Large-scale methane measurements on individual ruminants for genetic evaluations

Yvette de Haas and Jan Lassen

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It all started in 2012 ☺

EAAP

Starting date: Dec 9th, 2013

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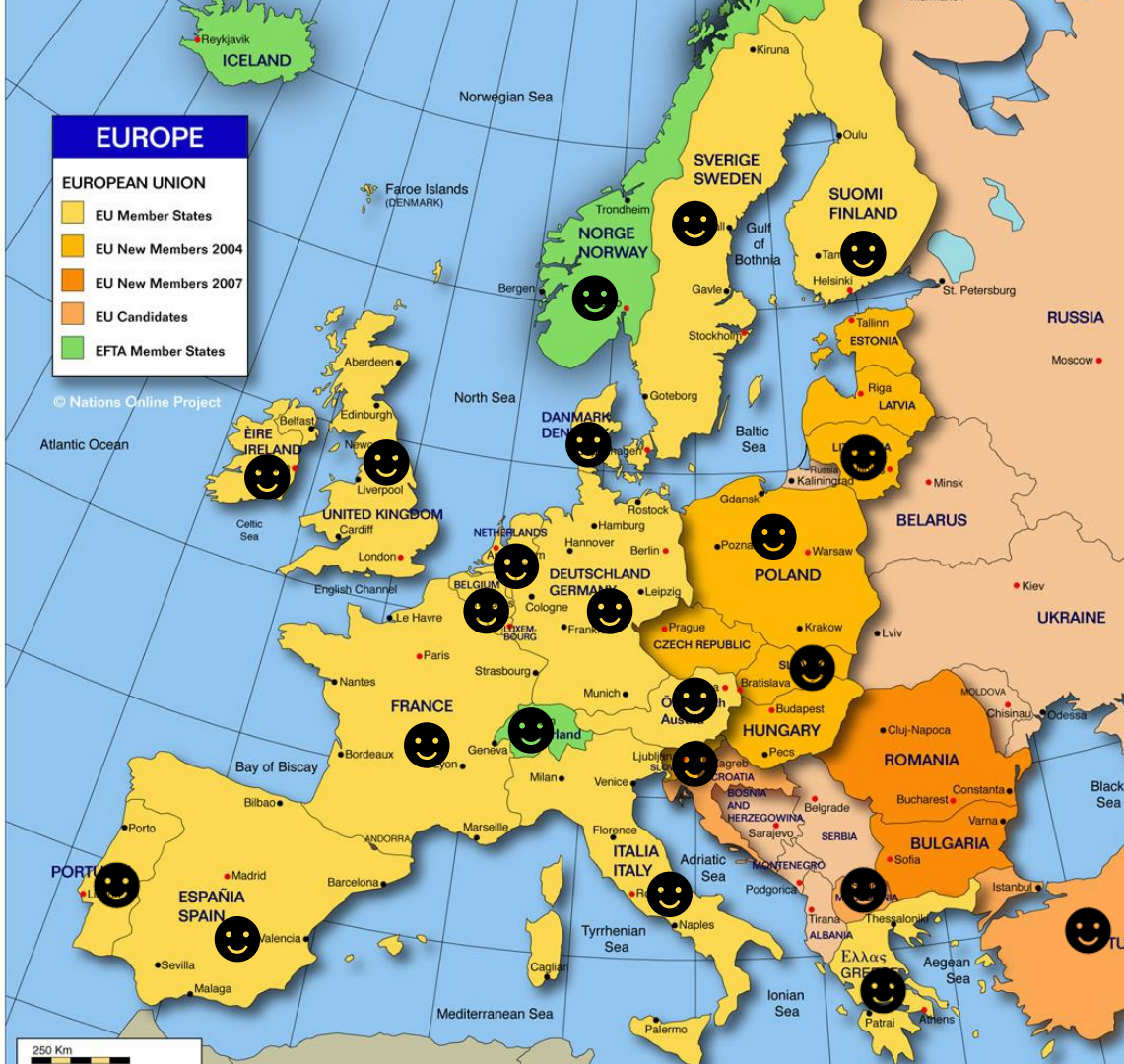

Objectives of METHAGENE

- Describe methane determining factors and decide on best trait for methane emission;
- Identify proxies for methane emissions to be used for genetic evaluations;
- Harmonise protocols for large-scale methane measurements using different techniques; and
- Quantify benefits for producers when incorporating methane emissions into national breeding strategies.

