

Where have we come with breeding for CH₄ emissions?

Update from international collaborations

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Where have we come with breeding for CH₄ emissions?



The Innovation Fund Denmark's Grand Solution Prize is awarded to three researchers for their breeding of climate-friendly cows

Peter Løvendahl from the Department of Molecular Biology and Genetics at Aarhus University, Jan Lassen from Viking Genetics and Henrik Bjørn Nielsen from the Technical University of Denmark receive the Innovation Fund Denmark's Grand Solution Prize for the breeding of climate-friendly cows, which alone in Denmark ensures a reduced emission equivalent to 90,000 tonnes of CO₂ a year. The prize was awarded by Søren Pind, Minister for Higher Education and Science.

2018.01.29 | [LISBETH HEILESEN](#)



The three recipients of the Innovation Fund Denmark's Grand Solution Prize. Left: Senior Researcher Peter Løvendahl, Department of Molecular Biology and Genetics, Aarhus University; Project Manager Jan Lassen, Viking Genetics and Chief Scientific Officer Henrik Bjørn Nielsen, The Technical University of Denmark. Photo: Maiken Kestner.

Discussion areas in different consortia focus on:

1. Pros and cons of several trait definitions for methane emission;
2. Proxies for methane emissions to be used for genetic evaluations;
3. Protocols for collating large-scale methane measurements using different techniques; and
4. Benefits for producers when incorporating methane emissions into national breeding strategies.



Definitions of methane phenotypes

Trait	Definition	Strength	Weakness
Methane production	Methane production per day (l or g/d)	The pure trait that we want to improve	Highly correlated to feed intake and production level
Methane intensity	Methane production per kg milk or live weight	The phenotype of interest for the user	Ratio trait so selection can be hard to incorporate properly
Methane yield	Methane production per DMI	The phenotype of interest for the user	Ratio trait so selection can be hard to incorporate properly
Residual methane production	Difference observed and predicted methane production	Nice statistical properties. Corrected for traits that influences methane production	Can be hard to explain for users

Ratio vs Residual vs Multi-trait



Aim: to reduce methane but still increase milk yield

- Ratio $I = \text{Milk} + \downarrow \text{Methane/Milk}$
 - Residual Methane $I(\text{Methane}) = \text{Milk} + \downarrow (\mu + \beta \text{Milk})$
 - Multi-trait $I = \text{Milk} + \downarrow \text{Methane}$
-
- r_g and r_e between CH_4 and Milk = 0.30
 - Genetic gain (ΔG) for milk was kept constant at 65.8 kg

Conclusions on methane phenotype

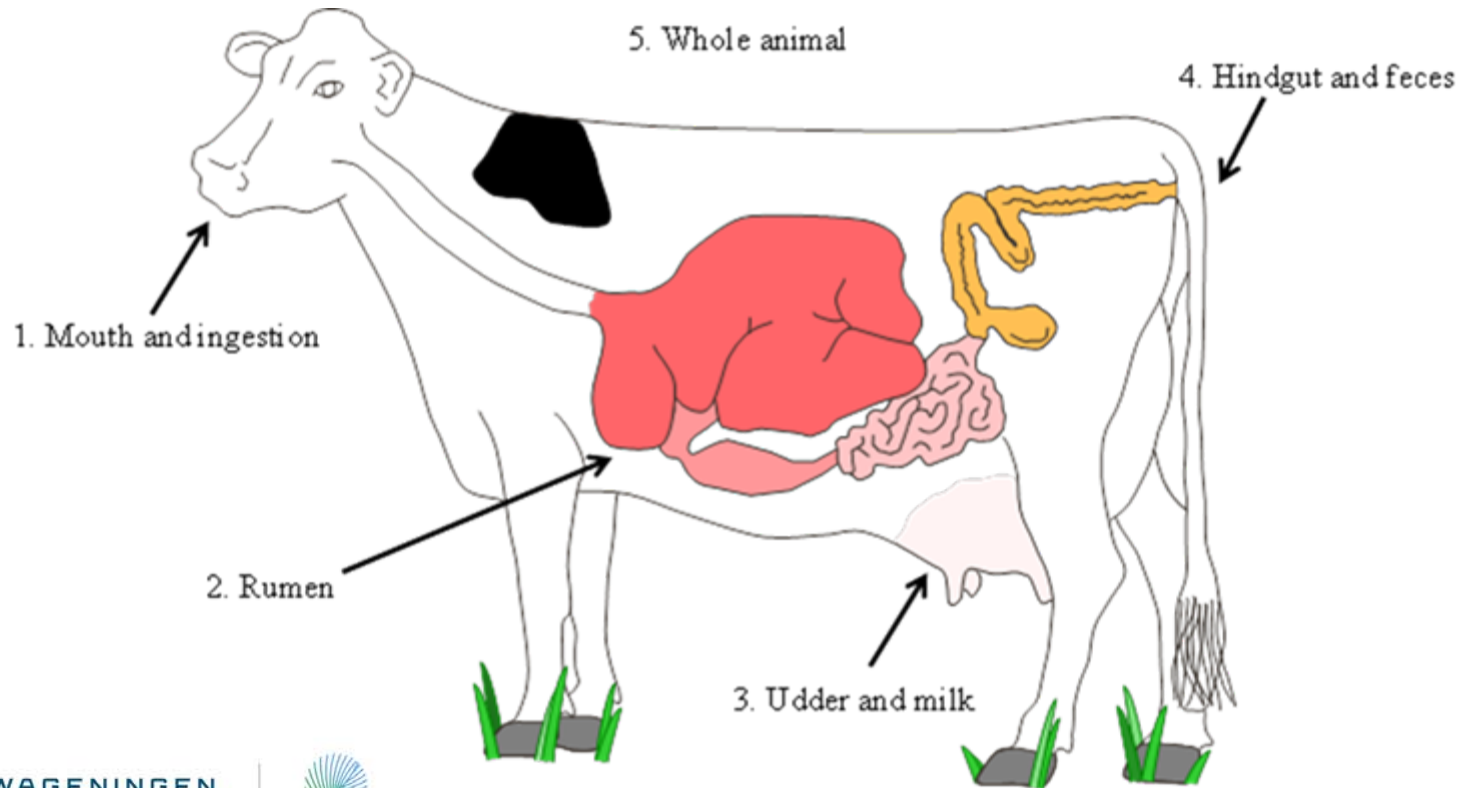
- In order to improve a trait defined as a ratio, selecting for its component traits brings highest genetic progress
- All trait definitions serve certain purposes
 - Collecting methane production is, however, key



