

GMG Asia: Webinar on methane recording techniques

Webinar GMG Asia, 05-11-2025

M. Spoelstra, A.E. van Breukelen, S. Meseret, R. Bonifazi, R.F. Veerkamp, B. Gredler-Grandl



Agenda

Part 1

- 09:00 Welcome (Mirjam)
- 09:05 General GMG update (Birgit)
- 09:15 Methane recording techniques (Anouk)
- 09:45 Questions

Short Break

Part 2

- 10:15 Experiences working with the Laser Methane Detector (Dr. Selam)
- 10:35 Working towards genomic evaluations & recommendations for genotyping (Mirjam)
- 10:45 Questions
- 10:55 Final Discussion & next steps for proposal development
- 11:30 Closure of meeting

GMG Asia: From Data to Impact

Webinar GMG Asia, 05-11-2025

M. Spoelstra, A.E. van Breukelen, Renzo Bonifazi, R.F. Veerkamp, B. Gredler-Grandl



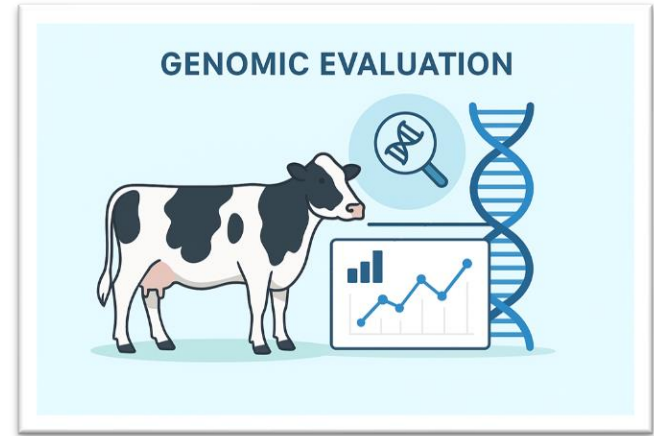
Genomic evaluation

■ Why?

- Direct measurements of CH4 expensive and labor-intensive
- Genomic evaluation enables indirect selection

■ How?

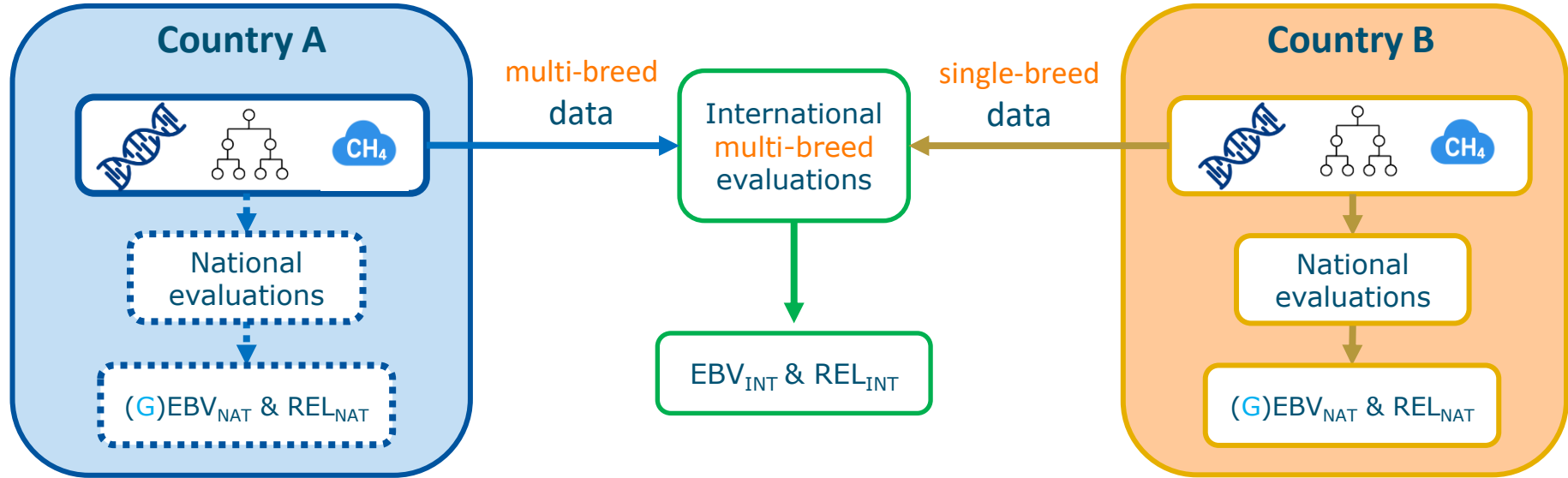
- Measuring CH4 on reference population (presentation Anouk)
- Estimating genetic relationship between SNPs and CH4
- Using these relationships to predict GEBVs (for animals without CH4 records)



National vs. International Genomic Evaluation

- National level
 - Reference population typically small
 - GEBVs are built only on national data, often with lower accuracy
- International level
 - Increase reference population size & improve prediction accuracy
 - Compare animals & performance in different environments
 - BUT data harmonization is essential:
 - Type of CH₄ measurements, accounting for management, diet, environmental effects (rG)
 - Aligning SNP panels

International genomic evaluations



Bonifazi, 2022,

<https://research.wur.nl/en/publications/d2508949-afa5-4e86-b7c9-cf3e30faf69b>

Size of reference population

- How many records needed for successful GEBV?
 - How many animals to select for recording CH4?
 - Important elements:
 - Trait definition & accuracy of GEBV
 - Heritability of the trait (0.11-0.32)
 - Genetic correlation between breeds
 - In case of crossbreeds; breed composition
- Corrections: farm-effects (management, diet, environment)

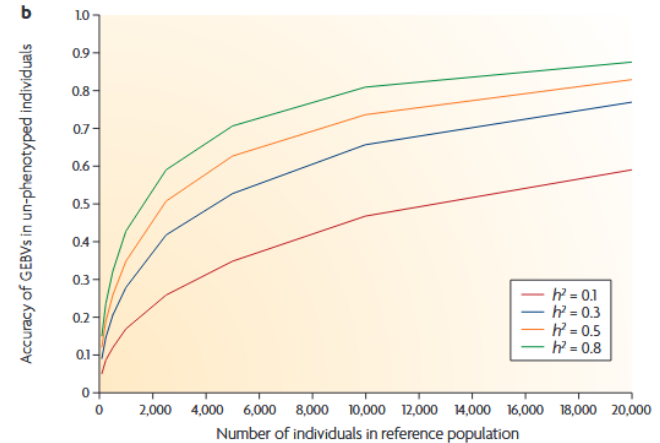


Figure 3 | **Calculation of number of animals in a reference population and accuracy of breeding values.** **a** | Number of animals needed in a reference population. To achieve an accuracy of 0.7 for estimated genomic breeding values (GEBVs) calculated from SNPs requires an increasing number of animals in the reference population as the heritability declines or the N_e of the population increases. **b** | Accuracy of GEBVs of un-phenotyped individuals with increasing number of phenotype records in the reference population used to estimate SNP effects, for different heritabilities (h^2). N_e was 100.

M. E. Goddard & B. J. Hayes (2009)

<https://www.nature.com/articles/nrg2575>

Multi-breed Genomic Evaluation

Separate vs. Combined Populations

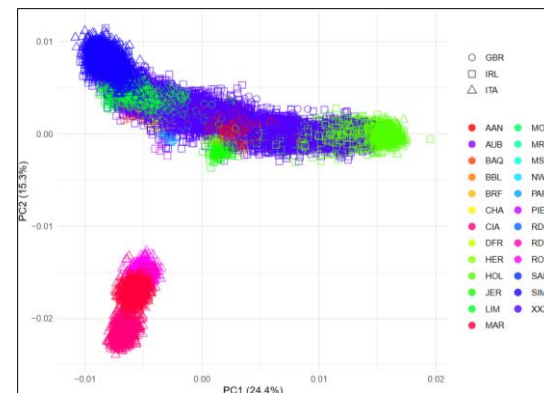
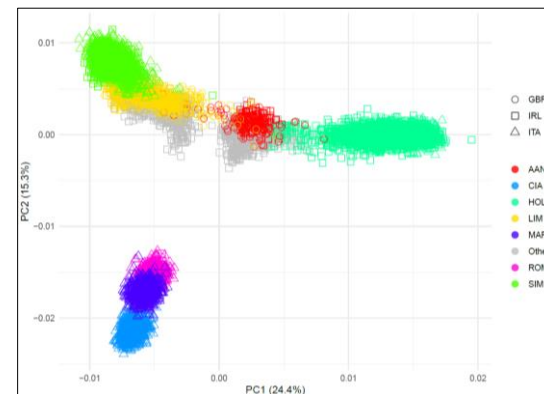
- Breeds can be analyzed as *separate populations* (top figure).
- Information from *crossbreeds* or *related populations* can be integrated to form *one combined population* (bottom figure).