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What factors affect methane?

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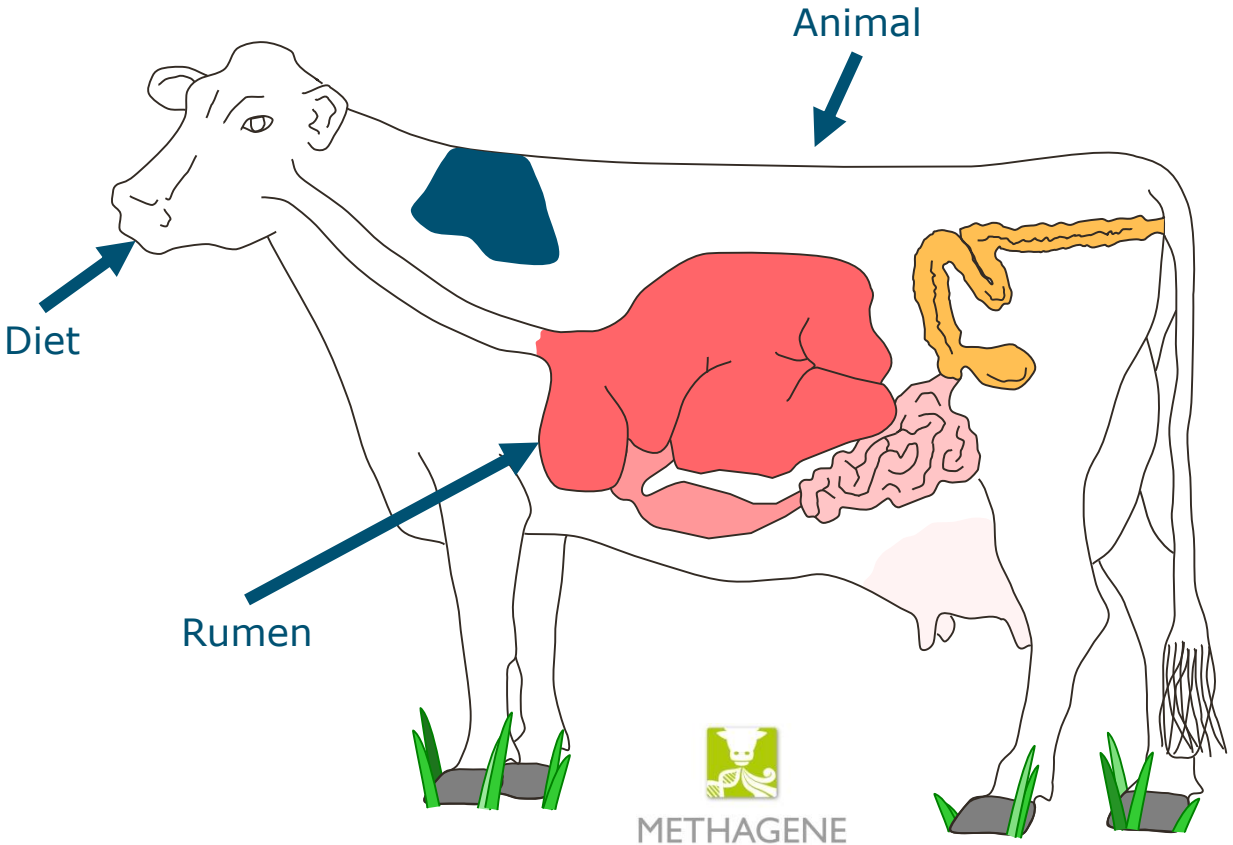
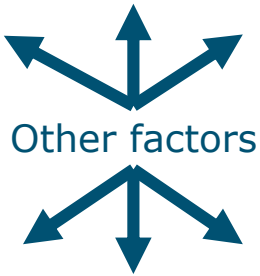
Methane-determining factors





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1. Diet

- Dry matter intake
- Diet composition
  - Fiber
  - Ether extract
  - Lignin
  - Starch
  - Suger
  - Protein
  - Fat
- Forage:concentrate ratio
- Grass:maize ratio
- Additives
  - Oil
  - Tannins
  - Nitrate
  - Enzymes
  - ...

