Linking genomics to efficiency and environmental traits in dairy cattle

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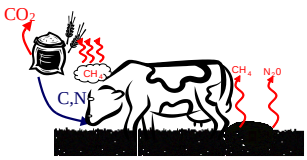
This is what we want a cow to do ...

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

... but that's also what causes problems!



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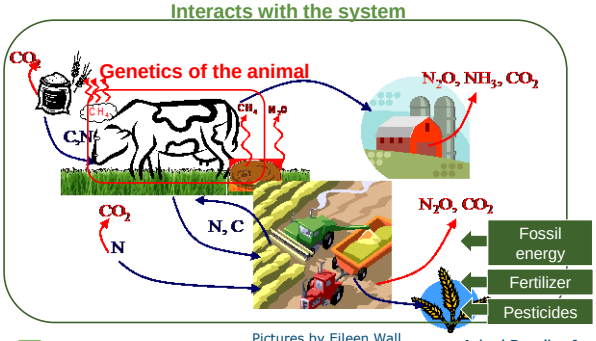
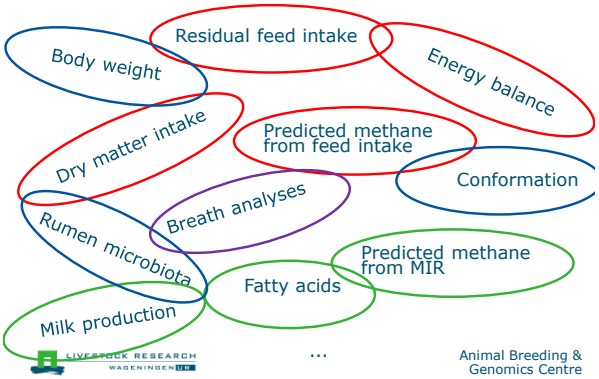


Pictures by Eileen Wall

Role of genetics

- Making use of natural variation between animals
  - Cost-effective
  - Permanent and cumulative changes in performance
- Information on phenotypes is needed!
  - Efficiency and environmental phenotypes are expensive and difficult to measure
    - Indicator traits
    - New technologies
    - Genomic selection

Efficiency and environmental phenotypes



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Outline of presentation

- Traits based on feed intake records
  - Link with genomics
- Traits based on breath analyses
  - Performance of new technologies
  - Monitoring strategies
- Traits based on cow characteristics and milk composition
  - Predictors for efficiency and environmental traits
- Future outlook

Traits based on feed intake records

Genomic prediction of RFI and PME

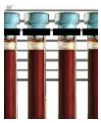
- Residual feed intake (RFI in MJ/d)
  - Energy intake – energy requirements for milk, fat, protein, and maintenance (as function of metabolic body weight)

- Predicted methane emission (PME in gram/day):
  = feed intake (in kg DM/d)
  x energy content of kg DM (= 18.4 (MJ/kg DM))
  / energy generated by methane (= 0.05565 (MJ/g))
  x percentage methane of gross energy (= 0.06)
  x scaling factor [1 + (2.38 – level of intake (multiples of maintenance level)) x 0.04]

Pilot study - available data

- Experimental farm: 613 cows (1990-1997)
  - Feed intake + ration (daily)
  - Body weight (weekly)
  - Milk production & milk contents (weekly)

- Blood samples: 588 cows
  - Illumina 50k Chip



Genetic parameters

	RFI	PME
RFI	0.40	0.72
PME	0.32	0.35

Heritability; phenotypic correlation; genetic correlation

De Haas et al., JDS, 2011

Accuracy of predicting BV for RFI and PME

	RFI	PME
Pedigree	0.37	0.21
Pedigree + SNP	0.52	0.37

Verbyla et al., JDS, 2010
De Haas et al., JDS, 2011

Conclusions – RFI and PME

- Genetic correlation PME with feed efficiency is positive: Cows with low RFI (i.e. high feed eff.) have low PME
- The use of SNP information showed an increase in the accuracy to predict BV for environmental phenotypes
- In future, selection for environmental phenotypes could be performed using genomic selection

Phenotype is king → collaboration

Combining DMI data of AUS-NL-UK

Country	Heifer type	No. anim.	No. SNPs	Rec. period
Australia	Growing	843	624,930	For 60-70d starting at age of 200d
Netherlands	Lactating	599	37,069	First 100d in lactation
UK	Lactating	359	37,069	First 100d in lactation