Connectivity enhances accuracy of predictions

- The more connected populations are the more beneficial it is to combine them

Practical Implications

- Constraints on the number of animals per breed, especially for local breeds.
- To achieve accurate genomic predictions and build a sufficiently large reference population; we need to link and share data across populations.
- Data from Holstein crosses can enhance predictions, given the large amount of methane data available from Holstein populations.



M3GE project
Bonifazi et al., 2025,
Interbull Bulletin

SNP arrays

- Examples of available SNP arrays (relevant for Bos Indicus breeds)
 - GGP Indicus 50K (€23)
 - GGP Bovine 100K (€23)
 - Illumina Bovine HD (777K - €79)
 - Affymetrix Bovine 25K
 - Axiom Bovine
 - DSN200k SNPs
 - Bovine Skimseek (millions of SNPs, lower depth €45)
- Arrays differ in selected SNPs



Image courtesy of Illumina Inc.

Genotyping strategies

- Combining genotypes from different SNP arrays:
 - Array's information:
 - Map: SNP name, rsID (if available), physical position of SNPs on chromosomes
 - Genome assembly version
 - Imputation to a common reference panel
- Risks: SNPs shared between multiple arrays can dramatically decrease with increasing number of different arrays
 - General recommendation: at least 20k overlap to be useful
- Research design; ideally prevent using too many different arrays if the main goal is to combine data

Questions



Countries & organisations

Bangladesh
(BAU, DLS)

India
(BAIF)

Indonesia
(BRIN)

Nepal
(ILRI)

Pakistan
(University
of Karachi)

Vietnam
(NASI)

GHG Asia – template breeding program

- Vietnam: Native yellow cattle, Holstein Friesian
 - Method: GreenFeed/GC?, n=?
- Indonesia: Bali Cattle, Ongole cross, Brahmman cross, Madura, Aceh, Pesisir
 - Method: LMD, n = 120-600 per year
- Pakistan: Cholistani cattle
 - Method: NIL, n = 500 per year

GHG Asia – template breeding program

- India: Gir, Sahiwal, Crossbreed, Murrah, Jaffarabadi
 - Method: LMD, Greenfeed, n=5000 per year
- Bangladesh: Red Chittagong cattle
 - Method: SF6, n =2000 per year
- Nepal: Jersey and Holstein cross, Murrah cross, Parkote, Lime and Gaddi
 - Method: Greenfeed or LMD, n=500 cattle & 500 buffalo per year

Next steps

- Number of animals to be sampled per (cross)breed (genotype + phenotype)
 - What do we consider as minimum?
 - Useful to assess breed that is very disconnected to other populations?
- Methane phenotyping
 - Choose method
 - Frequency and measurement length (consult SOPs)
- Genotyping
 - Send info on already used SNP arrays (arrays' information)
 - Check for overlap with available commercial arrays
 - Reach consensus on array(s) to be used

Two-page proposal

- i. Title
- ii. Funding: amount requested, amount leverage funding
- iii. Proposal grant period

- iv. Project summary
- v. Use of funds
- vi. Short high-level overview of activities
- vii. Global milestones
- viii. Anticipated impact
- ix. Budget narrative

Next steps in proposal development

Each country to summarize in bullet points:

- High-level overview of activities
- Global milestones
- Anticipated impact
- Budget, and if available leverage funding

Global Methane Genetics initiative

Acceleration of genetic progress for reduced methane emission in ruminants

Global
Methane
Genetics
initiative

Led by



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In Partnership with



BEZOS
EARTH
FUND



Global
Methane
Hub

Birgit Gredler-Grandl, Y. de Haas, R. F. Veerkamp



GMG: Why? How? What?



- Genetic progress can make a **permanent** and **impressive** contribution to reducing methane output from livestock systems globally
 - Aim: **accelerate genetic progress** and to implement **breeding strategies** for reduced methane emissions in ruminants in the **global North and South** by supporting:
 - sharing of protocols and data
 - expanding phenotyping, breeding program design
 - genetic evaluations & development of
- Global Livestock Genetics and Genomics Programs

Global Methane Genetics initiative

Investment of 27M US\$

25 countries, 50 partners, 25 breeds

Methane pheno- & genotypes ~110k cattle & sheep, ~20k microbiome

Dairy:

Holstein (~42k)

Jersey (~8k)

(Nordic) Red Breeds
(~7.3k)

Brown Swiss (~3.3k)

Beef:

North America (~6k)

Australia, Ireland,
UK, NZ (~18.5k)

Sheep: world-wide reference population

Australia & New Zealand

UK & Ireland

Uruguay (~17k)

Africa

Local breeds & crosses (~4k)

Latin America

Beef (~7k)

Microbiome:

World-wide reference
population
(~20k samples)

Global Methane Genetics initiative

Investment of 27M US\$

25 countries, 50 partners, 25 breeds

Methane pheno- & genotypes ~110k cattle & sheep, ~20k microbiome

Dairy:

Holstein (~42k)

Jersey (~8k)

(Nordic) Red Breeds
(~7.3k)

Brown Swiss (~3.3k)

Develop protocols

Phenotyping

World-wide sharing

Genetic evaluation

Africa

Local breeds & crosses (~4k)

Latin America

Beef (~7k)

Beef:

North America (~6k)

Australia, Ireland,
UK, NZ (~18.5k)

Sheep: world-wide reference population

Australia & New Zealand

UK & Ireland

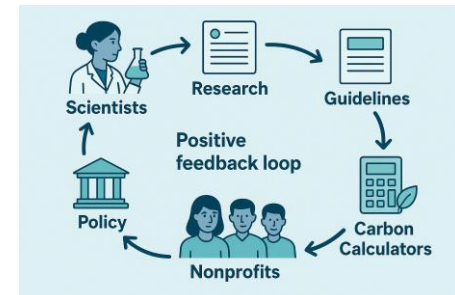
Uruguay (~17k)

Microbiome:

World-wide reference
population
(~20k samples)

Key activities

- GMG global database
 - fair share principle (GMG internal & external data sharing)
- Sniffer SOP & methane recording device testing center
- Adoption of genetic selection as mitigation strategy & incentivization



Microbiome-driven breeding for lower emissions



■ Microbiome to **predict methane** phenotype

scientific reports

OPEN

Methane prediction equations including genera of rumen bacteria as predictor variables improve prediction accuracy

Boyang Zhang¹, Shili Lin^{2,3}, Luis Morales^{4,5}, Jeffrey Fikins¹, Alexander N. Hristov⁶, Ernieas Kebreab⁶, Peter H. Janssen⁶, André Blanton⁶, Alireza R. Bayat⁷, Les A. Crompton⁸, Jan Dijkstra⁹, Magrey A. Eugène¹⁰, Michael Kreuzer¹¹, Mark McGee¹², Christopher K. Reynolds¹³, Angela Schwarm¹⁴, David R. Yáñez-Ruiz¹⁵ & Zhongtang Yu¹⁶

Bilton et al. *Genetics Selection Evolution* (2023) 57:23
<https://doi.org/10.1186/s12711-023-00879-3>

Genetics Selection Evolution

RESEARCH ARTICLE

Open Access

Rumen metagenome profiles are heritable and rank the New Zealand national sheep flock for enteric methane emissions

Timothy P. Bilton¹, Setegn W. Alemu², Ken G. Dodds³, Hannah Henry⁴, Melanie K. Hess⁵, Ronan Jordan¹, Fern Booker⁶, Sharon M. Hickey⁷, Neville Amyes⁸, Kevin Knowler⁹, Edgar Sandoval¹⁰, Jacqueline Peers-Adams¹¹, Tracey C. van Soest¹², Hayley Baird¹³, Trevor Watson¹⁴, Wendy Bain¹⁵, Barry Vennart¹⁶, Gerard Pile¹⁷, Brooke Bryson¹⁸, Shannon M. Clarke¹⁹, Patricia L. Johnson²⁰, John C. McEwan²¹ and Suzanne J. Rowe²²

■ Microbiome as **correlated trait** with methane

ORIGINAL ARTICLE

Animal Breeding and Genetics | WILEY

Structural equation models to disentangle the biological relationship between microbiota and complex traits: Methane production in dairy cattle as a case of study

Alejandro Saborío-Montero^{1,2} | Mónica Gutiérrez-Rivas¹ | Aser García-Rodríguez³ | Raquel Atxaerandio³ | Idoia Goiri³ | Evangelina López de Maturana⁴ | José Antonio Jiménez-Montero⁵ | Rafael Alenda⁶ | Oscar González-Reco^{1,4}



J. Dairy Sci. 106:2198–2212
<https://doi.org/10.3168/jds.2022-22578>

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Invited review: Recursive models in animal breeding: Interpretation, limitations, and extensions

L. Varona^{1*} and O. González-Reco²

¹Instituto Agroalimentario de Aragón (IA2), Facultad de Veterinaria, Universidad de Zaragoza, C/ Miguel Servet 177, 50013 Zaragoza, Spain
²Departamento de mejora genética animal, INIA-CSIC, Crta. de la Coruña km 7.5, 28040 Madrid, Spain



Global Methane Genetics -



THE UNIVERSITY of EDINBURGH
The Royal (Dick) School
of Veterinary Studies



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Key objectives



- Establish a **reference population** with metagenomic and genomic data
- Harmonize pipelines for metagenomic and genomic evaluation for microbiome composition
- Target different breeds and systems (20k samples)
- Help partners to integrate the microbiome profile as a correlated trait in breeding programs for accelerating methane emissions reduction



ICAR Feed&Gas guidelines

ICAR Wiki: <https://wiki.icar.org/index.php/Guidelines>

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Section 20 – Methane Emission for Genetic Evaluation

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NOTE: This version of Section 20 has been approved by the working group's Chair. Please be aware that further revisions may occur before final review and approval by the Board and ICAR members per the [Approval of Page Process](#).

