Analysis of methane measured in young dairy sires after accounting for variation in dry matter intake

Rhiannon Handcock
The Helical Company - rhiannon@helicalco.com
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Data Collection Timeline

- **LIC**
  - 138 bulls
  - Aged 6-10 months

- **CRV**
  - 122 bulls
  - Aged 12-16 months

Feb 2021 → Dec 2022
Data Collection Timeline

Feb 2021

LIC
- 138 bulls
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CRV
- 122 bulls
- Aged 12-16 months

Dec 2022
Data Collection Timeline

Feb 2021

LIC
- 138 bulls
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CRV
- 122 bulls
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LIC
- 226 bulls
- Aged 6-10 months

Dec 2022
Data Collection Timeline

- LIC
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  - Aged 6-10 months

- CRV
  - 122 bulls
  - Aged 12-16 months

- LIC
  - 226 bulls
  - Aged 6-10 months

- CRV
  - 45 bulls
  - Aged 12-16 months

Feb 2021

Dec 2022

531 bulls
Data

- Daily methane (CH4; g/day)
  - Measured via Greenfeed visits
  - Visits vary in number and duration
  - Total time per day 120 to 4,222s (2-70 min)
  - Mean time was 893s (~15min)

- Daily dry matter intake of pen-fed animals

- Genotypes
  - A mix of panels of varying densities
  - Approximately 6,300 SNPs in common
Model

• JWAS in Julia
• MCMC chains of 200,000 plus 25,000 chain burn-in keeping every 10th sample

• \( Y = CG + Year + pJ + \text{het} + \text{BullPermEnv} + \text{BullBV} + e \)

  • CG – day-group-pen assignment
  • Year – location-year combination
  • \( pJ \) – proportion of Jersey breed
  • \( \text{het} \) – heterosis coefficient between Holstein-Friesian and Jersey
  • \( \text{BullPermEnv} \) – random permanent environmental effect of bull
  • \( \text{BullBV} \) – random genetic effect of bull
<table>
<thead>
<tr>
<th></th>
<th>CH4 (g/day)</th>
<th>DMI (kg/day)</th>
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<tbody>
<tr>
<td><strong>Heritability</strong></td>
<td><strong>0.10</strong></td>
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<td>(0.06, 0.16)</td>
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95% lower and upper credibility intervals in parentheses
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<tr>
<td>Genetic Variance</td>
<td>202</td>
<td>0.43</td>
</tr>
<tr>
<td></td>
<td>(113, 325)</td>
<td>(0.22, 0.76)</td>
</tr>
<tr>
<td>Perm Env Variance</td>
<td>395</td>
<td>1.13</td>
</tr>
<tr>
<td></td>
<td>(295, 498)</td>
<td>(0.85, 1.41)</td>
</tr>
<tr>
<td>Residual Variance</td>
<td>1,365</td>
<td>2.63</td>
</tr>
<tr>
<td></td>
<td>(1,331, 1,398)</td>
<td>(2.57, 2.70)</td>
</tr>
<tr>
<td>Phenotypic Variance</td>
<td>1,961</td>
<td>4.19</td>
</tr>
<tr>
<td></td>
<td>(1,869, 2,077)</td>
<td>(3.97,4.47)</td>
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95% lower and upper credibility intervals in parentheses.
Methane and Dry Matter Intake

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<tr>
<td>Genetic</td>
<td>0.48</td>
<td>(0.12, 0.73)</td>
</tr>
<tr>
<td>Phenotypic</td>
<td>0.28</td>
<td>(0.24, 0.32)</td>
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- Genetic correlations higher than phenotypic correlations
- 95% CI wider for genetic correlations than phenotypic correlations
- All have significant density above zero
- Selection for lower methane would be associated with lower intakes
Residual Methane

• Residual methane EBVs from a selection index using methane and DMI EBVs

• Residual methane that is independent of **phenotypic** DMI
  • Selection for genetic residual methane where correlated changes in DMI do not compromise the overall selection efforts

• Residual methane that is independent of **genetic** DMI
  • Selection for residual methane while holding DMI EBV constant
Phenotypic regression

\[ \begin{align*}
P &= \begin{array}{ccc}
\text{CH4} & 1961 & 25.4 \\
\text{DMI} & 25.4 & 4.19
\end{array} \\
G &= \begin{array}{ccc}
\text{CH4} & 202 & 4.6 \\
\text{DMI} & 4.6 & 0.43
\end{array}
\end{align*} \]

\[ \begin{bmatrix}
\text{var}(y_f) & c_s' \\
 c_s & P_s
\end{bmatrix} \]

\[ b'_s = c'_s P_s^{-1} \]

\[ b' = (1 - b'_s) \]

\[ b' = [1 \quad -6.06] \]

\[ \text{CH4\_phen\_EBV} = \text{CH4\_EBV} + -6.06*\text{DMI\_EBV} \]
Genetic regression

\[ \begin{bmatrix}
\text{var}(y_f) & c'_s \\
c_s & P_s
\end{bmatrix} \]

\[ b'_s = g'_s G_s^{-1} \]

\[ b' = (1 - b'_s) \]

\[ b' = [1, -10.7] \]

\[ \text{CH4_gen_EBV} = \text{CH4_EBV} + -10.7 \times \text{DMI_EBV} \]
EBV correlations

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<tr>
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<th>CH4_gen</th>
<th>DMI</th>
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<tr>
<td>CH4</td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH4_phen</td>
<td>0.97</td>
<td>1.00</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH4_gen</td>
<td>0.90</td>
<td>0.98</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>DMI</td>
<td>0.46</td>
<td>0.23</td>
<td>0.02</td>
<td>1.00</td>
</tr>
</tbody>
</table>

- $\text{CH4}_{\text{phen}}_{\text{EBV}} = \text{Methane}_{\text{EBV}} - 6.06 \times \text{DMI}_{\text{EBV}}$
- $\text{CH4}_{\text{gen}}_{\text{EBV}} = \text{Methane}_{\text{EBV}} - 10.7 \times \text{DMI}_{\text{EBV}}$
Summary to date:

- Heritability and repeatability of daily methane yield in bulls were low to moderate
- Repeatability is not high so more measurements will improve prediction accuracy
  - but this comes at a cost (fewer bulls or larger facility)
- Genetic and phenotypic correlations between methane and DMI were positive
- After accounting for genetic variation in DMI, there was genetic variation in methane remaining
  
  Scope exists to reduce daily methane yields while maintaining DMI