Proxies for methane

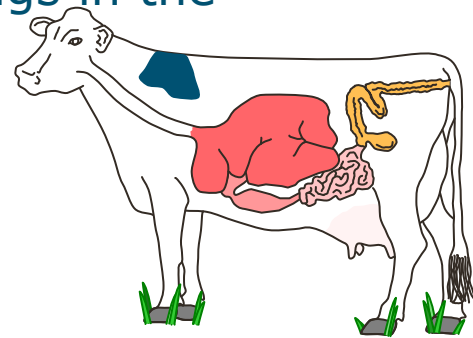


Proxies for methane

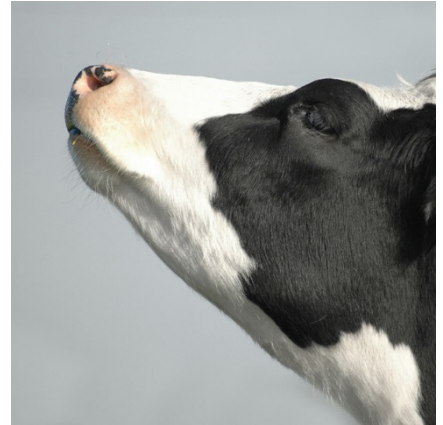


Conclusions on proxies

- No single proxy was found to accurately predict CH_4
- A combination of two or more proxies is a better solution
 - Combining proxies can increase the accuracy of predictions by up to 15 - 35%
 - Different proxies describe independent sources of variation in CH_4 and one proxy can correct for shortcomings in the other(s)



Protocols to collate methane data



Measuring methane



Respiration chambers



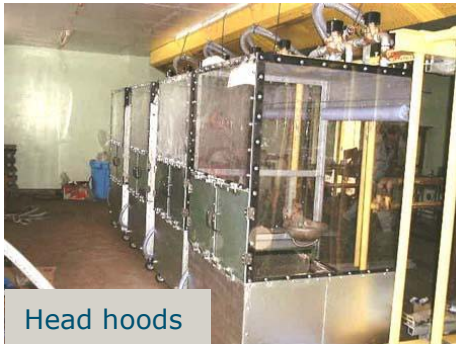
Laser



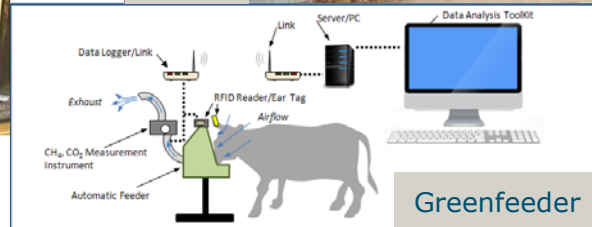
Boxes



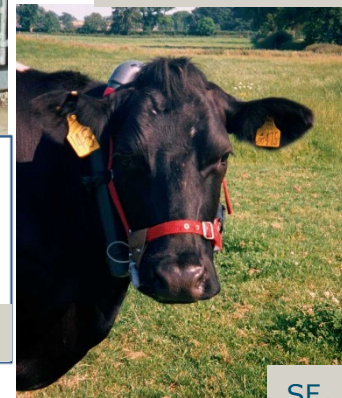
Sniffers (robot)