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Contact us!

gmg@wur.nl

Newsletter:

https://www.wur.nl/en/project/global-methane-genetics-initiative.htm?wmstepid=thank_you

**Global
Methane
Genetics
initiative**

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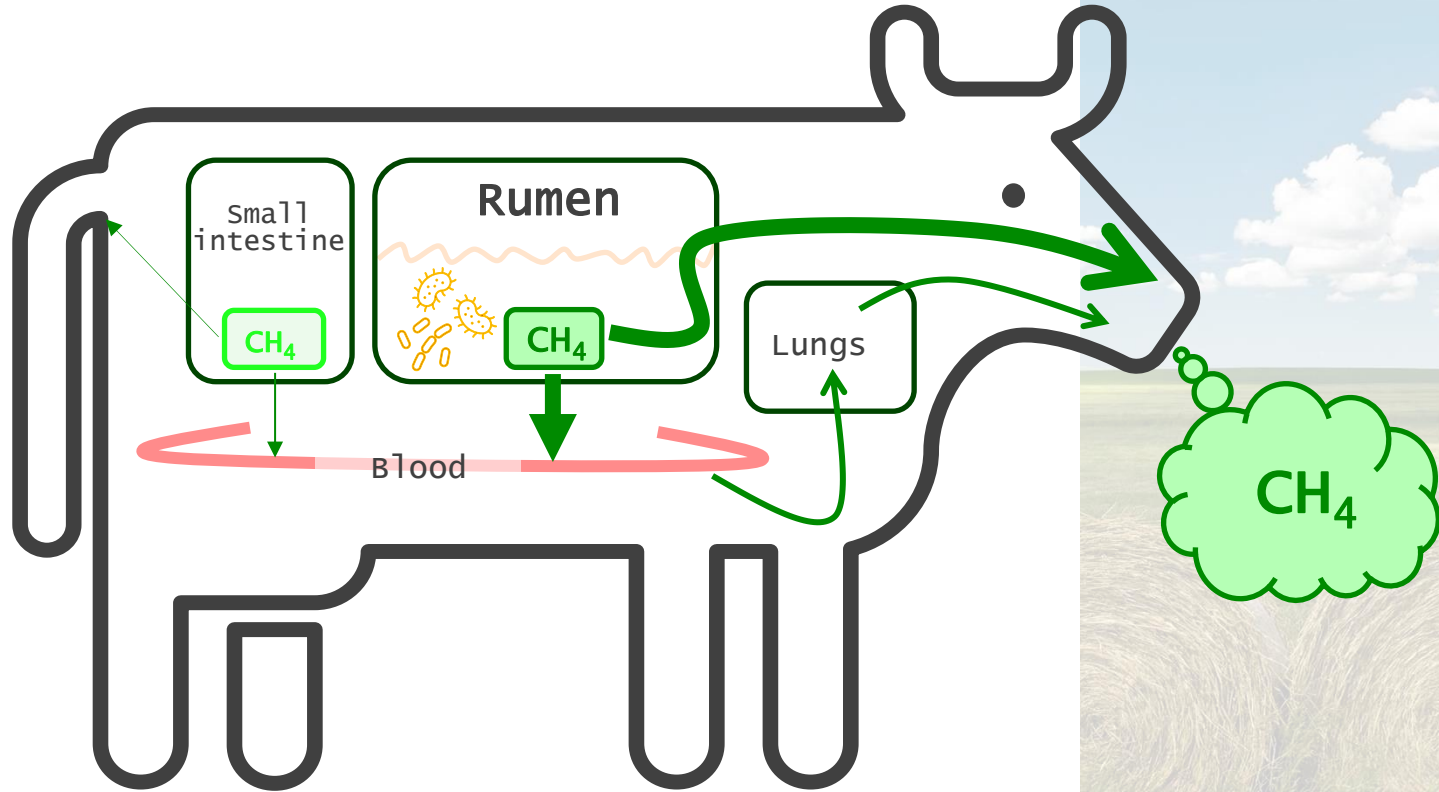
GMG Asia: Methane recording techniques

Online, 05-11-2025

A.E. van Breukelen, M. Spoelstra, R.F. Veerkamp , B. Gredler-Grandl

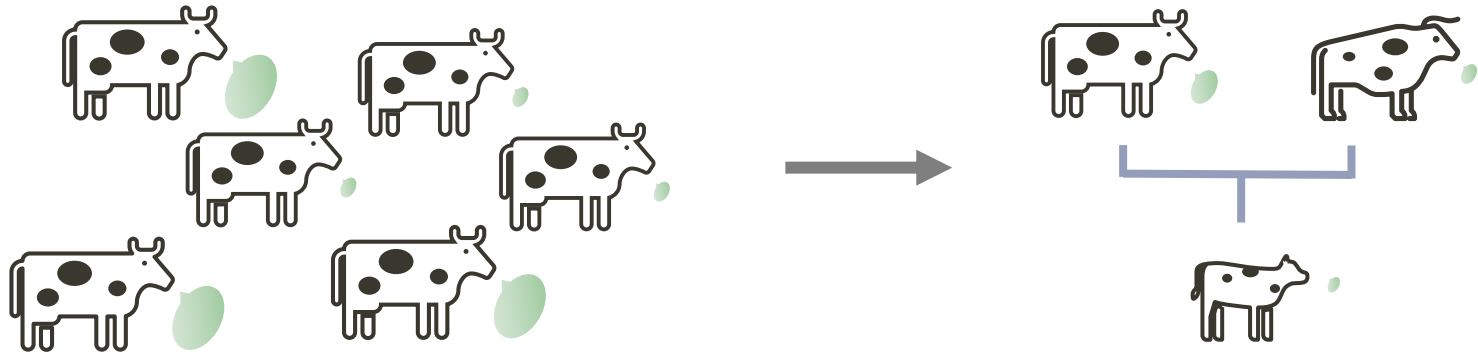


Enteric methane



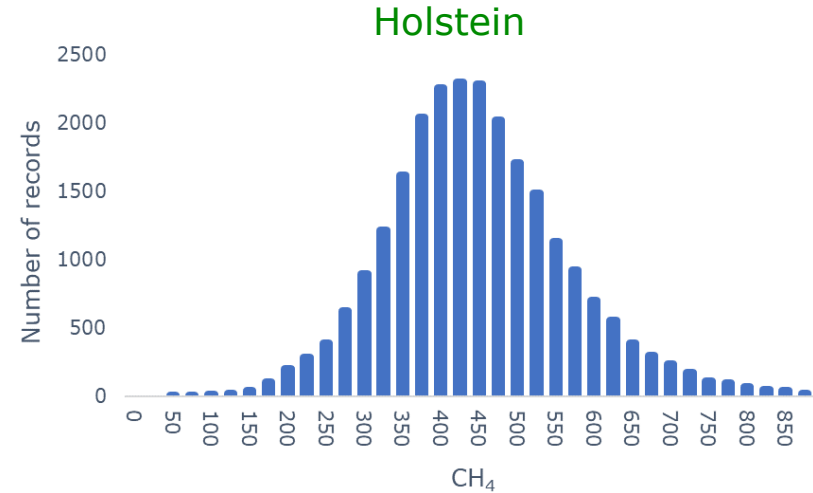
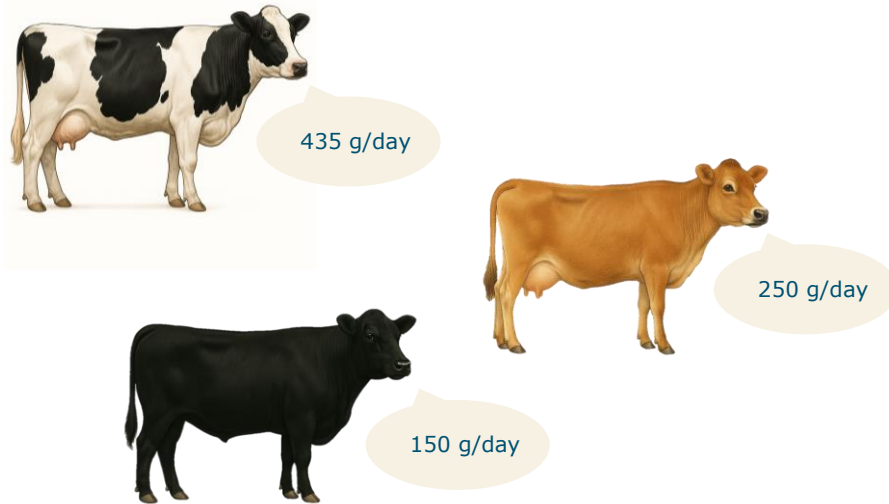
Animal breeding as a mitigation strategy

