GMG Asia: Methane recording techniques

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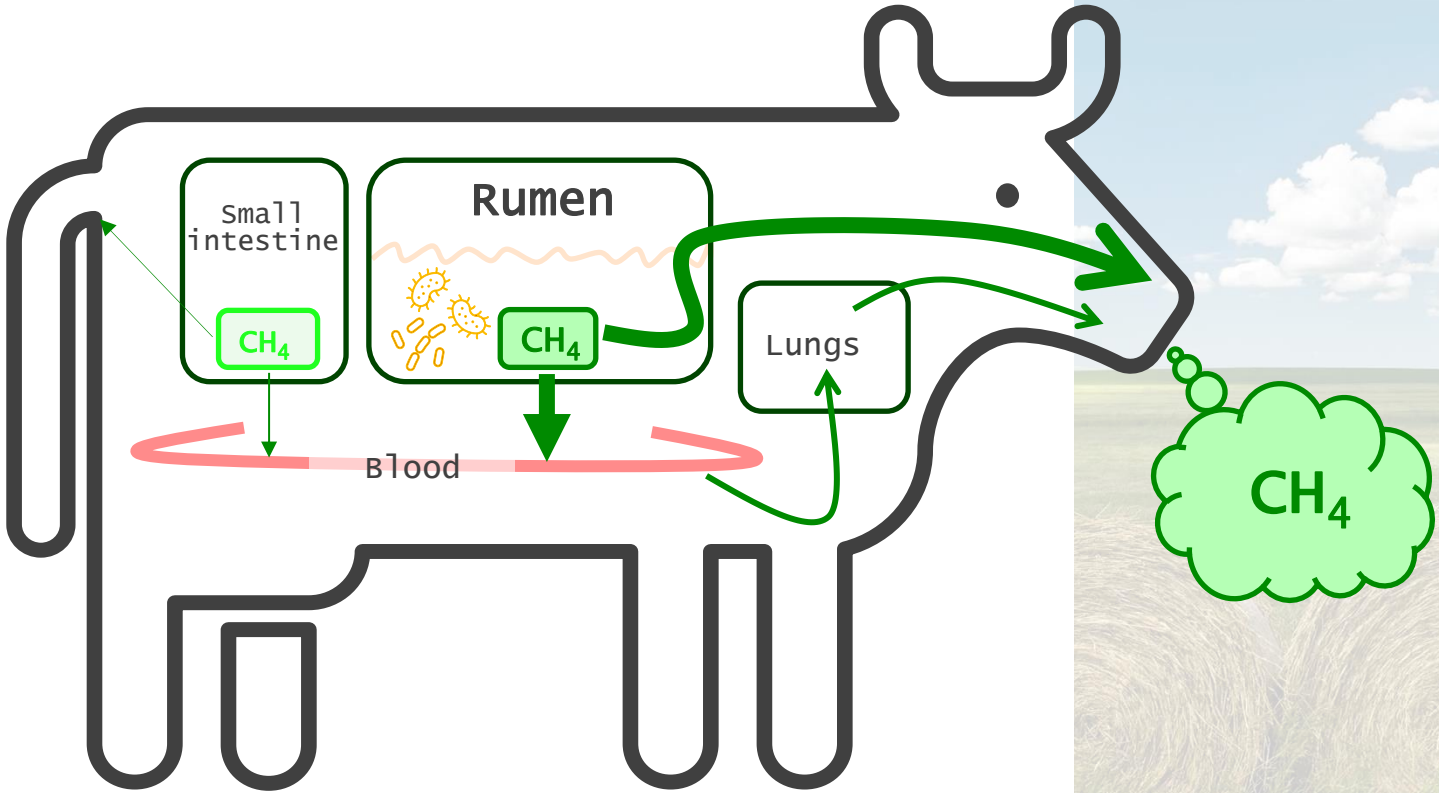
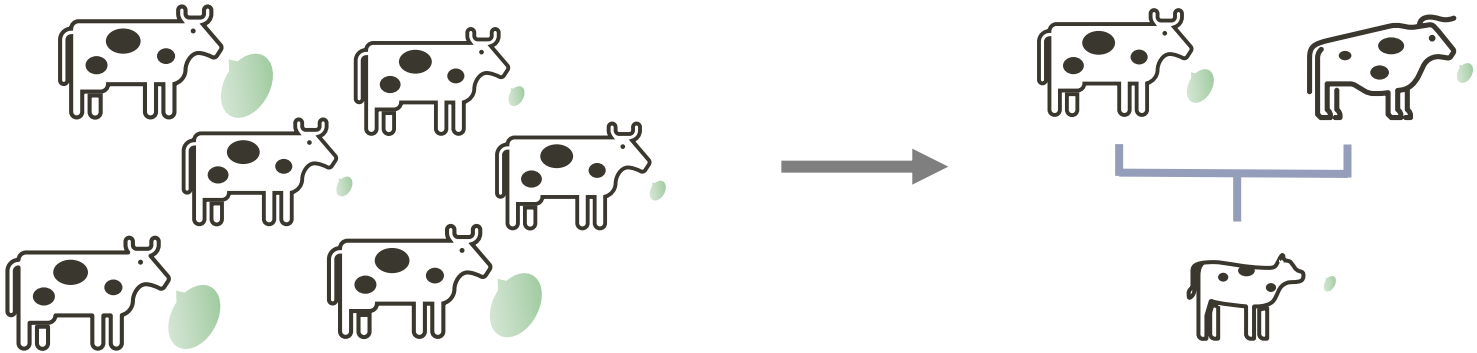
Enteric methane