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2. Rumen

- Microbial types
  - Protozoa
  - Fungi
  - Archaea
  - Bacteria
  - Virus
- Rumen volume
- Rumen size
- Rumen shape
- Retention time
- Passage rate
- Digestibility

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3. Animal

- Body weight
- Body conformation
- Lungs
- Production level + composition
- Lactation stage
- Parity
- Genetics
- Breed
- Gender
- Immune system

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4. Other

- Diurnal pattern
  - Feeding behaviour?
- Seasonal pattern
  - Diet?
  - Weather?
- Disease
  - Feed intake?

Best methane phenotype

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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 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

Design of the experiment

Multitrait	I = Milk + ↓Methane
Ratio	I = Milk + ↓Methane/Milk
Residual Methane	I(Methane) = Milk + ↓(μ+βMilk)

- r_g and r_e between CH_4 and Milk = 0.30
- Genetic gain (ΔG) for milk was kept constant at 65.8 kg

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Zetouni et al. (2017) - J. Anim. Sci. 95:1921–1925

Table 1. Expected genetic gain methane (in L) for the three selection indexes, in scheme calibrated to keep ΔG_{milk} = 65.8 kg

Indexes	CH_4
Multitrait	**24.8**
Ratio	**27.1**
Residual Methane	**27.3**

ΔG_{meth} was most favourable for the Multitrait index, when keeping the Δg_{milk} constant (65.8 kg)

Table 2. Estimated genetic and residual correlations between traits

	Milk	Meth	ResM	Ratio
Milk	-	0.30	-0.002	-0.97
Meth	0.30	-	NA	-0.082
ResM	-0.10	NA	-	-0.083
Ratio	-0.98	-0.12	-0.13	-

r_g between Methane and Ratio are small, implying that selection for the ratio wouldn't be effective in reducing methane emissions.

Zetouni et al. (2017) - J. Anim. Sci. 95:1921–1925

Larissa's conclusion

In order to improve a trait defined as a ratio, selecting for its component traits brings higher genetic progress

Zetouni et al. (2017) - J. Anim. Sci. 95:1921–1925

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Conclusion of METHAGENE consortium

Best methane phenotype

It depends!

How you express it, depends:

- On the audience
- On the purpose
- On your discipline

But for all you need methane production

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Which proxies for methane?