- There is variation between individual cows
- Around 20% is estimated as genetic variation (heritability)



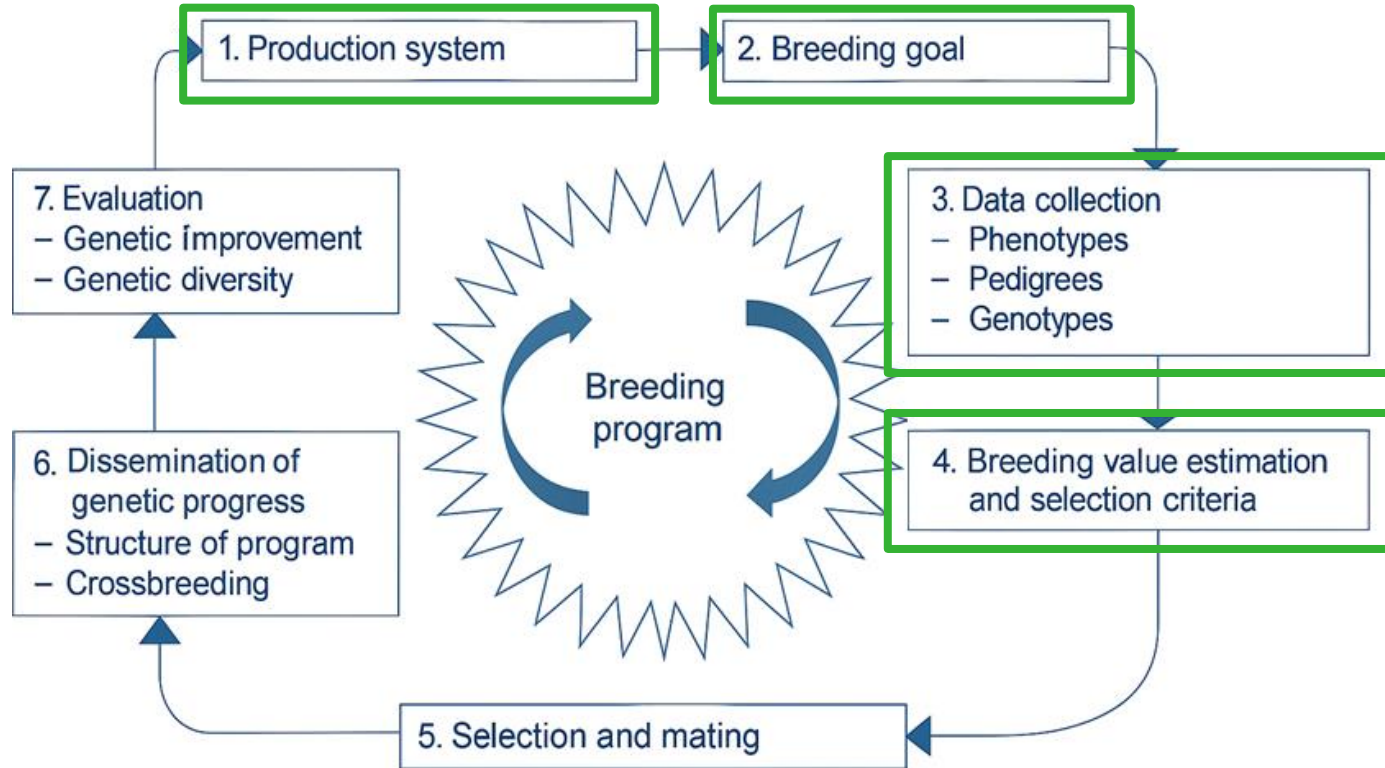
Quantitative genetics theory

- Continuous variation, differences **between** and **within** breeds



- many genes with a small effects , exact drivers of genetic variation largely unknown

What is needed to breed for CH₄ mitigation?

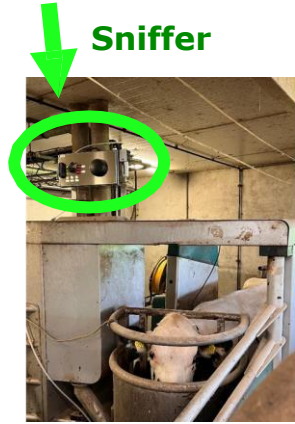


Phenotyping

Respiration chamber



Sniffer



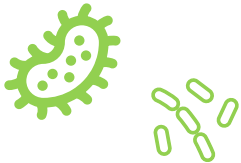
SF6



GreenFeed



Predictions from
microbiome



Predictions from
MIR spectra



Portable accumulation
chamber



Laser methane
detector



Chamber methods

Respiration chamber

- Individual animal in chamber
- Flux method (g/day)
- All emissions are measured
- Low throughput
- Costly



Portable accumulation chambers

- Individual animal in chamber
- Estimate production g/day
- Spot sample method (10-30 minutes)
- Medium throughput
- Cost effective



SF6

SF6

- Used in barn and on pasture
- 24h measurement in g/day
- Medium throughput
- Labour intensive
- Costly



Ellinbank Smartfarm, Agriculture Victoria, Australia

Spot sampling methods

Sniffer

- Installed at milking robot
- Measures concentration (ppm)
- Does not record head position
- High throughput
- Cost effective



GreenFeed

(C-lock Inc. Rapid City, SD, US)

- Placed in the barn/ pasture
- Flux method (g/day)
- Records head position
- Medium throughput
- Costly



Laser methane detector

- Handheld
- Measures concentration (ppm)
- Medium throughput
- Labour intensive
- Cost effective



Methods in development

Wearables



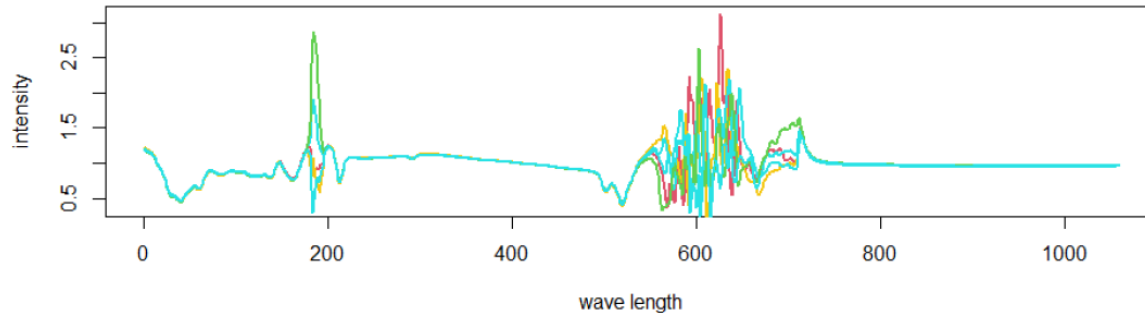
Zelp LTD, London, UK

Cubicle hoods



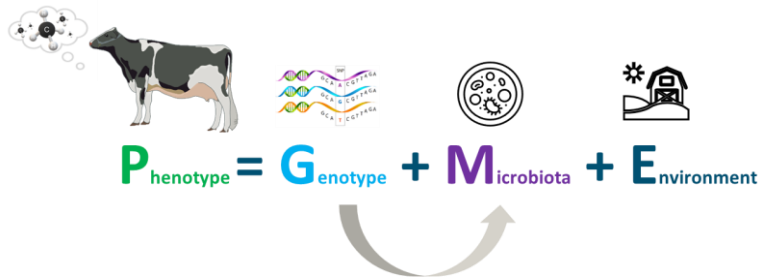
MIR prediction

- Phenotypes on methane needed to train prediction models!
- Mixed results from literature, successful but predictions not always accurate for farms without methane measurements
- A cheap method to substantially increase the number of animals with information

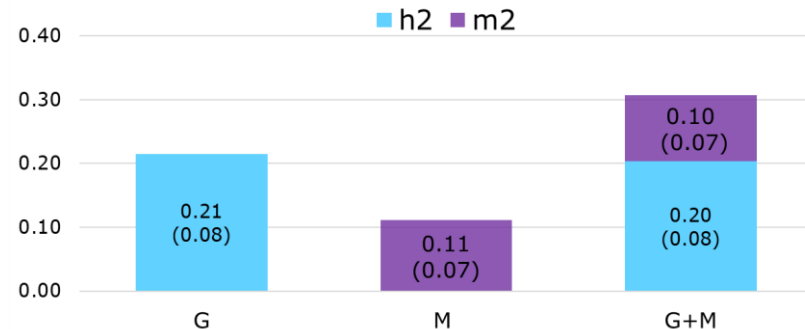


Rumen Microbiome

- Either to predict methane OR use microbiome composition as direct trait
- Phenotypes on methane needed to train prediction models!
- Heritabilities: 148 genera heritable, h^2 up to 0.57
- Association: 80 genera associated with methane
- In total, 30 microbial genera potentially most relevant for breeding on lower methane!