Head hoods

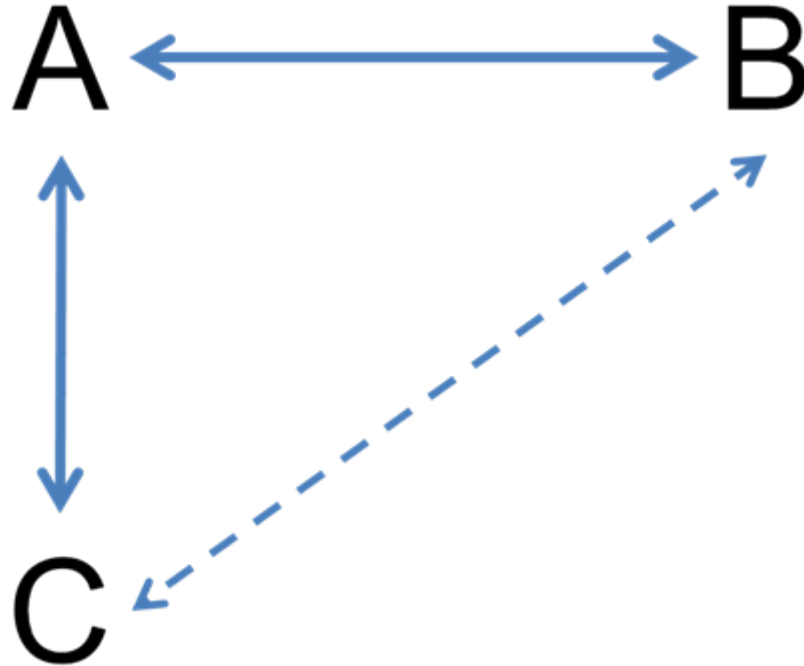


Greenfeeder



SF₆

Can we link methods?



How well do methods correlate?

	Mass Flux Methods			Concentration Methods				
	Chamber	SF ₆	GF	LMD	NDIR Peaks	NDIR CO ₂ tracer1	FTIR CO ₂ tracer1	PAIR CO ₂ tracer2
Respiration Chamber	1							
SF ₆	0.87	1						
GreenFeed	0.81	0.40^B	1					
LMD			0.77	1				
NDIR Peaks	0.89^A				1			
NDIR CO ₂ tracer1	0.72^A		0.64	0.56	0.58	1		
FTIR CO ₂ tracer1				0.60	0.53	0.97	1	
PAIR CO ₂ tracer2	0.80^{AB}							1

How well do methods correlate?

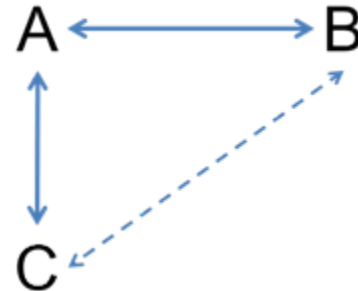
	Mass Flux Methods			Concentration Methods				
	Chamber	SF ₆	GF	LMD	NDIR Peaks	NDIR CO ₂ tracer1	FTIR CO ₂ tracer1	PAIR CO ₂ tracer2
Respiration Chamber	1							
SF ₆	0.87	1						
GreenFeed	0.81	0.40^B	1					
LMD	(0.41 – 0.71)	(0.32 - 0.62)	0.77	1				
NDIR Peaks	0.89^A	(0.36 - 0.74)	(0.24 - 0.82)	(0.36 - 0.96)	1			
NDIR CO ₂ tracer1	0.72^A	(0.08 - 0.81)	0.64	0.56	0.58	1		
FTIR CO ₂ tracer1	(0.31 - 0.76)	(-0.26 – 0.71)	(0.48 - 0.70)	0.60	0.53	0.97	1	
PAIR CO ₂ tracer2	0.80^{AB}	(0.44 – 0.80)	(0.18 - 0.80)	(0.16 - 0.89)	(0.59 - 0.85)	(0.01 - 0.83)	(-0.23 - 0.83)	1

How well do methods agree?

