

Genetic and genomic analyses of enteric methane emissions of dairy cattle

Yvette de Haas, Jennie Pryce, Eileen Wall,
Sinead McParland, Gareth Difford, Jan Lassen



Acknowledgements



SEQSEL



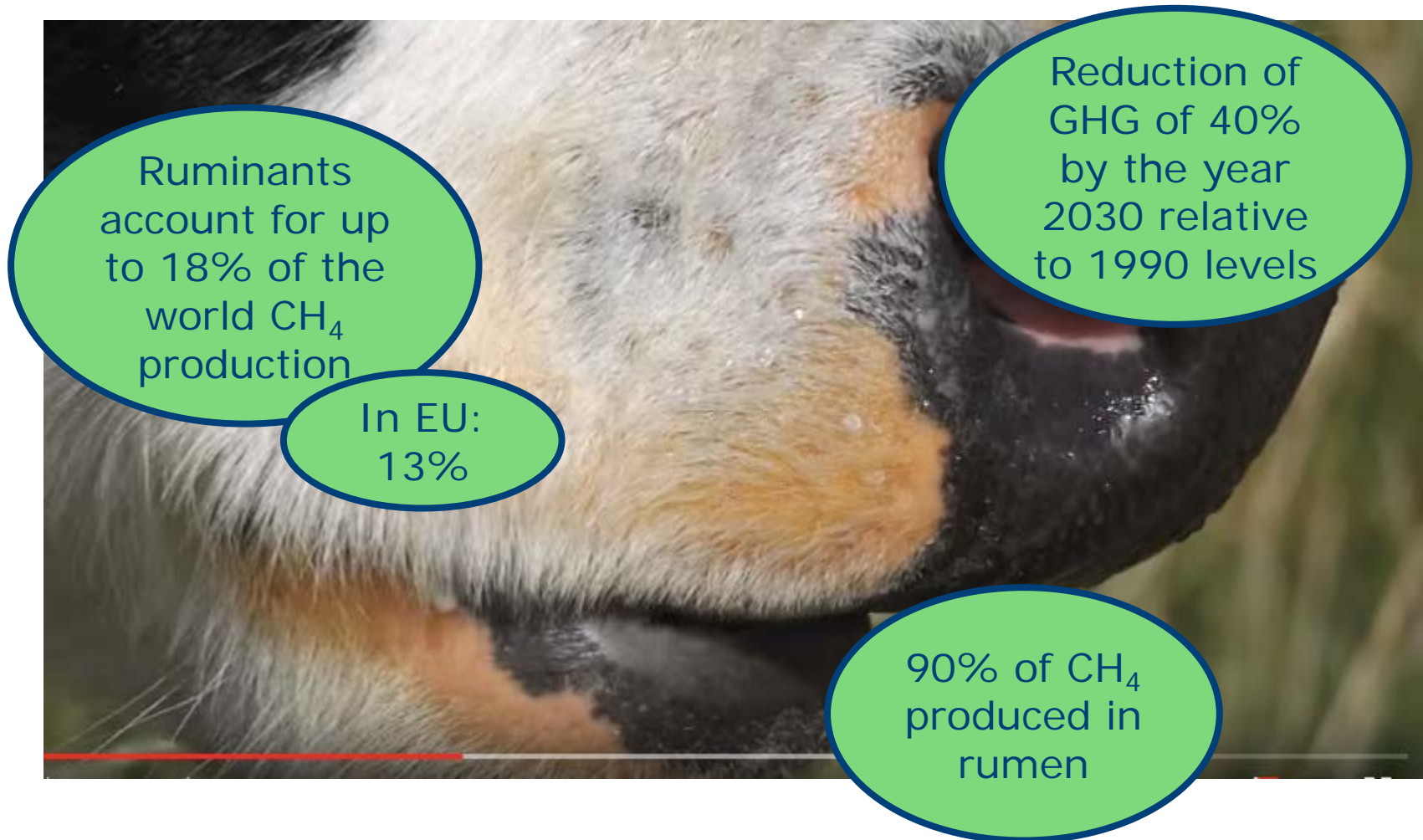
METHAGENE

This is what we want a cow to do ...