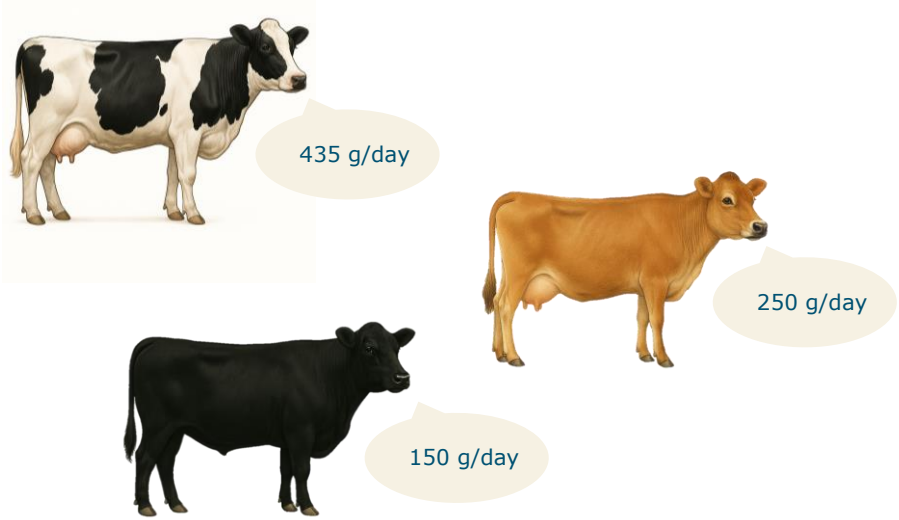
Animal breeding as a mitigation strategy

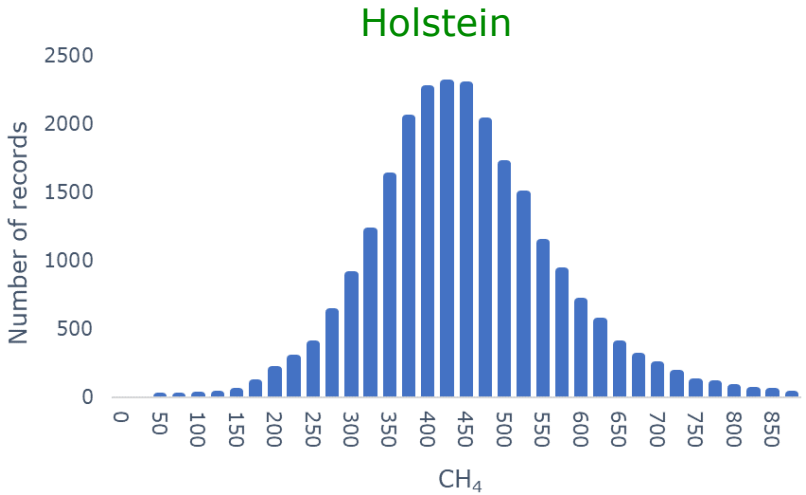
- There is variation between individual cows
- Around 20% is estimated as genetic variation (heritability)