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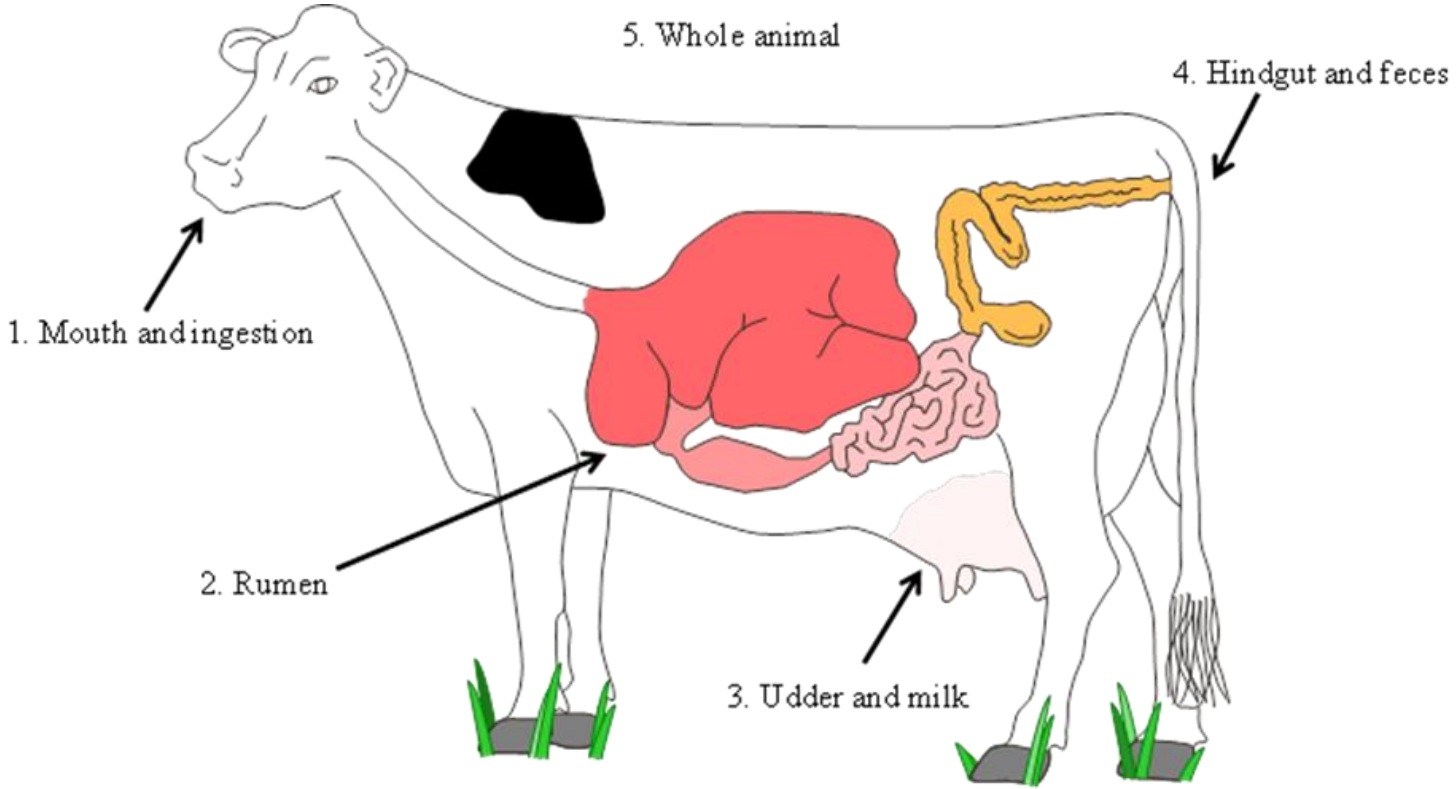
Proxies for methane



Negussie et al. (2017) - J. Dairy Sci. 100:2433-2453

1. Mouth and ingestion

Dry Matter Intake

Rumination time

Feeding behaviour

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2. Rumen

Rumen microbiome

Methanogens

Rumen volume

Protozoa

Retention time

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3. Udder and milk

Milk yield and composition

Milk fatty acids

MIR spectra

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4. Hindgut and faeces

Faecal ether lipids

Digestibility

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5. Whole animal

Body weight – conformation traits

Lactation stage

Animal type

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Best proxy

It depends!

- 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)

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Negussie et al. (2017) - J. Dairy Sci. 100:2433-2453

How to record methane?

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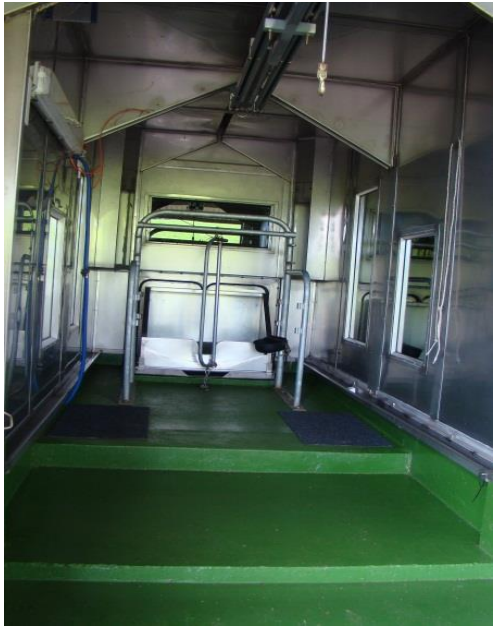
Measuring equipments (1/3)



Respiration chamber
Gold standard!

