>
Part III

Genetic parameters for methane indicator traits obtained directly from MIR spectra in first lactation dairy cows

P. B. Kandel¹, M-L. Vanrobays¹, A. Vanlierde², F. Dehareng², E. Froidmont², P. Dardenne², S. McParland³, N. Gengler¹ and H. Soyeurt¹

¹Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium
²Walloon Agricultural Research Center, Gembloux, Belgium
³Animal & Grassland Research and Innovation Center, TEAGASC, Moorepark, Co. Cork, Ireland
Equation applied to Walloon spectral database (Holstein)

<table>
<thead>
<tr>
<th>Traits</th>
<th>Lactation 1 (N=412, 520)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CH$_4$ g/day</td>
<td>545.91±109.34</td>
</tr>
<tr>
<td>CH$_4$ g/kg of milk</td>
<td>25.01±8.88</td>
</tr>
<tr>
<td>Milk yield (kg/day)</td>
<td>23.44±5.97</td>
</tr>
<tr>
<td>Fat yield (kg/day)</td>
<td>0.92±0.23</td>
</tr>
<tr>
<td>Protein yield (kg/day)</td>
<td>0.78±0.19</td>
</tr>
</tbody>
</table>
Model: Two trait random regression test day

\[ y = X\beta + Q(Z_p + Z_u) + e \]

- **y**: MIR CH\(_4\) indicators and milk traits (two traits-each pair)
- **\(\beta\)**: herd x test day, 24 classes of days in milk, and 3 classes of age at calving \(\rightarrow\) fixed effects
- **p**: random permanent environmental effects
- **u**: additive genetic effects
- **e**: random residual effect
- **Q**: coefficients of 2\(^{nd}\) order Legendre polynomials

Variance components: REML
Fixed effects: BLUP
Averaged daily heritability

<table>
<thead>
<tr>
<th>Traits</th>
<th>heritability</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\text{CH}_4$ g/day</td>
<td>$0.07\pm0.01$</td>
</tr>
<tr>
<td>$\text{CH}_4$ intensity (g/kg of milk)</td>
<td>$0.16\pm0.01$</td>
</tr>
</tbody>
</table>
Model: Multi-trait random regression test-day model

\[ y = X\beta + Q(Z_p + Z_u) + e \]

- \( y \): MIR CH\(_4\) indicators and milk traits (total 5 traits)
- \( \beta \): herd x test day, 24 classes of days in milk, and 3 classes of age at calving \( \rightarrow \) fixed effects
- \( p \): random permanent environmental effects
- \( u \): additive genetic effects, \( e \): random residual effect
- \( Q \): coefficients of 2\(^{nd}\) order Legendre polynomials

Prior variance components - REML
Variance components – Gibbs Sampling
Fixed effect - BLUP
Relative CH$_4$ emission across lactation

For comparison first lactation first day was made zero

Fixed effect – after model
Relative CH$_4$ intensity across lactation
For comparison first lactation first day was made zero
### Averaged daily heritability

<table>
<thead>
<tr>
<th>Lactation</th>
<th>CH$_4$ (g/d)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lactation 1</td>
<td>0.10±0.01</td>
</tr>
<tr>
<td>Lactation 2</td>
<td>0.10±0.01</td>
</tr>
<tr>
<td>Lactation 3</td>
<td>0.09±0.01</td>
</tr>
</tbody>
</table>

### Averaged daily heritability

<table>
<thead>
<tr>
<th>Lactation</th>
<th>CH$_4$ intensity (g/kg FPCM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lactation 1</td>
<td>0.15±0.01</td>
</tr>
<tr>
<td>Lactation 2</td>
<td>0.15±0.01</td>
</tr>
<tr>
<td>Lactation 3</td>
<td>0.16±0.02</td>
</tr>
</tbody>
</table>
**Phenotypic (below diagonal) and genetic (above diagonal) correlations**

<table>
<thead>
<tr>
<th>Traits</th>
<th>MIR CH₄ (g/d)</th>
<th>MIR CH₄ intensity</th>
<th>FPCM</th>
<th>Fat yield</th>
<th>Protein yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>MIR CH₄ (g/d)</td>
<td></td>
<td>0.52</td>
<td>-0.01</td>
<td>0.16</td>
<td>-0.02</td>
</tr>
<tr>
<td>CH₄ intensity (g/kg of FPCM)</td>
<td>0.21</td>
<td></td>
<td>-0.84</td>
<td>-0.68</td>
<td>-0.78</td>
</tr>
<tr>
<td>FPCM</td>
<td>-0.02</td>
<td>-0.65</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fat yield</td>
<td>0.01</td>
<td>-0.58</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Protein yield</td>
<td>-0.01</td>
<td>-0.60</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Estimated Breeding Values

Sires which have daughters with MIR CH₄ records

Population mean = 166 kg
EBV = -16.6 kg
Expected methane next gen = 166 - 16.6 = 149.4 kg (if both selected sire and dam) 10% reduction
If only selected sire and average cow = 166 - (16.6/2) 8.3 = 157.7 kg (5% reduction)
Conclusions

• Production on less CH$_4$ (g/day) during peak milk production
• First lactations and second lactation different genetically and within lactations
• Obtained heritability- selection for these traits possible
• Selection of methane intensity decreases yield of milk production traits
• Genetic variability seems to exist
Perspectives

• Extend to the Walloon genetic evaluation system to access the profitability (+ve/-ve) from inclusion of methane traits in the selection index
• Genome wide association study to detect potential region of chromosome for methane emissions (50k SNP data will be utilized from DairySNP project)
Acknowledgements

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- Mathew Deighton
- Sinead McParland
- Donagh Berry

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