Quantitative genetics theory

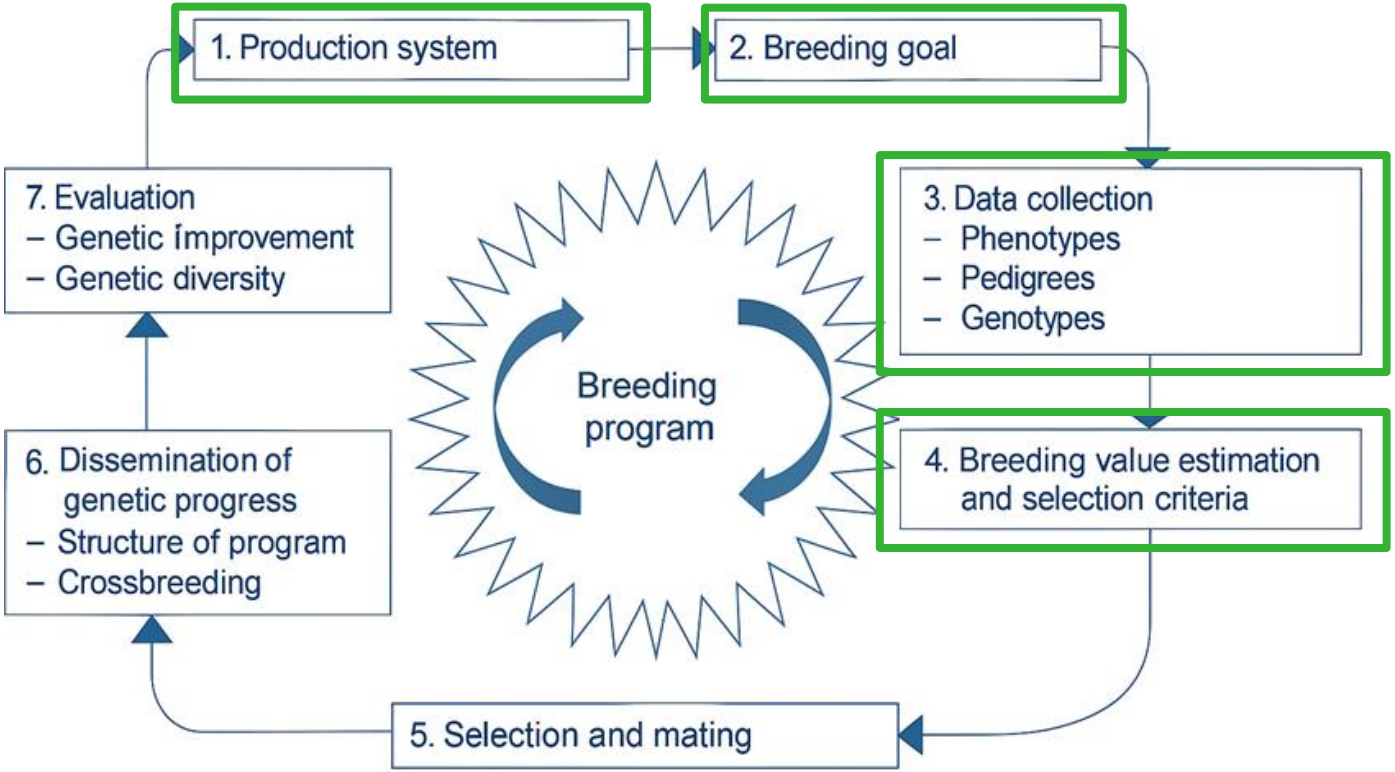
- Continuous variation, differences **between** and **within** breeds





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

What is needed to breed for CH_4 mitigation?