Variance explained



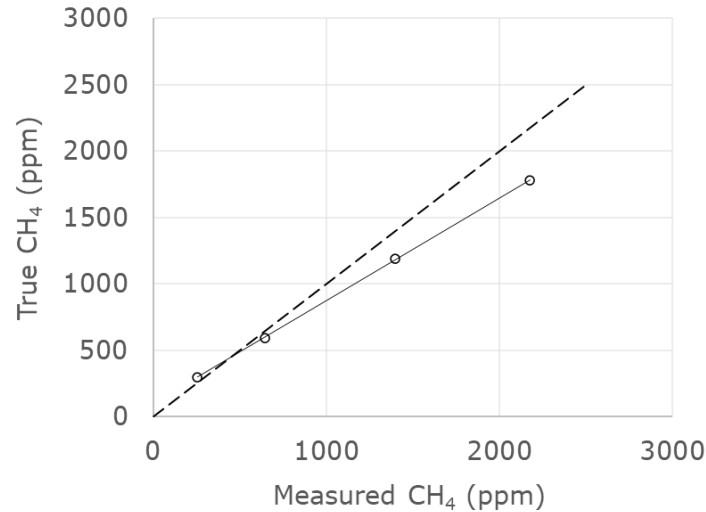
How to choose a method?

- What is the available budget and labour?
- What does the farming system look like?
- **Considerations:**
- Genomic reference populations need to continuously be updated with phenotypes on new progeny!
 - Same holds for predictions from MIR, microbiome, etc.
- Indirect methods (MIR, microbiome, ...) need to be predicted from phenotyped cows in a production system and with a genetic profile similar to what is in the reference population (have sufficient variability in the reference population!)

Be critical about the method and device!

- What is the measurement range?
- What is the sensitivity?
- How can data be accessed?
- How often is calibration of IR sensors required?
- Will the device be serviced, are replacement parts available and at what costs?
- Is the device suitable for farm conditions (dirt, dust, high moisture levels, wind)?
- Will handlers be trained? And how can we monitor the measurement?
- How do we connect the measurement to animal IDs?

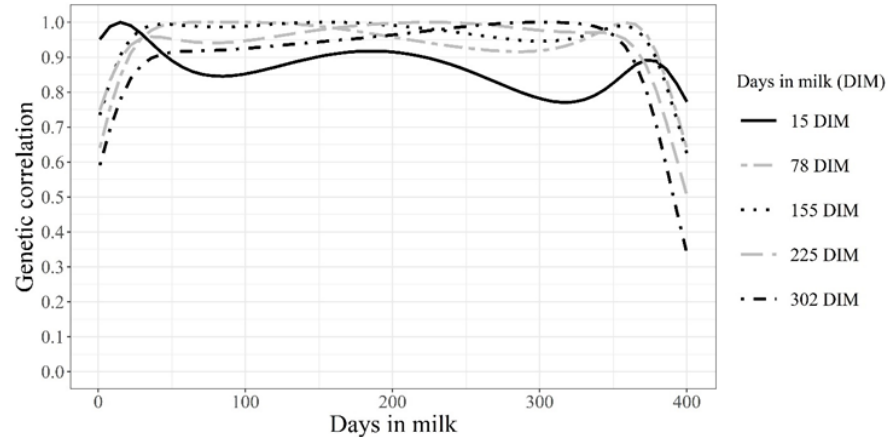
Calibration is an issue for all IR sensors!



- Severity highly depends on the type of sensor, e.g. NDIR, FTIR, TDL, etc.
- From our experience, more expensive sensors drift less

When to measure?

- High correlations between lactation stages



- Frequency and measurement length depends on measurement method and trait
- Some methods require standardized timing relative to feeding

Information on recording methods by ICAR

■ ICAR Section 20: Methane measuring methods

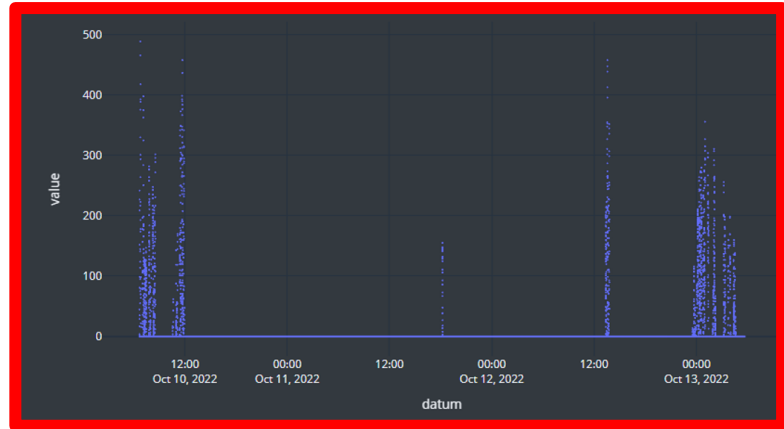
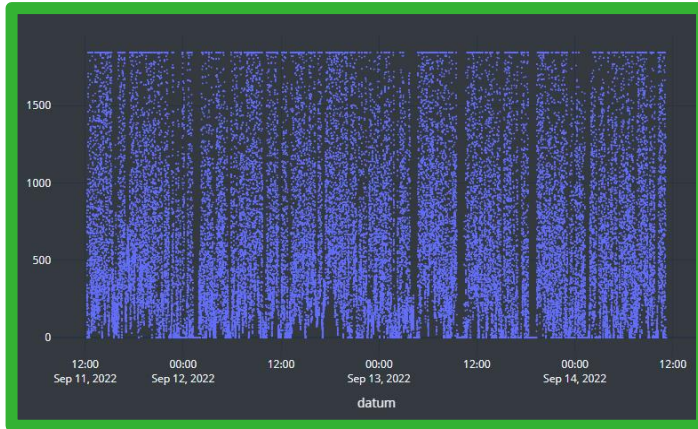
[https://wiki.icar.org/index.php/Section_20: Methane measuring methods](https://wiki.icar.org/index.php/Section_20:_Methane_measuring_methods)

- Respiration chamber
- Portable Accumulation Chambers
- SF6
- Breath sampling during milk and feeding
- Sniffer SOP
- Greenfeed SOP
- Laser Methane Detector