(4 to 9 hours/day - Hafez & Bouissou, 1975)



... but what also causes problems



Mitigation options

- Animal nutrition
 - Ration
 - Additives (3NOP)
- Microbiology
 - Microbial population – a host in a host!
- Animal breeding
 - Cost-effective
 - Permanent and curative changes in performance



Animal breeding at mitigation tool

- Breeding goal
- Phenotype
- Genetic parameters
- Genetic markers

Breeding goal

■ *What is it that we want to decrease?*

1. The overall emission?

- methane production in g/d

2. The intensity?

- methane prod per kg of output; e.g. milk/meat

3. The yield?

- Methane prod per kg of input; e.g. DMI

Phenotype

- *What is the best suitable phenotype related to the breeding goal?*
 - Intrusiveness
 - Costs
 - Labour
 - Throughput

Ways to measure:



Respiration chamber
Gold standard!

Animal Breeding &
Genomics Centre



Ways to measure:



Head hoods



Ways to measure:



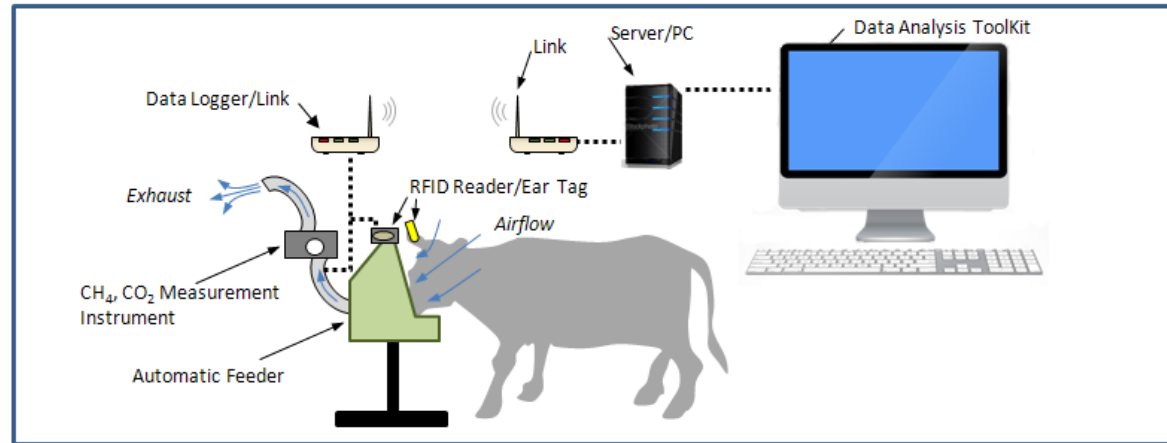
SF₆



Ways to measure:



Laser



GreenFeeder



Butter boxes

Ways to measure:



3
Sniffer



Genetic parameters & Genetic markers

- Example in beef
 - Coralia's talk, 15.15h



- Example in dairy



Genomic selection for CH₄ in dairy



De Haas et al. (2016) *Combining methane traits in dairy cattle from multiple sources for genetic evaluations*. In prep for Journal of Dairy Science

Multiple sources



Available data - Australia



- DEDJTR farm: Ellinbank
- 354 cows
- SF₆ methane phenotypes over 3 days
 - 2013, 2014, 2015
- Genotyped with 50k chip, imputed to HD (338 animals)

Available data - Denmark

- 1769 Danish Holsteins
 - 374 Sires; 1306 Dams
- Sniffer methane records
 - CH₄ and CO₂ concentration
- 11 Herds; each visited 1 week
- 2012 & 2013
- 56k Genotyped
 - 1758 animals



Available data - Ireland



- 352 cows
 - 4,360 records
 - 2009, 2010, 2011
- Holstein, Jersey, crossbreds
- SF₆ methane records; 5 consecutive 24h periods
- 64 animals genotyped
 - Illumina 50k v01
 - Custom chip with 16k SNPs

Available data - Netherlands

- 460 cows at Dairy Campus
 - 12,088 weekly records
 - 2013-2014-2015
- Sniffer methane records (CH₄, CO₂ concentrations)
- 452 are genotyped
 - Eurogenomics 10k chip – imputed to CRV custom chip (76k SNPs)



Available data - UK

- 216 cows
- Laser methane detector
- Recording every 0.5 sec over c. 5 minutes
- 2 x 2 factorial analysis
 - => Langhill data (genetic line, ration)
- 192 are genotyped (50k Illumina v01 and v02)



Methane traits

Selected phenotypes (weekly averages)