	Mass Flux Methods			Concentration Methods				
	Chamber	SF ₆	GF	LMD	NDIR Peaks	NDIR CO ₂ tracer1	FTIR CO ₂ tracer1	PAIR CO ₂ tracer2
Respiration Chamber	1	0.30	0.41	(0.10 – 0.69)	0.88^A	0.38	(0.09 -0.49)	0.70^A
SF ₆	0.87	1	0.34	(0.07 - 0.56)	(0.09 - 0.55)	(-0.14 - 0.68)	(-0.25 - 0.53)	(0.06 - 0.84)
GreenFeed	0.81	0.40^B	1	0.18	(0.04 - 0.51)	0.14	(-0.29 - 0.55)	(0.06 - 0.66)
LMD	(0.41 – 0.71)	(0.32 - 0.62)	0.77	1	(0.31 - 0.86)	0.18	0.20	(0.31 - 0.67)
NDIR Peaks	0.89^A	(0.36 - 0.74)	(0.24 - 0.82)	(0.36 - 0.96)	1	0.14	0.15	(0.32 - 0.65)
NDIR CO ₂ tracer1	0.72^A	(0.08 - 0.81)	0.64	0.56	0.58	1	0.79	(0.11 - 0.74)
FTIR CO ₂ tracer1	(0.31 - 0.76)	(-0.26 – 0.71)	(0.48 - 0.70)	0.60	0.53	0.97	1	(-0.29- 0.75)
PAIR CO ₂ tracer2	0.80^{AB}	(0.44 – 0.80)	(0.18 - 0.80)	(0.16 - 0.89)	(0.59 - 0.85)	(0.01 - 0.83)	(-0.23 - 0.83)	1

Conclusions on collating data

- Generally good correlation between methods
- Concordance is less good, but generally positive
- Combining predictions shows promise, but reveals some biases
- Combining data for genetic analysis – does it require perfect agreement?



Genetics of methane



What is the genetic component of methane?

Heritabilities:

■ Sheep

- MeP: 0.29 (0.05)
- MeY: 0.13 (0.02)

Pinares-Patino et al., 2016

■ Beef

- MeP: 0.29 (0.05)
- MeY: 0.13 (0.10)

Donoghue et al., 2013

■ Dairy

- MeP: 0.29 (0.05)
- MeY: 0.13 (0.04)

Pinares-Patino et al., 2016

- MeP w DMI: 0.35
- De Haas et al., 2012*

- MeP w MIR: 0.12
- Kandel et al., 2013*

Heritabilities range between 0.1 and 0.4

What are correlations with other traits?

Genetic correlations (MeI)

- Milk yield and content
 - $\sim -0.6, -0.1, -0.4$
- Fertility: 0.3
- BSC: 0.3
- Longevity: -0.1

Kandel et al., 2017

Genetic correlations (MeP)

- Milk yield
 - 0.1
- Body weight: -0.2

Lassen et al., 2016

Selection index with methane



- Starting from current total merit indices in



- Scenario 1: Including CH_4 in current breeding goals
- Scenario 2: Including CH_4 , whilst restricting the genetic gain of CH_4 to zero
- Scenario 3: Including CH_4 , whilst assigning an economic cost to CH_4 (3 shadow prices were investigated)

Scenarios

	Scenario 1		Scenario 2		Scenario 3	
	Index value	Genetic gain CH ₄				
UK	£85.2	8.48g/d				
ES	€91.9	7.30g/d				
NL	€228.3	3.93g/d				

Scenarios

	Scenario 1		Scenario 2		Scenario 3	
	Index value	Genetic gain CH ₄	Total change	Percentage change		
UK	£85.2	8.48g/d	-£12.85	-14%		
ES	€91.9	7.30g/d	-€11.09	-12%		
NL	€228.3	3.93g/d	-€7.23	-3%		

Scenarios

	Scenario 1		Scenario 2		Scenario 3	
	Index value	Genetic gain CH ₄	Total change	Percentage change	Carbon price (lit)	Carbon price (high)
UK	£85.2	8.48g/d	-£12.85	-14%	-0.59	-1.75
ES	€91.9	7.30g/d	-€11.09	-12%	-0.63	-1.85
NL	€228.3	3.93g/d	-€7.23	-3%	-0.31	-0.88

Conclusions on benefit for producers

- Breeding is a mitigation tool
 - Heritabilities 0.1-0.4
- Benefit for producers depends on incentives and carbon taxes/prices

Climate change means meat taxes are 'increasingly probable'

By Matt Mace | edie.net

📅 15 dec. 2017

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Summarizing conclusions

- Enteric methane is a heritable trait
 - highly genetically correlated with DMI
- Most useful proxies relate to feed intake, milk mid-infrared spectral data, and fatty acids in the milk
- International collaboration is essential to make progress in this area
 - sharing ideas, experiences, protocols and phenotypes
 - coming to a consensus regarding what phenotype to collect and to select for
 - collating large enough datasets for genetic evaluations

Acknowledgements



METHAGENE



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ASGGN

The animal selection, genetics
and genomics network.