LMD SOP and webinar organized soon

Breeding value estimation - phenotypes

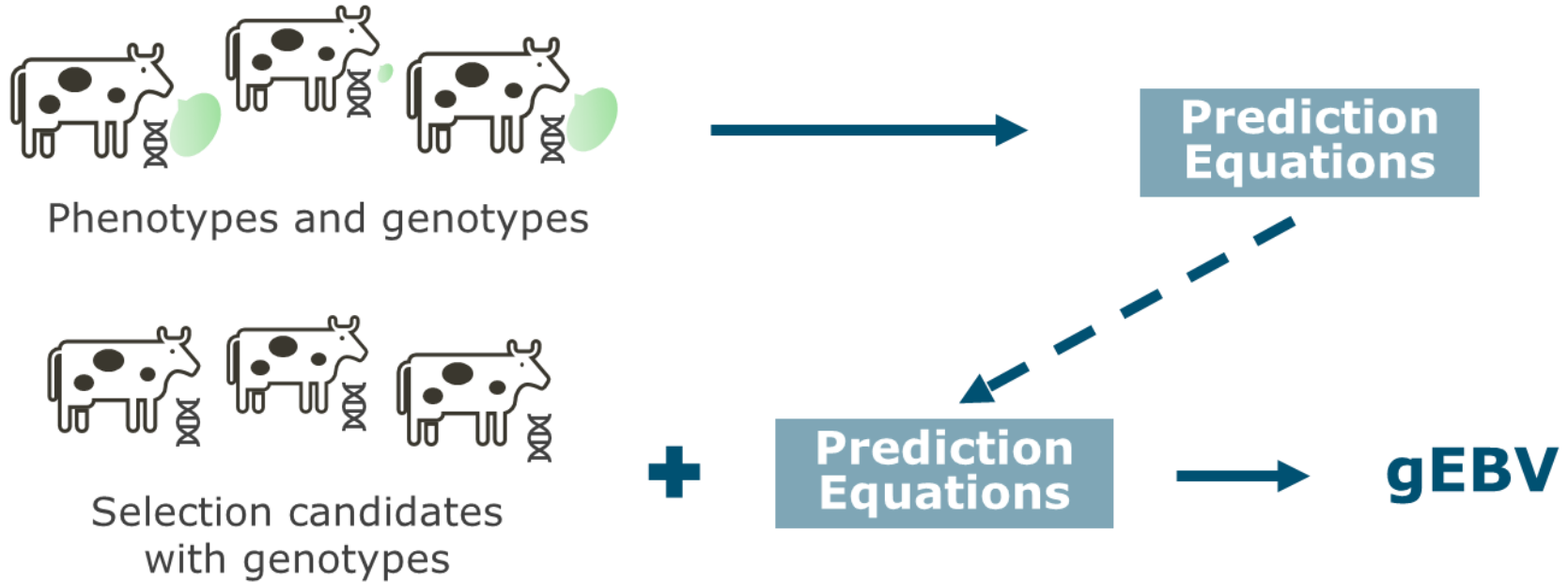
- Large volumes of data (phenotypes, pedigree and genotypes)
- Methane data can be very noisy



- Is it possible to combine measurements from several methods?

Breeding value estimation - genotypes

- Using all information in genomic evaluations



Breeding value estimation - models

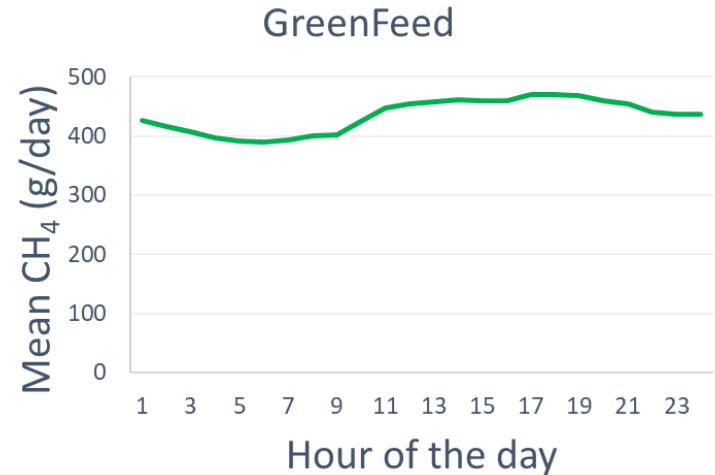
- Estimation of EBVs with linear mixed models (in e.g. ASReml, WOMBAT, BLUPF90, etc.)

Suggested fixed effects:

- Herd x Year x Season
- Experiment or ration
- Breed
- Parity
- Days in milk
- Diurnal effects

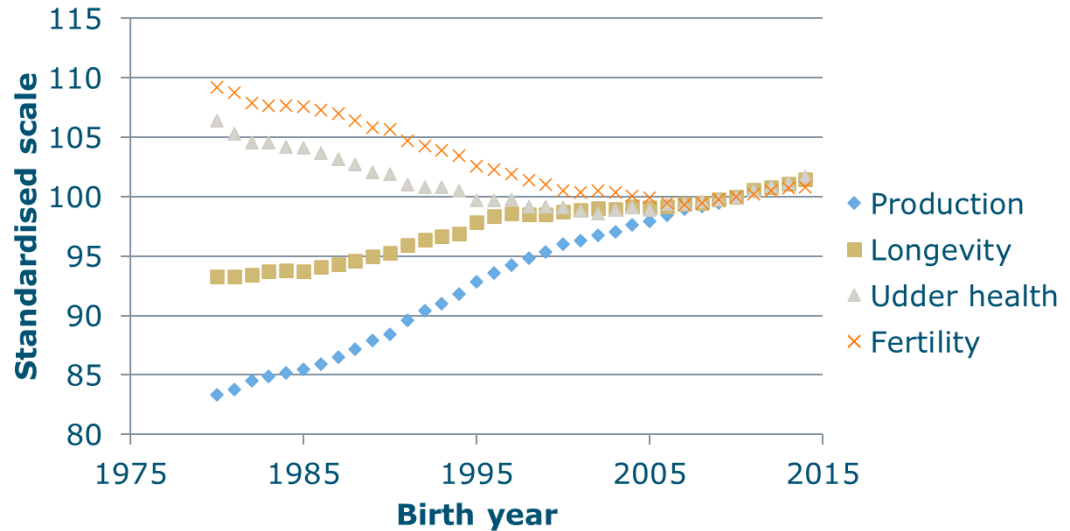
Random effects:

- Additive genetic (pedigree/ genotypes)
- Parity x permanent environmental
- Residual



Methane in a breeding goal

- Balanced breeding



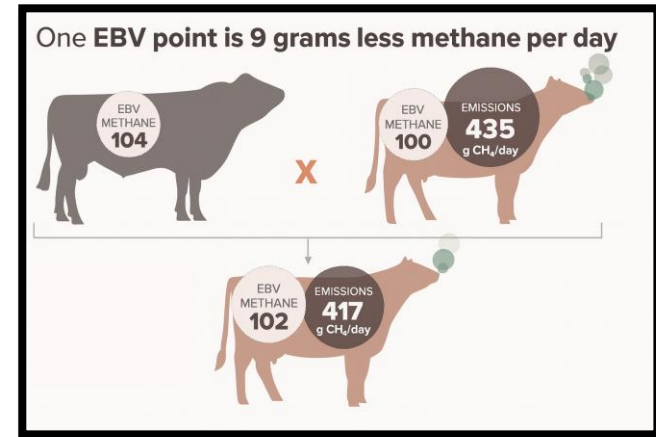
- Relationships with methane differ between studies
- Large datasets required and there appear to be species/ population differences

Methane in a breeding goal

- Methane efficiency vs methane production
 - Dilution of maintenance, increase of production a strong mitigation method per kg product for small local breeds!
- Adoption of breeding for low methane by farmers:
 - Should not be overlooked! Essential for successful implementation
 - Possible incentives
 - Training of farmers

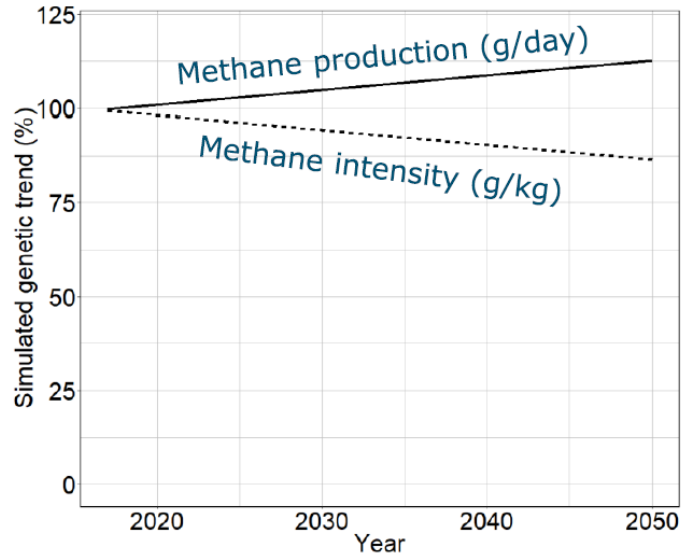
Examples of projects

- The Netherlands, Spain and Denmark, methane recorded with sniffers on dairy
- Application in sheep in New-Zealand
 - 4 year experiment, difference of -1.3 g CH₄/ kg DMI (12%)
 - Applied in breeding program since 2018
- Canada, breeding values for MIR predicted CH₄

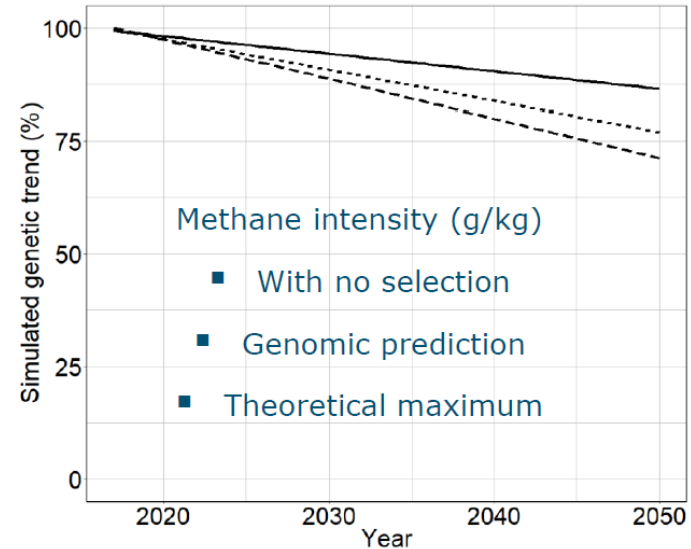


What can breeding bring us?

