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









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



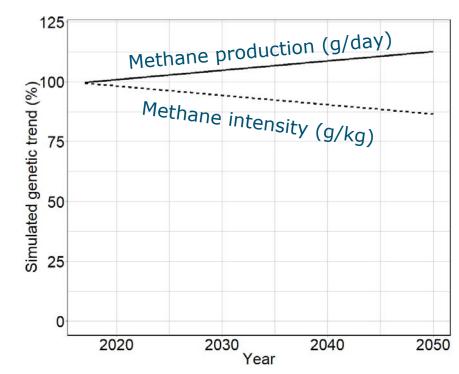
- Goal is to have breeding values available for selection
- Recording methane on 100 farms
- Parameter estimation and developing a selection index



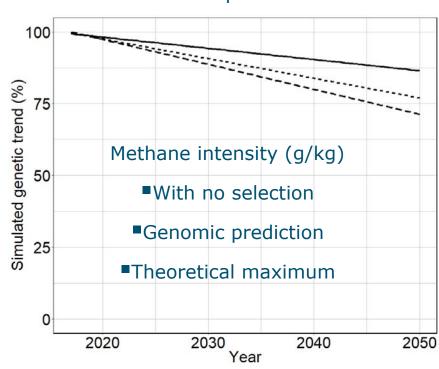


Why do we want to do large scale recording?

Current trends

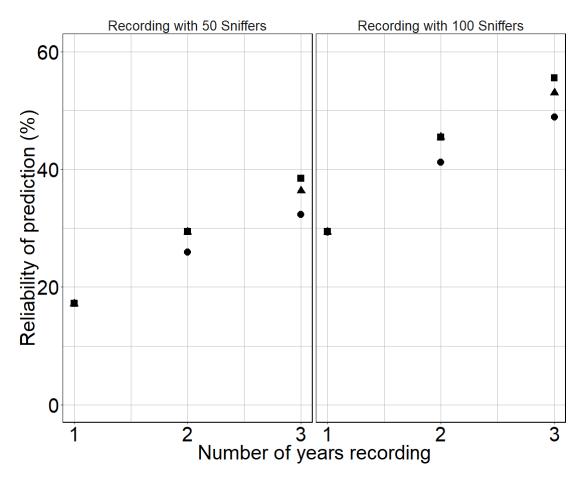


With CH₄ selection





Why do we want to do large scale recording?





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

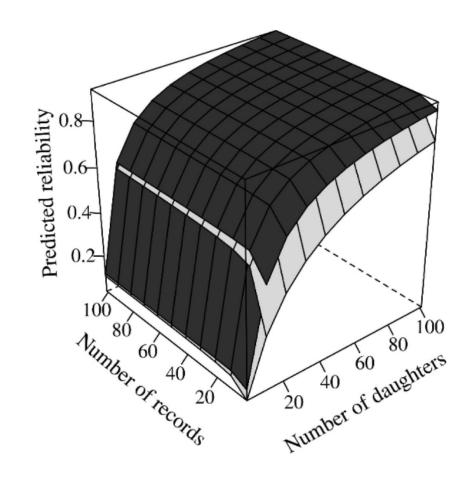






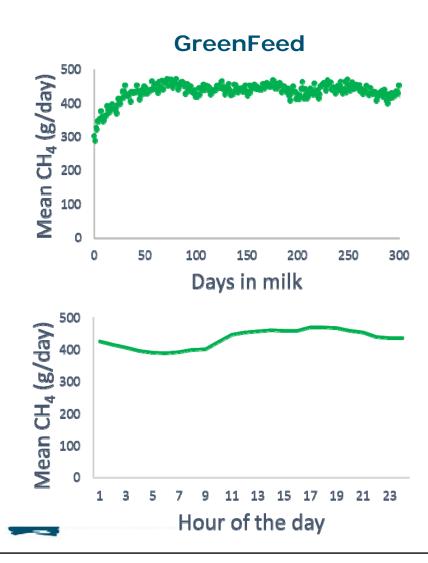
Use of large scale recording in genetics

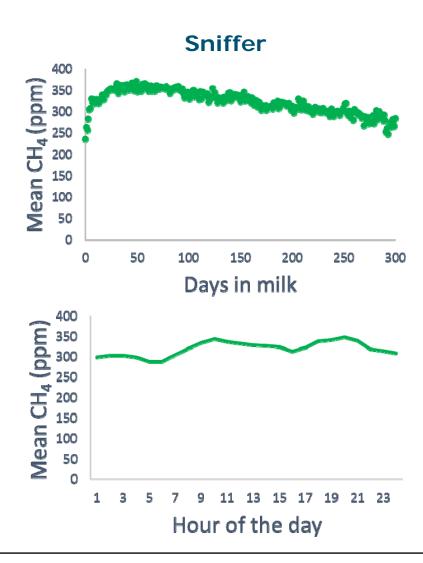
- Data processing is needed to match milking robot and sniffer information, identify sniffer malfunctions, and remove background methane.
- Visit, daily and weekly methane are:
 - Heritable (0.13 to 0.32)
 - Repeatable (0.30 to 0.68)





Phenotypic analyses





Parameter estimates

Daily methane parameter estimates

	GF CH ₄	Sniffer CH ₄
GF CH ₄	0.20 ± 0.02	0.39 ± 0.03
Sniffer CH ₄	0.71 ± 0.13	0.18 ± 0.01

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

Estimates for CO₂ and weekly methane are available in an additional slide if you are interested.



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

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Daily methane parameter estimates

	GF CH ₄	GF CO ₂	Sniffer CH ₄	Sniffer CO ₂
GF CH ₄	0.20 ± 0.02	0.69 ± 0.01	0.39 ± 0.03	0.20 ± 0.04
GF CO ₂	0.94 ± 0.03	0.26 ± 0.03	0.32 ± 0.04	0.25 ± 0.04
Sniffer CH ₄	0.71 ± 0.13	0.54 ± 0.15	0.18 ± 0.01	$0.78 \pm < 0.01$
Sniffer CO ₂	0.39 ± 0.16	0.51 ± 0.15	0.93 ± 0.01	0.20 ± 0.01

Weekly methane parameter estimates

	GF CH ₄	GF CO ₂	Sniffer CH ₄	Sniffer CO ₂
GF CH ₄	0.33 ± 0.04	0.76 ± 0.01	0.37 ± 0.05	0.19 ± 0.06
GF CO ₂	0.65 ± 0.05	0.34 ± 0.05	0.31 ± 0.05	0.24 ± 0.06
Sniffer CH ₄	0.76 ± 0.15	0.72 ± 0.16	0.32 ± 0.02	$0.84 \pm < 0.01$
Sniffer CO ₂	0.41 ± 0.18	0.60 ± 0.17	0.93 ± 0.01	0.32 ± 0.02