SF_6

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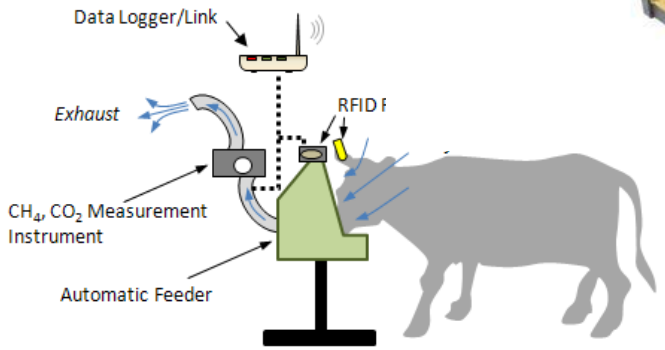
Measuring equipments (2/3)

Laser

Sniffers (FTIR)



GreenFeed

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Measuring equipments (3/3)

Butter boxes

Head hoods

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Features of equipments

- Robustness
- Intrusiveness
- Costs of 1 measurement
- Throughput
- Total time in life that animal can be recorded
- Labour intensity
- Automated matching with animal ID (risk on mistakes)
- Flow / Flux
- Concentration

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Best device

It depends!

- No method is completely ideal for large scale monitoring
- Need to be aware of limitations
- All methods (used properly) provide valuable information
- All methods provide variable information
- Can we combine data sets from different methods?

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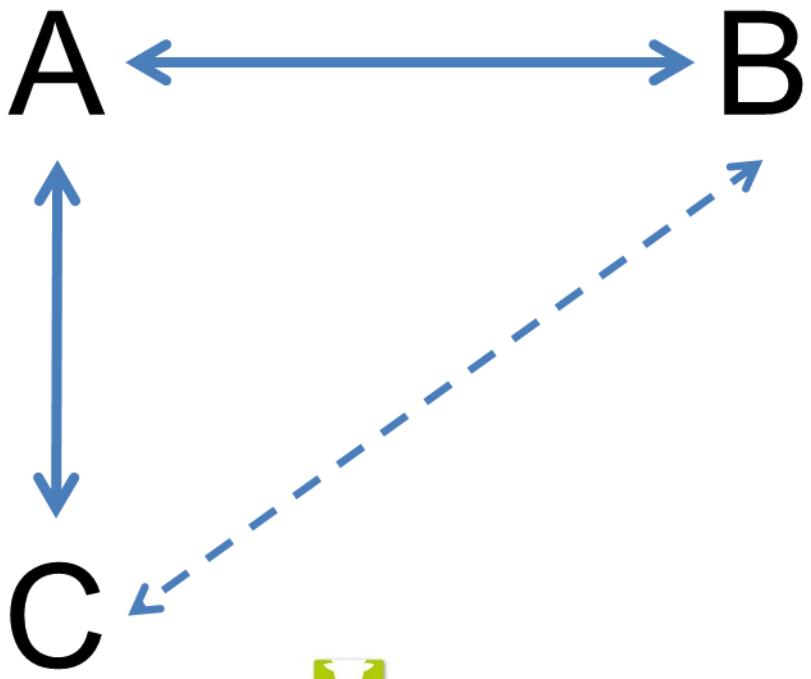
Can we link methods?



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How well do methods correlate?

	Mass Flux Methods			Concentration Methods				
	Chamber	SF_6	GF	LMD	NDIR Peaks	NDIR CO_2tracer1	FTIR CO_2tracer1	PAIR CO_2tracer2
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_2tracer1	**0.72**^{A}		**0.64**	**0.56**	**0.58**	1		
FTIR CO_2tracer1				**0.60**	**0.53**	**0.97**	1	
PAIR CO_2tracer2	**0.80**^{AB}							1

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Actual correlations

How well do methods correlate?

