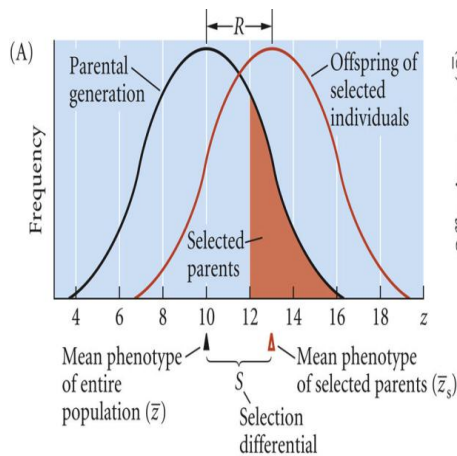# Genetic relationships between methane-related traits and milk composition in lactating dairy cows
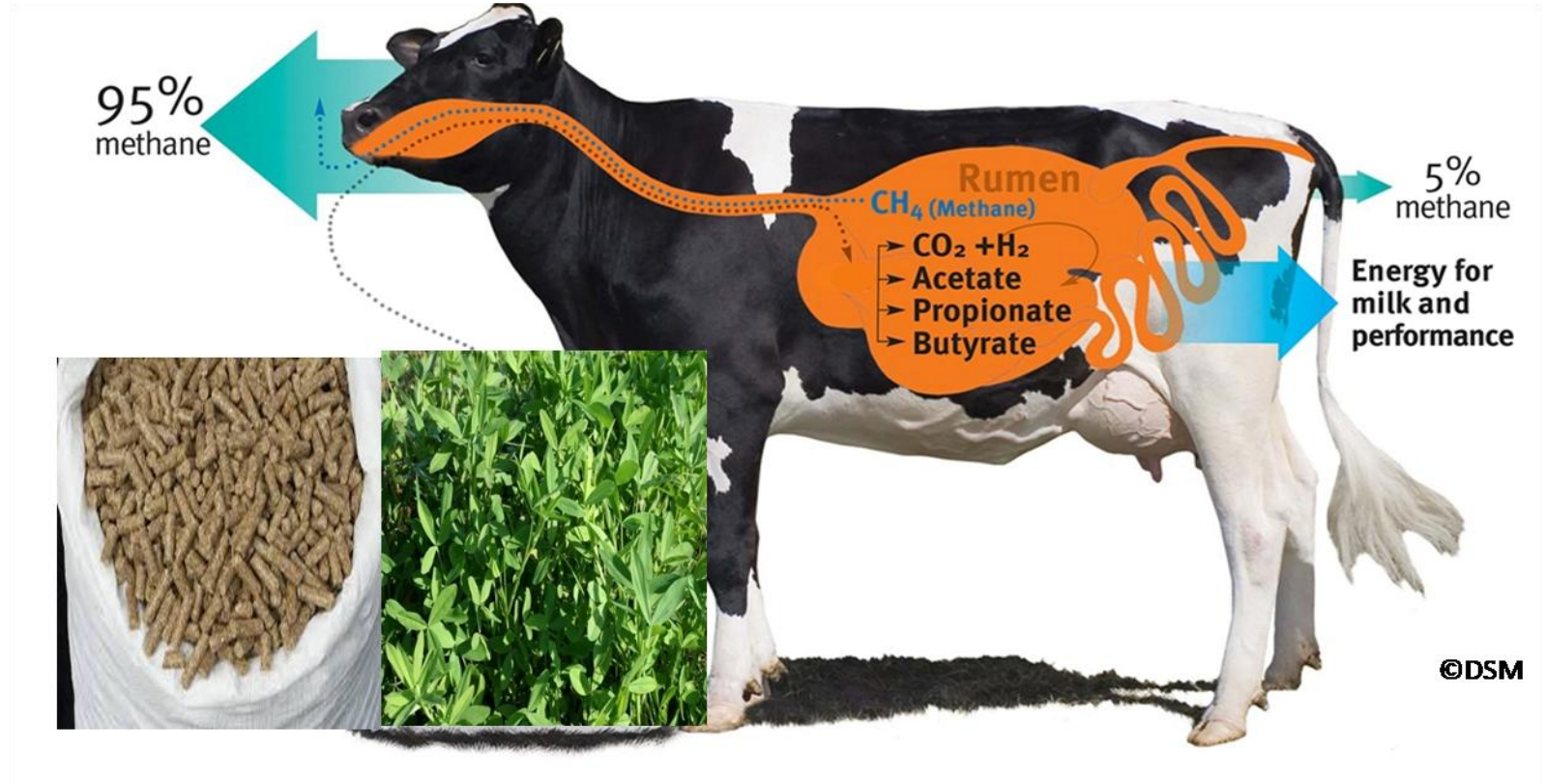

Purna Kandel

Supervisor: Nicolas Gengler
Co-Supervisor: Hélène Soyeurt

Jan 2018

Background

Background

37% of anthropogenic methane emissions from livestock (FAO, 2010)

- o Environmental pollutants
- o 2-12 % of dietary energy loss (Johnson and Johnson, 1995)

Measurements of methane emissions

Respiration chamber

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Measurements of methane emissions

Sulfur hexafluoride measurements

Measurements of methane emissions

Fourier transformed infrared method

Infrared gas analyser (FTIR)
Method used by Jan Lassen (Aarhus University, DK) and
Yvette de Haas (Wageningen UR Livestock Research, NL)

Pictures by Jan Lassn

LIVESTOCK RESEARCH
WAGENINGEN UR

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Measurements of methane emissions

GreenFeed System

Background

37% of anthropogenic methane emissions from livestock (FAO, 2010)