Current trends



With CH₄ selection



**Thank you for your
attention!**



Measuring Methane in Cattle Using Laser Methane Detector

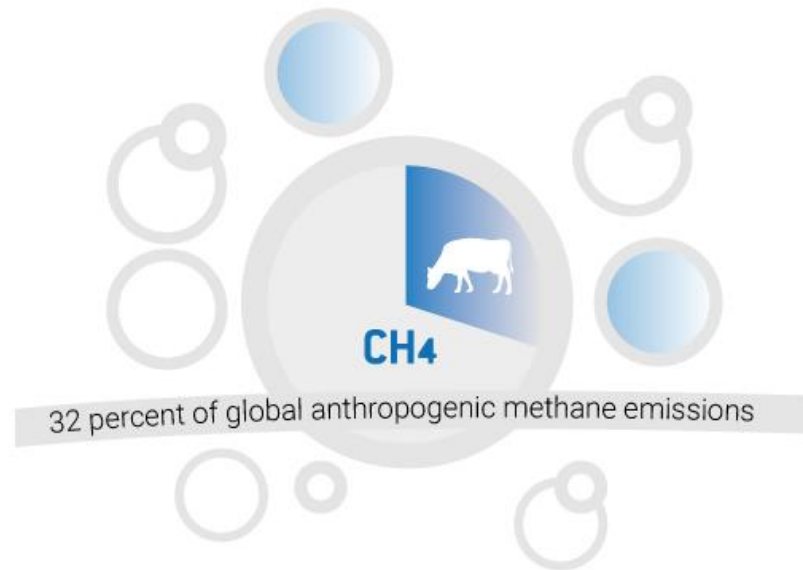


Selam Meseret, Alireza Ehsani, Raphael Mrode.
ILRI, Addis Ababa, Ethiopia & SRUC, Edinburgh , UK

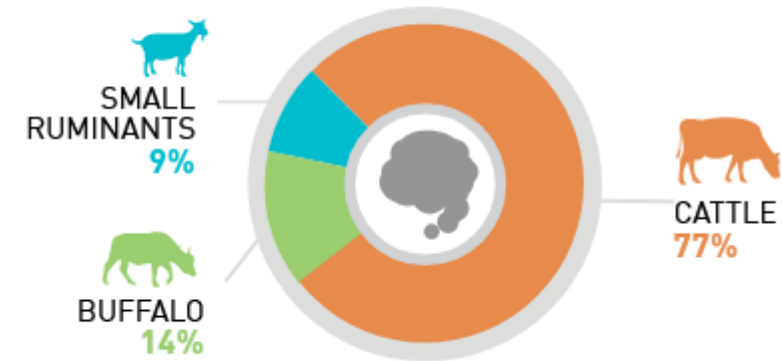
GMG Asia: Webinar on methane recording techniques
November 5, 2025



Enteric methane production



GLOBAL DISTRIBUTION OF ENTERIC METHANE EMISSIONS FROM RUMINANT (%)

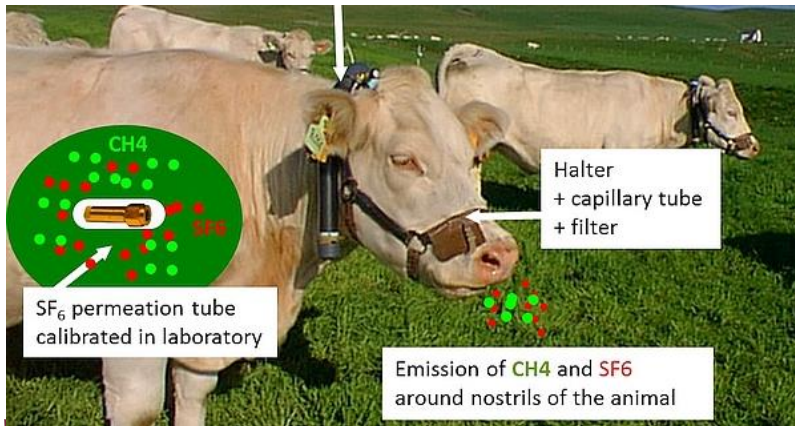


IPCC 2013

Measure to manage: Phenotyping enteric methane is essential for identifying low-emitting cows and developing effective mitigation and adaptation strategies.

CH₄ measuring technologies

3



Laser Methane Detector

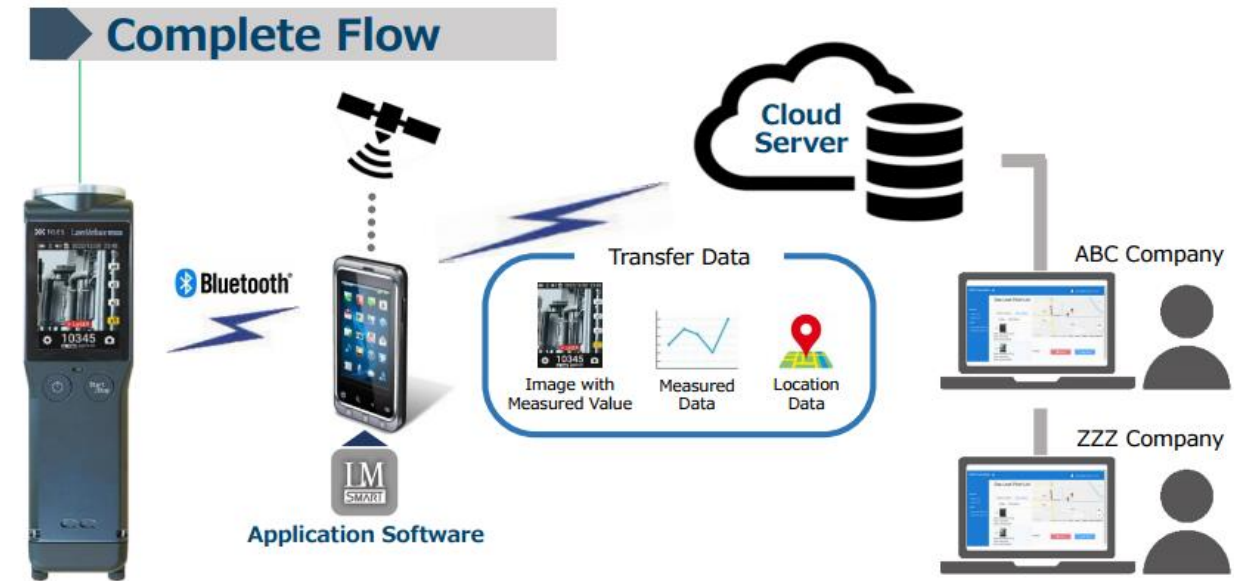
Tokyo Gas Engineering Solutions Corporation

- Laser methane mini
 - Software for Android Devices (GasViewer)



~ 13k USD

Laser Methane Smart



~ 9k USD

Data

No	yyyy/mm/	Intensity	Measured	Error	Location
1	20:20.8	395	16	1	http://map
2	20:21.3	410	13	1	http://map
3	20:21.8	325	8	1	http://map
4	20:22.3	173	12	1	http://map
5	20:22.8	278	28	1	http://map
6	20:23.3	482	8	1	http://map
7	20:23.8	283	18	1	http://map
8	20:24.5	1069	8	1	http://map
9	20:24.9	409	10	1	http://map
10	20:25.4	310	9	1	http://map

- 1: Values are measured normally.
- 5: 「Not enough reflection」 Value involving an **error**.
- 6: 「High density gas」 Value involving an **error**.
- 7: 「Too much reflection」 Value involving an **error**.

Operating time



eneloop Standard

2.5hours

eneloop Pro

3.5hours

eneloop Lite 1.3hours

LaserMethane **SMART**



Special Battery Pack

4hours

LaserMethane **mini**

Note) These are reference values at 25°C.

