Large scale phenotyping of methane for genetic evaluation is possible with Sniffers

ICAR - Recording and selection tools for feed efficiency and environmental impact

1/06/2022 Michael Aldridge, Anouk van Breukelen, Roel Veerkamp, Yvette de Haas

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Introduction

- The Dutch Government climate goals
  - 55% by 2030
  - Carbon neutral by 2050

- Breeding is a useful tool to help achieve these goals

- We have reviewed our decision and results on large scale recording with sniffers
Current Projects

- **Climate envelope**
  - Data collection with sniffers and GreenFeed
  - Preliminary genetic parameters
  - Microbiability
  - N and P use efficiency

- **Climate Smart Cattle Breeding**
  - Goal is to have breeding values available for selection
  - Recording methane on 100 farms
  - Parameter estimation and developing a selection index
Why do we want to do large scale recording?

Current trends

- Methane production (g/day)
- Methane intensity (g/kg)

Year

With CH$_4$ selection

- Methane intensity (g/kg)
  - With no selection
  - Genomic prediction
  - Theoretical maximum

Year

Why do we want to do large scale recording?

[Graph showing reliability of prediction (%) vs. number of years recording for recording with 50 and 100 sniffers.]

Developing a sniffer and lessons learned

- 15 first generation sniffers
  - To date, over 1,800 cows and over 300,000 individual visits
  - Prone to calibration drift
  - Accuracy limitations
  - Susceptible to environment
  - Difficult to carry and mount
  - Data transfer was constrained
Developing a sniffer and lessons learned

- 90 second generation sniffers
  - Still a developing technology
  - Higher accuracy (potentially)
  - Improved housing
  - Communication integration
Installation of sniffers

- 15-20 sniffers currently installed in barns
- 100 sniffers will be installed by the end of summer
- Sniffers will be installed for 2 years
- Recording methane on over 15,000 cows
Installation of GreenFeed

- GreenFeed has been installed on 16 farms
  - To date 822 cows phenotyped
  - GreenFeed continues to be used in the Climate Envelope
  - We are not actively using GreenFeed for large scale phenotyping
Use of large scale recording in genetics

- Data processing is needed to match milking robot and sniffer information, identify sniffer malfunctions, and remove background methane.
- Visit, daily and weekly methane are:
  - Heritable (0.13 to 0.32)
  - Repeatable (0.30 to 0.68)

https://doi.org/10.3168/jds.2021-21420 (Breukelen et al. 2022)
Phenotypic analyses

**GreenFeed**

![Graph showing Mean CH₄ (g/day) over Days in milk]

**Sniffer**

![Graph showing Mean CH₄ (ppm) over Days in milk]

![Graph showing Mean CH₄ (g/day) over Hour of the day]

![Graph showing Mean CH₄ (ppm) over Hour of the day]
## Parameter estimates

### Daily methane parameter estimates

<table>
<thead>
<tr>
<th></th>
<th>GF CH$_4$</th>
<th>Sniffer CH$_4$</th>
</tr>
</thead>
<tbody>
<tr>
<td>GF CH$_4$</td>
<td><strong>0.20 ± 0.02</strong></td>
<td>0.39 ± 0.03</td>
</tr>
<tr>
<td>Sniffer CH$_4$</td>
<td>0.71 ± 0.13</td>
<td><strong>0.18 ± 0.01</strong></td>
</tr>
</tbody>
</table>

Heritabilities are reported on the diagonal, phenotypic correlation above and genetic correlation below the diagonal.

Estimates for CO$_2$ and weekly methane are available in an additional slide if you are interested.

More information is available in WCGALP and will be submitted for publication soon (contact anouk.vanbreukelen@wur.nl)
Next steps

- Microbiome rumen sampling and parameter estimation
- Continue installation on 100 farms
- Genetic correlations with other traits in the selection index
- Develop a selection index
- Publish breeding values for methane
Thank you

Large scale phenotyping of methane for genetic evaluation is possible with Sniffers

Michael Aldridge, Anouk van Breukelen, Roel Veerkamp, Yvette de Haas
### Daily methane parameter estimates

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<tr>
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<th>GF CH₄</th>
<th>GF CO₂</th>
<th>Sniffer CH₄</th>
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</tr>
</thead>
<tbody>
<tr>
<td>GF CH₄</td>
<td><strong>0.20 ± 0.02</strong></td>
<td>0.69 ± 0.01</td>
<td>0.39 ± 0.03</td>
<td>0.20 ± 0.04</td>
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<tr>
<td>GF CO₂</td>
<td>0.94 ± 0.03</td>
<td><strong>0.26 ± 0.03</strong></td>
<td>0.32 ± 0.04</td>
<td>0.25 ± 0.04</td>
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<tr>
<td>Sniffer CH₄</td>
<td>0.71 ± 0.13</td>
<td>0.54 ± 0.15</td>
<td><strong>0.18 ± 0.01</strong></td>
<td>0.78 ± &lt;0.01</td>
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<tr>
<td>Sniffer CO₂</td>
<td>0.39 ± 0.16</td>
<td>0.51 ± 0.15</td>
<td>0.93 ± 0.01</td>
<td><strong>0.20 ± 0.01</strong></td>
</tr>
</tbody>
</table>

### Weekly methane parameter estimates

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<th>GF CO₂</th>
<th>Sniffer CH₄</th>
<th>Sniffer CO₂</th>
</tr>
</thead>
<tbody>
<tr>
<td>GF CH₄</td>
<td><strong>0.33 ± 0.04</strong></td>
<td>0.76 ± 0.01</td>
<td>0.37 ± 0.05</td>
<td>0.19 ± 0.06</td>
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<tr>
<td>GF CO₂</td>
<td>0.65 ± 0.05</td>
<td><strong>0.34 ± 0.05</strong></td>
<td>0.31 ± 0.05</td>
<td>0.24 ± 0.06</td>
</tr>
<tr>
<td>Sniffer CH₄</td>
<td>0.76 ± 0.15</td>
<td>0.72 ± 0.16</td>
<td><strong>0.32 ± 0.02</strong></td>
<td>0.84 ± &lt;0.01</td>
</tr>
<tr>
<td>Sniffer CO₂</td>
<td>0.41 ± 0.18</td>
<td>0.60 ± 0.17</td>
<td>0.93 ± 0.01</td>
<td><strong>0.32 ± 0.02</strong></td>
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