Phenotyping

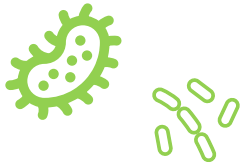
Respiration chamber

Sniffer

SF6

GreenFeed

Predictions from microbiome



Predictions from MIR spectra

Portable accumulation chamber

Laser methane detector

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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

Julius van der Werf, UNE Armidale, Australia

SF6

SF6

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

Ellinbank Smartfarm, Agriculture Victoria, Australia

https://www.farmonline.com.au/story/7790951/focus-on-reducing-dairys-methane-footprint/

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

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Methods in development

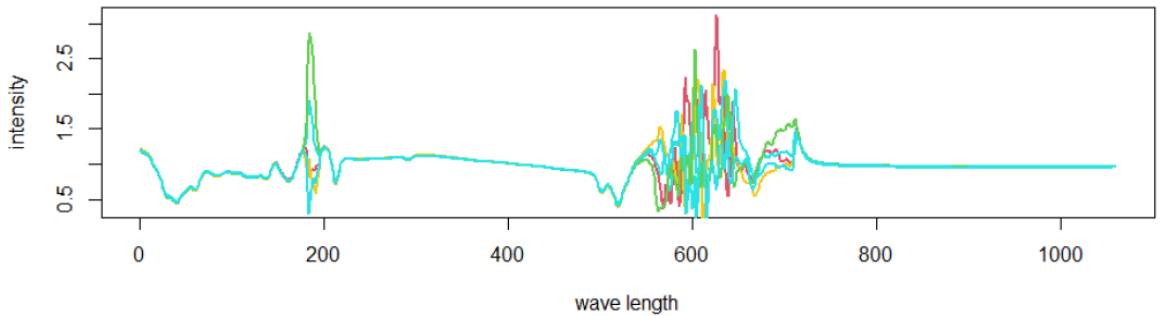
Wearables

Zelp LTD, London, UK

Cubicle hoods

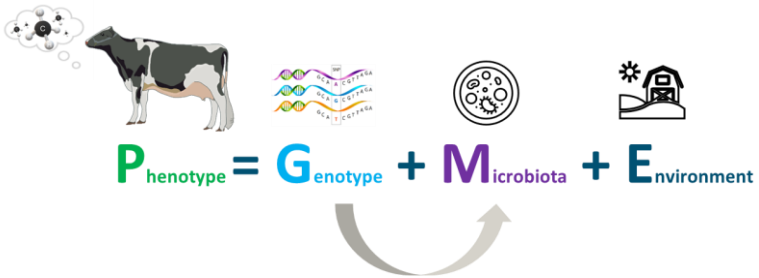
MIR prediction

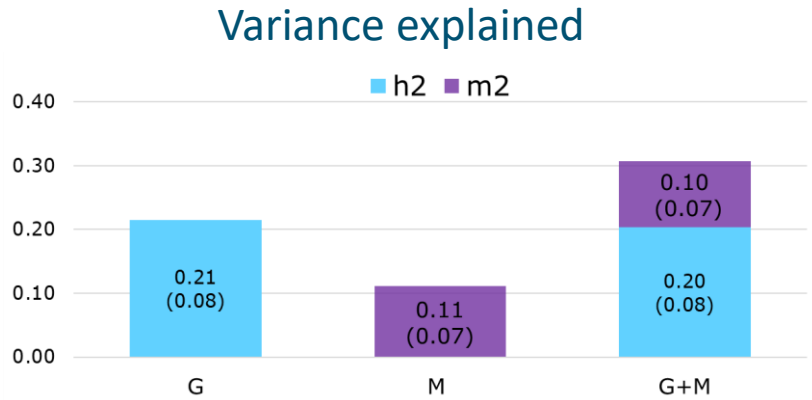
- Phenotypes on methane needed to train prediction models!
- Mixed results from literature, successful but predictions not always accurate for farms without methane measurements
- A cheap method to substantially increase the number of animals with information



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!