Commercial Batteries (4 Pieces)

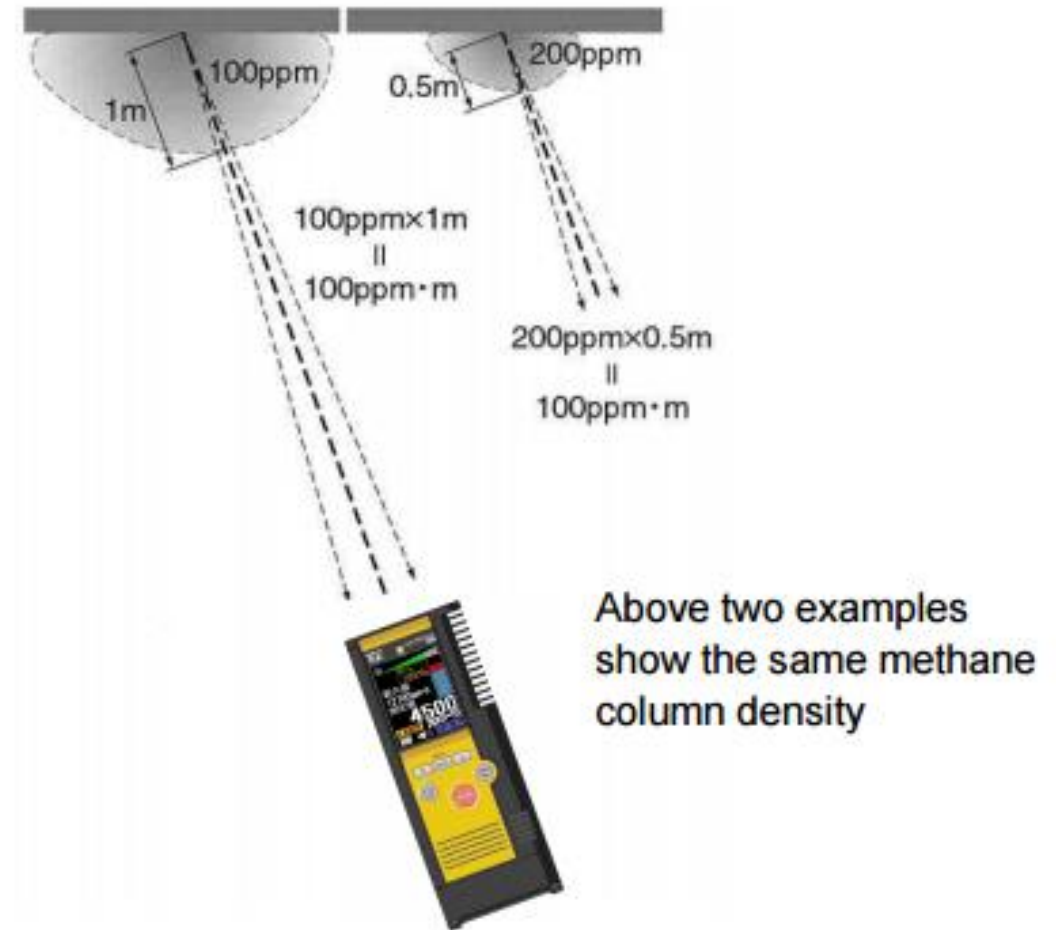


Battery pack: 1 pc.



Intensity and distance

- Light reception intensity bar
 - Be sure to measure when the reception intensity is indicated in green.



Proxy-Based Methods

- Milk Mid-Infrared Spectroscopy (MIR)

Principle: Predict CH₄ emission based on spectral properties of milk components

Advantages:

- Non-invasive and high-throughput
- Leverages routine milk testing data

Limitations:

- Indirect—requires calibration with direct CH₄ data



Indirect prediction of methane using MIR

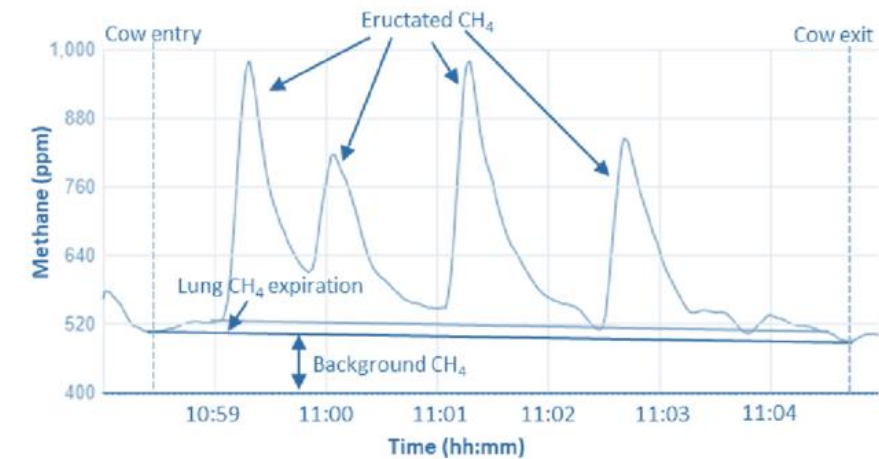
	All data		
	N	R	RMSE
MIR + body weight+ milk + fat% + prot%	479	0.45	103.3
MIR	620	0.40	111.9

Feeding status data		
N	R	RMSE
296	0.52	104.5
296	0.52	110.6

Number of records needed for prediction

Average Records	accuracy	RMSE
1	0.24	168
2	0.28	149
3	0.29	133
4	0.37	124
5	0.39	122
6	0.45	116
7	0.47	116
8	0.45	109
9	0.45	107
10	0.45	106
11	0.46	105
12	0.45	106

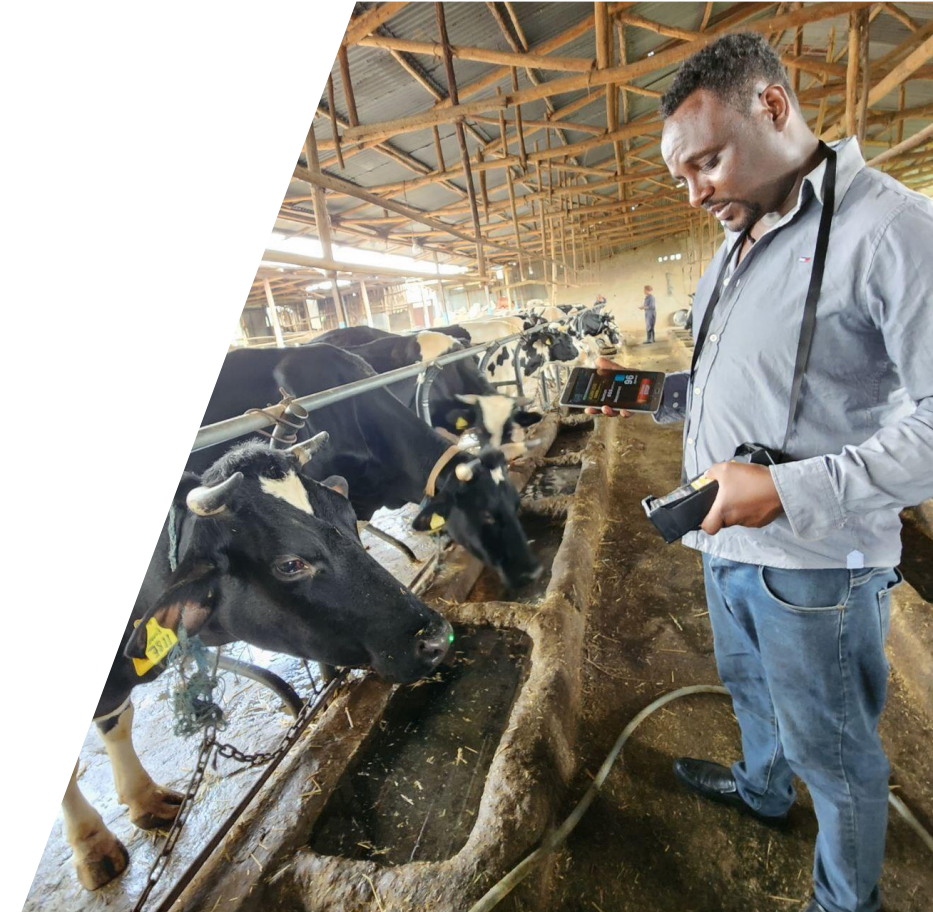
Duration: 5-10 min



Background methane : Correcting the methane measurement for the background data

Prediction inside cow status recordings

cowStatus	nAnim	nRec	accuracy
Feeding	410	2302	0.49
Ruminating	587	6437	0.33
Sleeping	185	555	0.33
Standing idle	345	2913	0.26
Drinking	12	18	0.21



Advantage and Limitation of LMD

Advantage	Explanation	Limitation	Explanation
Non-invasive	Reduces stress; allows repeated measures	Environmental sensitivity	Wind, humidity, and temperature affect readings.
Portable	Suitable for field/smallholder conditions	Measure concentration	Records ppm·m, not actual CH ₄ /day emission.
Real-time output	Immediate emission profiling	Movement effects	Animal or operator movement causes variation.
Cost-effective	Affordable compared to chambers	Needs repeated measures	Several readings required for accuracy.
Flexible use	Across activities and environments	Background interference	Nearby methane sources distort results.
Data integrable	Links with MIR/genomics databases	Missing Data Linkage	Not linked with animal id
Safe operation	No harm to animals or users		