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Aim of this study

Estimate the accuracy of genomic breeding values (GEBV's) across countries for dry matter intake, when analysed as one trait, or a separate trait per country (multitrait)

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Accuracy of genomic selection

	Uni within		
AU	0.38 *(0.03)*		
EU	0.31 *(0.05)*		
UK	0.30 *(0.04)*		
NL	0.33 *(0.09)*		

De Haas et al., JDS, 2012

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Accuracy of genomic selection

	Uni within	Uni multi	
AU	0.38 *(0.03)*	0.34 *(0.05)*	
EU	0.31 *(0.05)*	**0.32** *(0.05)*	
UK	0.30 *(0.04)*	**0.33** *(0.06)*	
NL	0.33 *(0.09)*	0.31 *(0.09)*	

De Haas et al., JDS, 2012

Accuracy of genomic selection

	Uni within	Uni multi	Tri: AU-UK-NL
AU	0.38 *(0.03)*	0.34 *(0.05)*	**0.39** *(0.04)*
EU	0.31 *(0.05)*	0.32 *(0.05)*	**0.33** *(0.05)*
UK	0.30 *(0.04)*	0.33 *(0.06)*	**0.33** *(0.03)*
NL	0.33 *(0.09)*	0.31 *(0.09)*	**0.33** *(0.09)*

De Haas et al., JDS, 2012

Conclusions – power of int. collaboration

- Accuracy of GEBVs for DMI can be increased by:
  - combining datasets across countries, and
  - using a multitrait approach
- "Proof-of-principle" is now shown
  - Start of global Dry Matter Initiative
    - More phenotypes (≈6,000 animals)
    - More SNPs (591,621)
    - More datasets (10 partners)

Breath analyses

Ways to measure:

Respiration chamber
Golden standard!

Ways to measure:

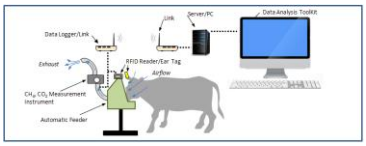
Head hoods

Ways to measure:

SF6

Ways to measure:

Laser



GreenFeeder

Butter boxes

Ways to measure:

1. Sampling unit
2. Pump unit
3. FTIR-Analyser
4. Laptop

FTIR
(pictures by Jan Lassen)

Ways to measure:

▪ Respiration chamber	Full day, continuous
▪ Head hoods	Full day, only mouth no hindgut
▪ SF6	Full day, large variation
▪ Butter boxes (sheep!)	Several moments per day
▪ GreenFeeder	While eating concentrates
▪ Laser	Short measurements
▪ FTIR – milking robot	During milking

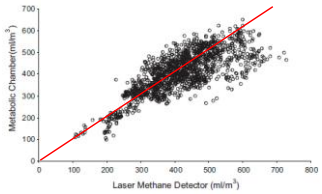
Ways to measure:

Question 1:

- How accurate are the measuring methods compared to Golden Standard?

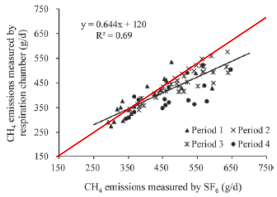
Validation of measuring method

- Few groups have validated a measuring strategy with the golden standard:
  1. Laser (Chagunda & Yan, AFST, 2011)



Validation of measuring method

- Few groups have validated a measuring strategy with the golden standard:
  2. SF6 (Munoz et al., JDS, 2012)



Ways to measure:

Question 2:

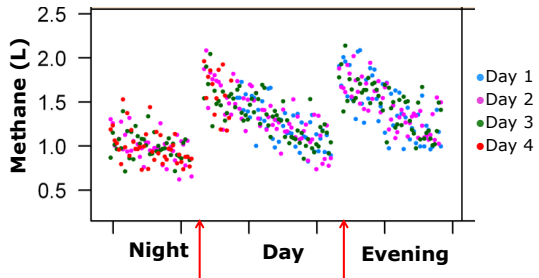
- How accurate can daily methane production be predicted with reduced sampling strategies?

Available data feasibility study

Wageningen respiration chambers

- 10 trials:
  - each involved a pair of cows
  - data reported over a 72 hour period spanning 4 calendar days

Methane production for 1 trial



3 scenarios

- Measuring
  - (1) during milking (i.e. twice daily, for 15 minutes);
  - (2) in concentrate feeder (i.e. 5x per day for 6 min.);
  - (3) in cubicles (i.e. 4 hours continuously).