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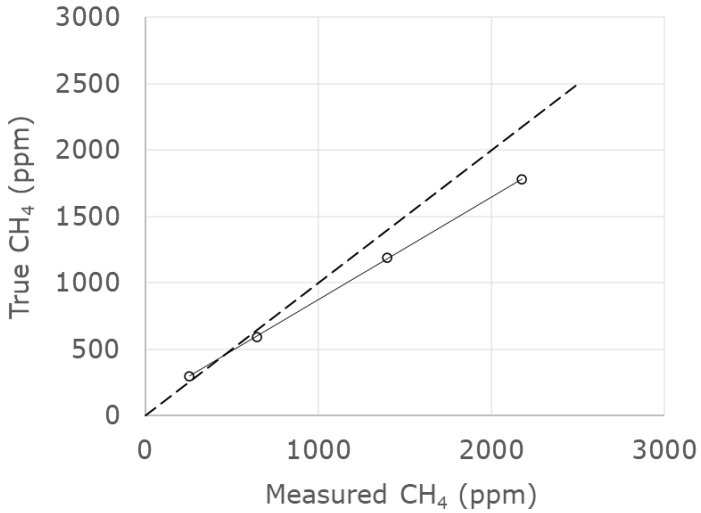
How to choose a method?

- 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?

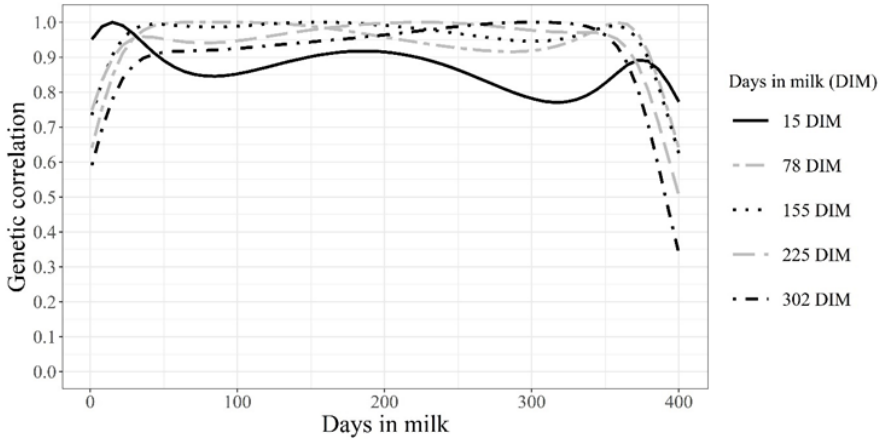
Calibration is an issue for all IR sensors!



- Severity highly depends on the type or 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

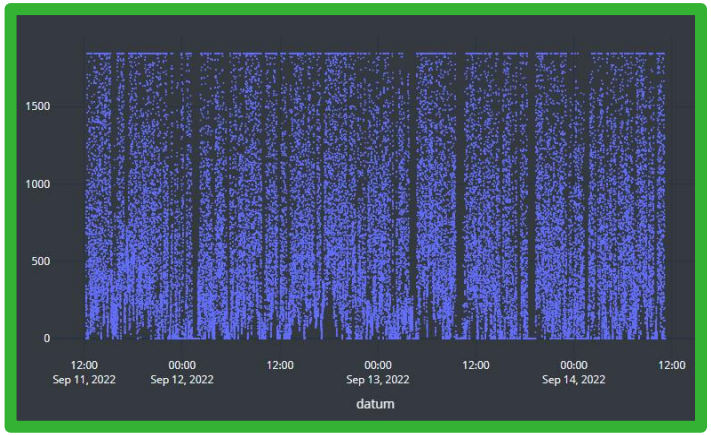
https://wiki.icar.org/index.php/Section_20:_Methane_measuring_methods