- Methane production = g/d
- Methane intensity = g/kg FPCM
- Methane concentration = ppm

- Standardized within country
 - Correcting for differences in variance between countries
 - Mean of 0, std. dev of 1

Methane traits - no. animals

Trait	No. of animals		
	Original	Edited	Genotyped
CH ₄ (g/d)	3,151	2,857	2,543
CH ₄ intensity	3,151	2,857	2,543
CH ₄ concentration	2,445	2,290	2,192
CH ₄ : CO ₂	2,229	2,088	2,014

Relationship matrices

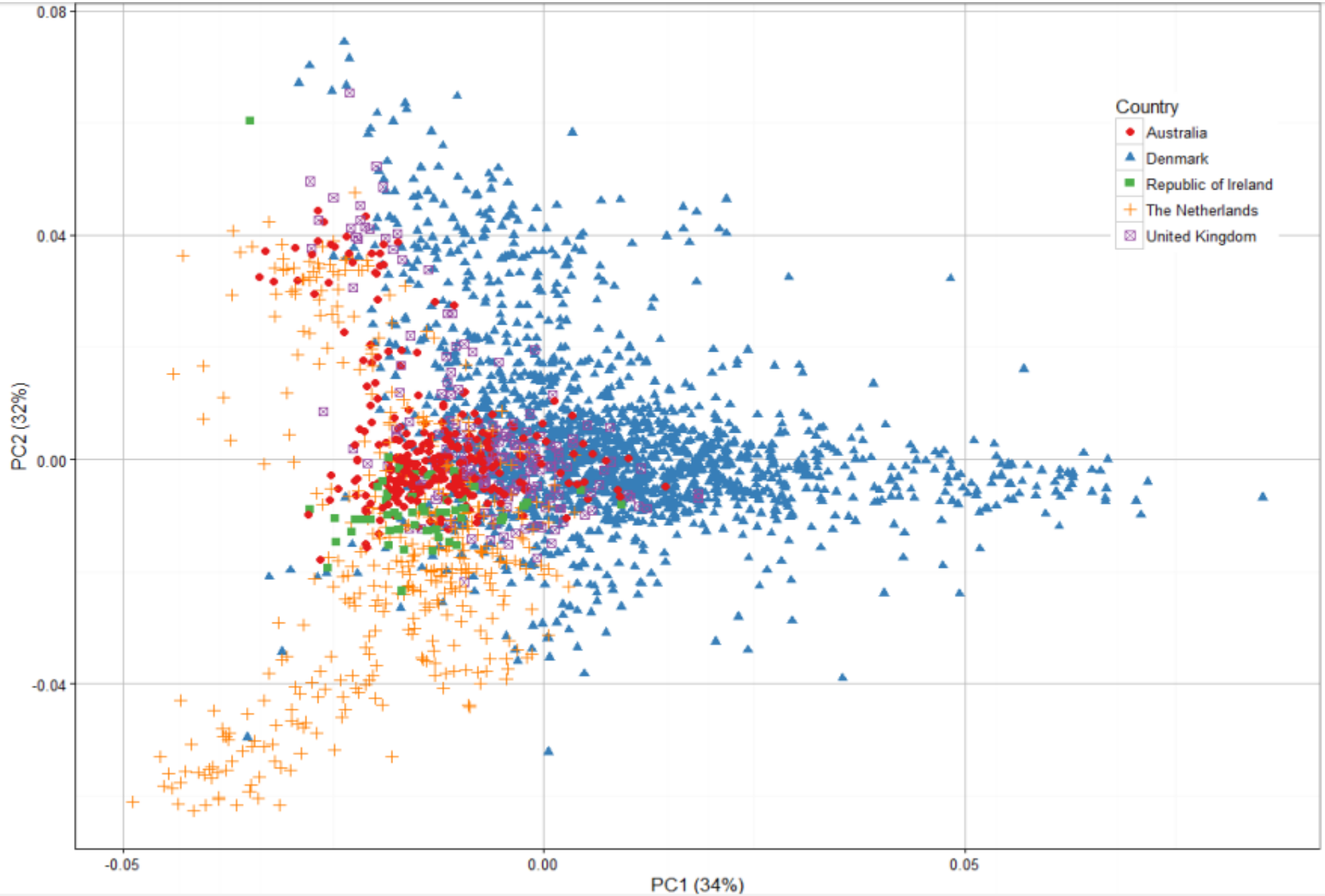
■ Pedigree

- Traced back to founder populations
- Using Interbull ID to remove aliases
- 28,317 animals