- Scenarios were simulated by omitting samples

Accuracies compared to resp. chambers

Scenario	CH_4	
During milking	0.85	
In concentrate feeder	0.89	
In cubicles	0.96	

De Haas et al. (in prep.)

Accuracies compared to resp. chambers

Scenario	CH_4	CH_4/CO_2
During milking	0.85	0.31
In concentrate feeder	0.89	0.33
In cubicles	0.96	0.39

De Haas et al. (in prep.)

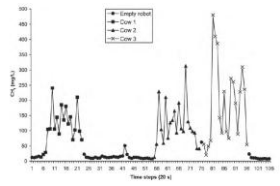
Ways to measure:

Question 3:

- Can variation within and between animals be picked up with reduced sampling strategies?

Variation within / between animals

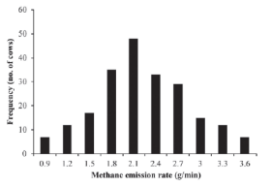
- Fourier transformed infrared sniffers



Lassen et al., JDS, 2012

Variation within / between animals

- Methane analyzers in Lely milking robots



Garnsworthy et al., JDS, 2012

Conclusions ways to measure

1. Cheaper equipment can measure methane accurately as well, but there is room for improvement
2. Daily methane production can be predicted reasonably accurate by collecting samples of all cows twice daily during milking
3. Variation between and within animals still picked up outside respiration chambers

- Opens up the possibility of creating a large database of individual methane emission phenotypes to be used for genetic and genomic studies

Predictor traits from cow characteristics and milk composition

1. Predictor traits for efficiency traits

- Data Dutch research herds
  - nearly 2,000 lactations with feed intake, ration, chemical composition, live weight (LW), production
- Can $LW^{0.75}$ and FPCM predict EBV for feed efficiency?

Predicting EBV for feed efficiency (35-70 DIM)

- EB = $NE_{intake} - (NE_{maintenace} + NE_{milk})$
- EFF = NE_{milk} / Ne_{intake}
- EFM = $NE_{milk} / (NE_{intake} - NE_{maintenance})$

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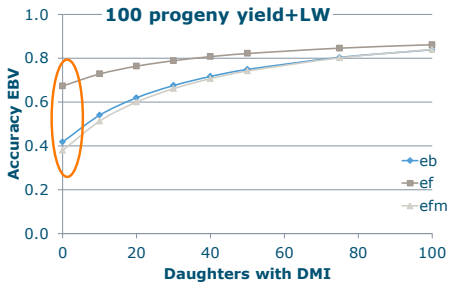
Predicting EBV for feed efficiency (35-70 DIM)



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2. Predictor traits for environment traits

- Potential use of milk mid-infrared spectra to predict individual methane emissions from dairy cows
  - Study Dehareng et al. (2012)

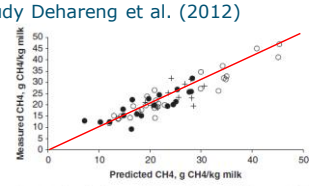

Figure 3 Infrared methane prediction on the basis of milk spectra of the day 1.5 for the different diets: corn silage (●), fresh pasture (○) and grass silage (+). PCA = principal component analysis.

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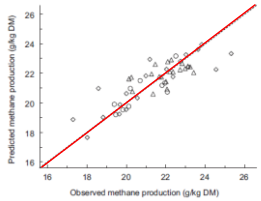
2. Predictor traits for environment traits

- Relationships between methane production and milk fatty acid profiles in dairy cattle
  - Study Dijkstra et al. (2011)



Conclusions predictor traits

- Feed intake expensive to measure on large scale
  - Yield and type to make the first step
  - Genomics should identify 'net efficient cows'
- Direct methane hard to measure on large scale
  - Predictor traits based on milk composition provide opportunities for large scale collections

Future outlook

Linking genomics to efficiency and environmental traits

- Selection for feed efficiency impossible a few years ago, with genomics a realistic prospect for future
  - Power of international collaboration
- New technologies open opportunities to start collecting individual methane output on large scale
  - Balance between costs and accuracy
  - Still room for improvement

Linking genomics to efficiency and environmental traits

- Indicator traits for both efficiency and environmental traits look promising
  - Large scale/national collection
  - Genomics should identify net efficient/environment-friendly cows

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Thank you for your attention

Questions??

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