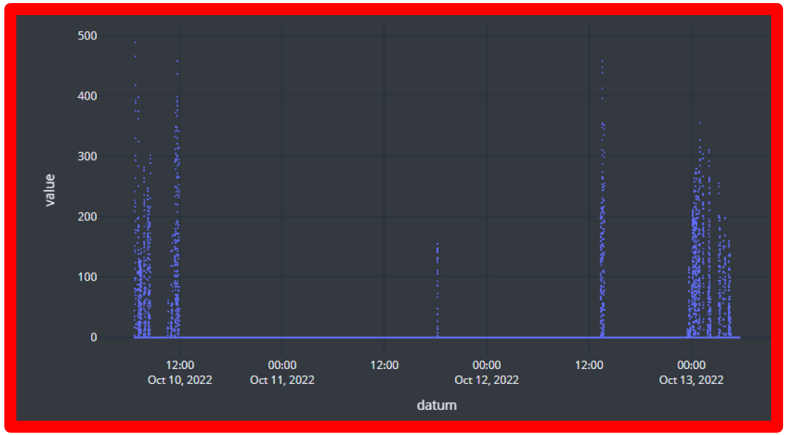
- Respiration chamber
- Portable Accumulation Chambers
- SF6
- Breath sampling during milk and feeding
- Sniffer SOP
- Greenfeed SOP
- Laser Methane Detector