	Mass Flux Methods			Concentration Methods				
	Chamber	SF_6	GF	LMD	NDIR Peaks	NDIR CO_2tracer1	FTIR CO_2tracer1	PAIR CO_2tracer2
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_2tracer1	**0.72**[A]	(0.08 - 0.81)	**0.64**	**0.56**	**0.58**	1		
FTIR CO_2tracer1	(0.31 - 0.76)	(-0.26 – 0.71)	(0.48 - 0.70)	**0.60**	**0.53**	**0.97**	1	
PAIR CO_2tracer2	**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

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Inferred correlations

How well do methods agree?

	Mass Flux Methods			Concentration Methods				
	Chamber	SF_6	GF	LMD	NDIR Peaks	NDIR CO_2tracer1	FTIR CO_2tracer1	PAIR CO_2tracer2
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_2tracer1	**0.72**[A]	(0.08 - 0.81)	**0.64**	**0.56**	**0.58**	1	**0.79**	(0.11 - 0.74)
FTIR CO_2tracer1	(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_2tracer2	**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

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Concordance (CCC)

Conclusions – comparing and harmonizing

- 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?

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The genetic component of methane

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Is there a genetic component in methane?

Heritabilities:

- Sheep
  - MeP: 0.29 (0.05)
  - MeY: 0.13 (0.03)

  Pinares-Patino et al., 2013
- Beef
  - MeP: 0.40 (0.11)
  - MeY: 0.19 (0.10)

  Donoghue et al., 2013
- Dairy
  - MeP: 0.21 (0.06)
  - MeI: 0.16 (0.04)

  Lassen et al., 2016
- Predicted methane
  - MeP w DMI: 0.35

  De Haas et al., 2012
  - MeP w MIR: 0.12

  Kandel et al., 2013

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Is there a genetic component in methane?

Genetic correlations (MeI)

- Milk yield and content
  - ~ -0.6, -0.1, -0.4
- Fertility: 0.3
- BSC: 0.3
- Longevity: -0.1

Kandel et al., 2014

Genetic correlations (MeP)

- Milk yield
  - 0.1
- Body weight: -0.2

Lassen et al., 2016

- *RFI: 0.3*

De Haas et al., 2012

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Selection index with methane

- Starting from current total merit indices in
  - UK, ES, NL

- 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/y				
ES	€91.9	7.30g/d/y				
NL	€228.3	3.93g/d/y				

Scenarios

	Scenario 1		Scenario 2		Scenario 3	
	Index value	Genetic gain CH_4	Total change	Percentage change		
UK	£85.2	8.48g/d/y	-£12.85	-14%		
ES	€91.9	7.30g/d/y	-€11.09	-12%		
NL	€228.3	3.93g/d/y	-€7.23	-3%		

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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/y	-£12.85	-14%	-0.59	-1.75
ES	€91.9	7.30g/d/y	-€11.09	-12%	-0.63	-1.85
NL	€228.3	3.93g/d/y	-€7.23	-3%	-0.31	-0.88

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Conclusion of METHAGENE consortium

Benefit for producers

It depends!

- 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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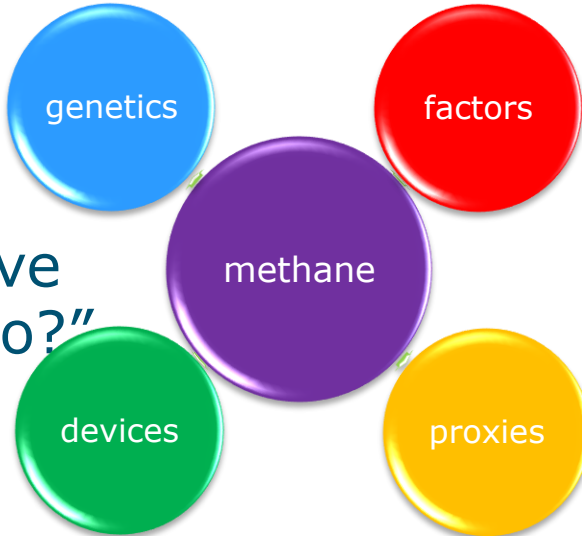
Conclusion – METHAGENE

- Within METHAGENE we have come a long way
  - Good discussions
  - New insights
  - Clear guidelines

- But ... We need a research project to give a conclusive answer to “what should I do?”



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Thank you!

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