■ Genomic

- Combining genotypes of all countries on matching SNP names
- Imputing => 45,873 SNPs
- Quality control => 44,936 SNPs

Principal components GRM



Descriptive statistics – overall

	Mean	Min	Max	σ_p
CH ₄ g/d	540.6	150.4	999.5	117.9
CH ₄ int.	17.6	3.2	74.5	5.1
CH ₄ ppm	321.0	17.0	909.7	125.8
Ratio	0.08	0.01	0.18	0.017
FPCM	32.2	9.2	63.1	7.6
LW	606.4	358.0	928.9	71.1

Descriptive statistics – per country

	Mean	Min	Max	σ_p
<i>CH₄ production</i>				
AUS	450.7	230.8	753.8	78.3
DK	554.2	443.1	820.3	50.1
IRL	357.5	176.2	651.0	91.2
NL	549.9	150.4	999.5	119.1
UK	323.6	158.1	523.5	61.6
<i>CH₄ intensity</i>				
AUS	21.5	8.2	74.5	11.7
DK	13.6	8.6	27.5	2.7
IRL	18.7	7.6	45.3	5.9
NL	18.2	3.2	59.3	4.7
UK	13.1	6.3	37.5	4.4

Overall heritabilities

	Pedigree	GRM
CH ₄ g/d	0.07 (0.03)	0.04 (0.02)
CH ₄ int.	0.21 (0.05)	0.11 (0.03)
CH ₄ ppm	0.16 (0.05)	0.07 (0.03)
Ratio	0.09 (0.04)	0.04 (0.02)
FPCM	0.41 (0.05)	0.26 (0.03)
LW	0.57 (0.05)	0.35 (0.03)

Country-specific heritabilities

	Pedigree	GRM
<i>CH₄ production</i>		
AUS	0.00 (0.15)	0.05 (0.14)
DK	0.05 (0.04)	0.05 (0.03)
IRL	0.14 (0.18)	N.E.
NL	0.09 (0.09)	0.04 (0.07)
UK	0.12 (0.17)	0.15 (0.17)
<i>CH₄ intensity</i>		
AUS	0.17 (0.17)	0.23 (0.15)
DK	0.29 (0.07)	0.14 (0.04)
IRL	0.16 (0.24)	N.E.
NL	0.09 (0.10)	0.05 (0.08)
UK	0.34 (0.23)	0.18 (0.21)



Correlations with milk and live weight

	CH ₄ (g/d)	CH ₄ intensity
<i>Pedigree relationship matrix</i>		
FPCM	0.90 (0.22)	-0.87 (0.06)
LW	0.63 (0.19)	-0.21 (0.12)
<i>Genomic relationship matrix</i>		
FPCM	0.86 (0.20)	-0.86 (0.07)
LW	0.79 (0.22)	-0.15 (0.12)

Correlations between countries

■ “Countries”

- Different equipment
- Different protocol
- Different production system
- Different ration
- Different genetic strain
- Different

=> Now it gets interesting ... But so hard to get done!

Correlations (Rg) between “countries” *methane production (g/d)*

	AUS	DK	IRL	NL
AUS	-			
DK	0.69 (0.99)	-		
IRL	*	*	-	
NL	0.74 (0.99)	0.82 (0.99)	*	-
UK	0.02 (0.99)	-0.95 (0.93)	*	0.46 (0.99)

Next steps

1. Run analyses with H-matrix
 - Include mainly the Irish animals
2. Update model
 - Currently overparametizing?
3. Phenotype definition
 - Take the original record, independent on unit
 - Apples *versus* Pears?
4. Genomic prediction for enteric methane
5. Link methane to feed efficiency
6. Proxies for methane, e.g., MIR profiles in milk

Conclusions

- The (preliminary!) results show that
 - Genetic variation in methane of dairy exists
 - Heritability slightly lower than published recently
 - Mainly positive genetic correlations between “countries”, large standard errors
 - GRM is more accurate at detecting relationships among animals in some countries
- Seems feasible to collate methane data on larger scale
 - G x E should be accounted for
 - Trait definition needs attention

Thank you!

Questions?



Yvette.deHaas@wur.nl