LMD SOP and webinar organized soon

Breeding value estimation - phenotypes

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

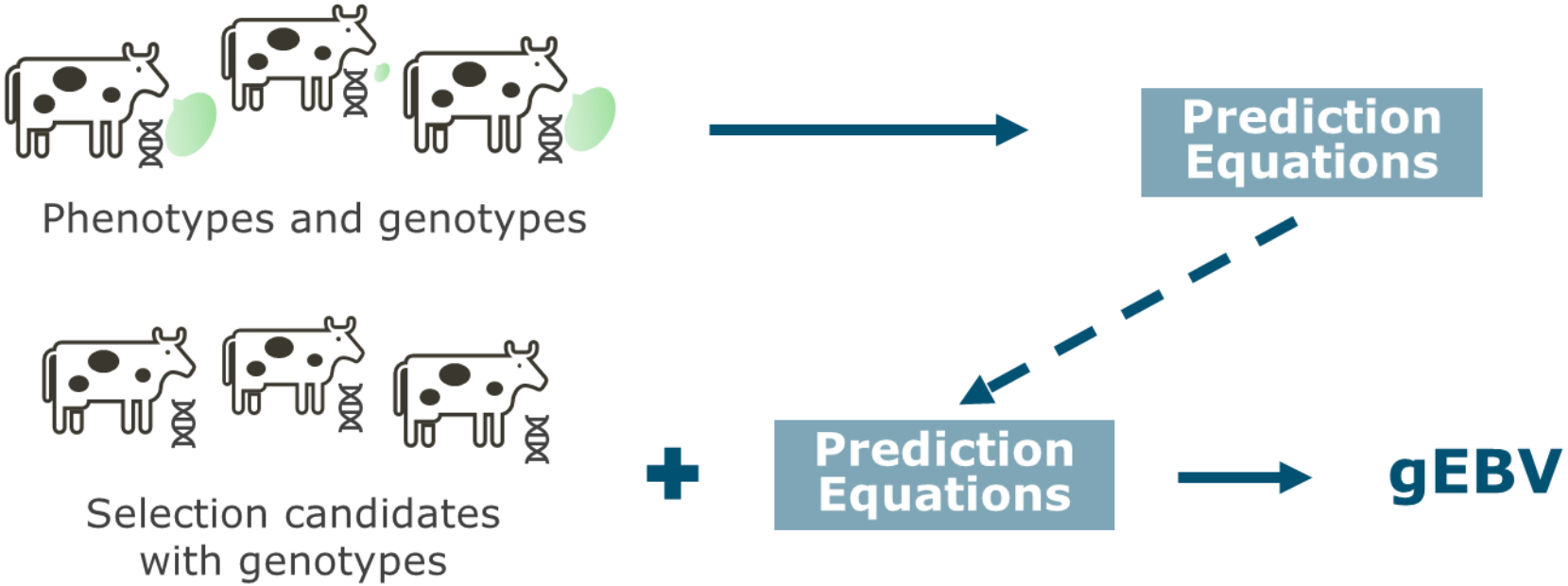




- Is it possible to combine measurements from several methods?

Breeding value estimation - genotypes

- Using all information in genomic evaluations



Breeding value estimation - models

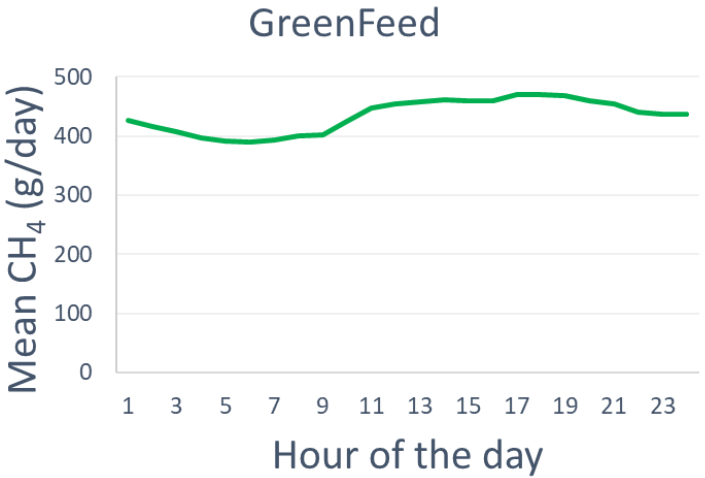
- Estimation of EBVs with linear mixed models (in e.g. ASReml, WOMBAT, BLUPF90, etc.)

Suggested fixed effects:

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

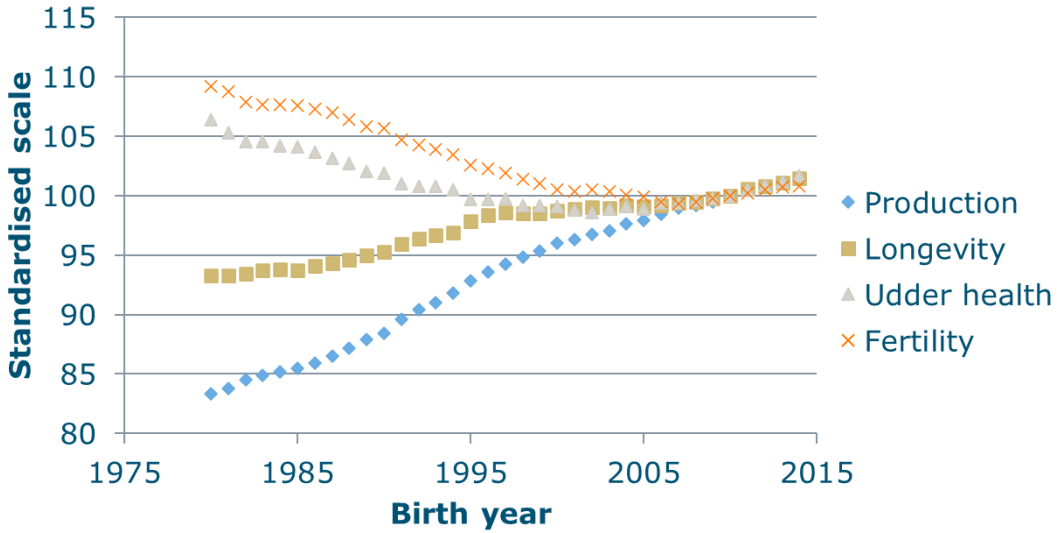
Random effects:

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



Methane in a breeding goal

- Balanced breeding



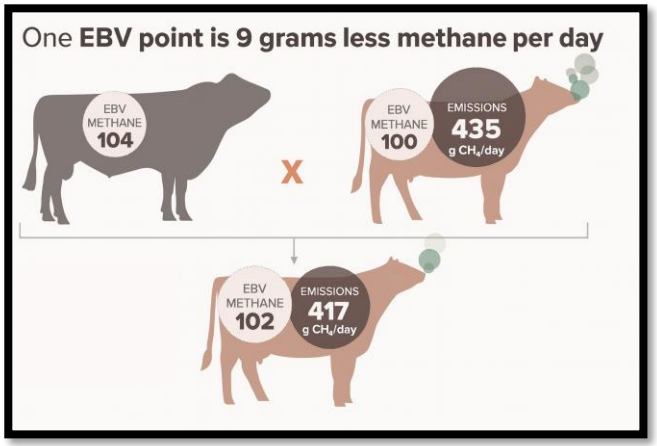
- Relationships with methane differ between studies
- Large datasets required and there appear to be species/ population differences

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

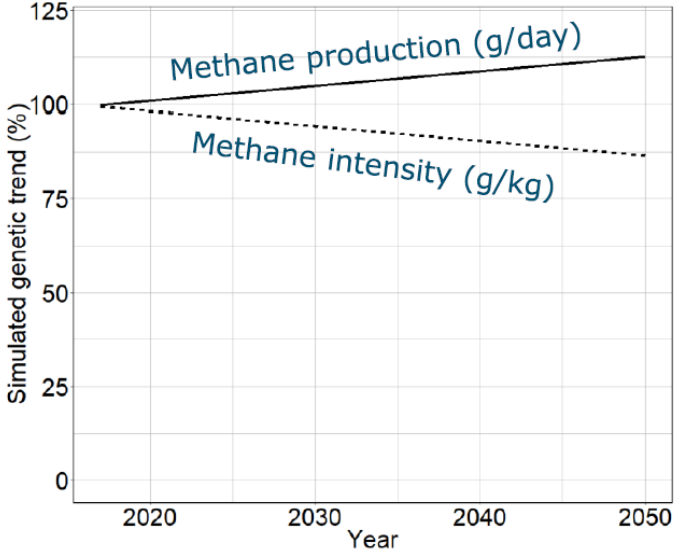
Examples of projects

- 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 CH_4/ kg DMI (12%)
  - Applied in breeding program since 2018
- Canada, breeding values for MIR predicted CH_4

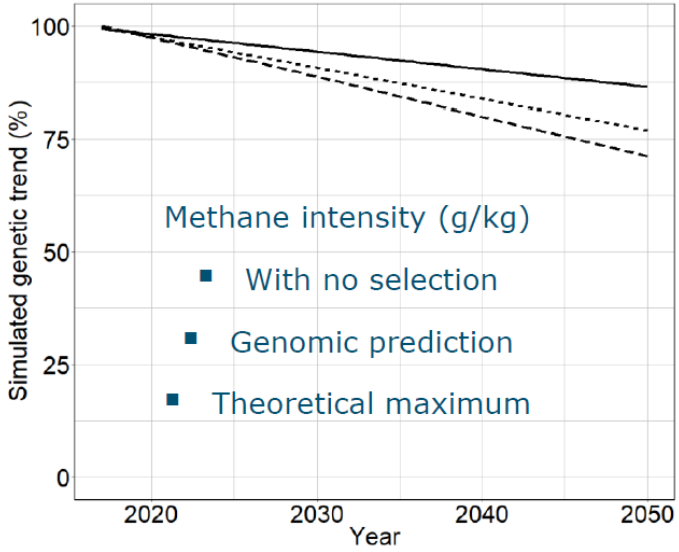


What can breeding bring us?

Current trends



With CH_4 selection



https://doi.org/10.1016/j.animal.2021.100294 (de Haas et al. 2021)

Thank you for your attention!

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