- o Environmental pollutants
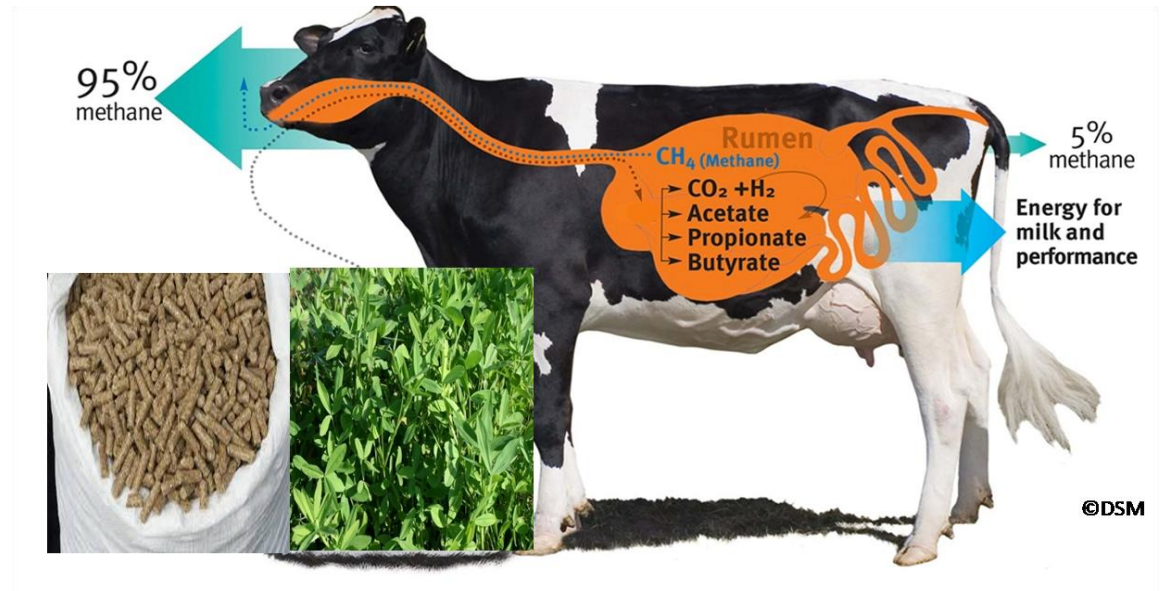- o 2-12 % of dietary energy loss (Johnson and Johnson, 1995)

Genetic gain

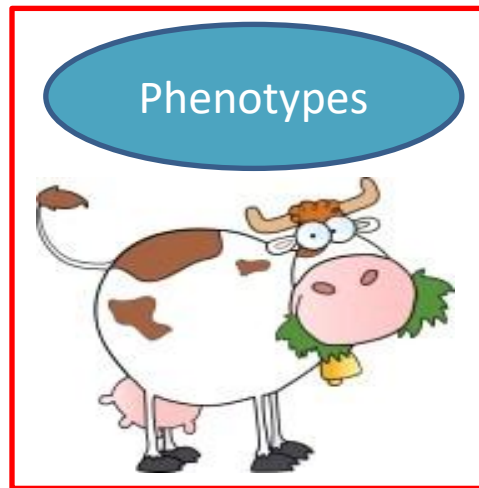- o Permanent and adds up every generation
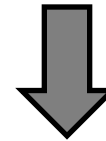
Direct methane measurements

Direct method :
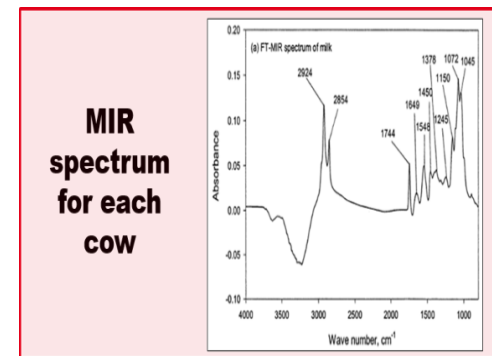- expensive
- difficult to measure
- low number of phenotypes

95% methane

Rumen
CH_4 (Methane)
→ $CO_2 + H_2$
→ Acetate
→ Propionate
→ Butyrate

5% methane

Energy for milk and performance

©DSM

➔ Indirect measurements through milk composition (fatty acid and mid-infrared spectra)

Milk Mid-Infrared Spectroscopy

Phenotypes

Equations

MIR spectrum for each cow

e.g., Milk fatty acids

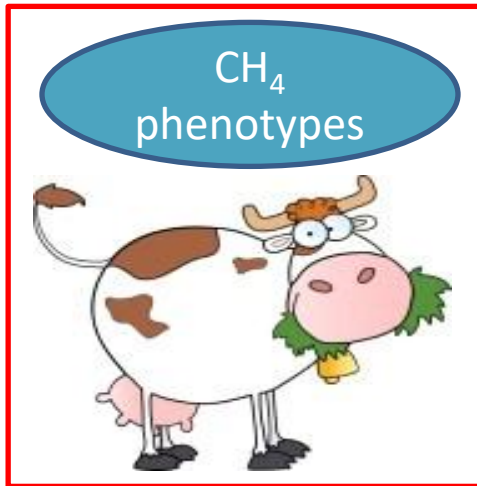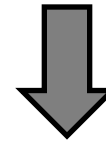LIÈGE université
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Prediction from milk MIR fatty acids

Original equations Chilliard et al., 2009   602 samples

Prediction	Equation	R^2ref	R^2CV
Methane1 *g/day*	9.97 x (C8:0 to C16:0) - 80	0.88	0.92
Methane2 *g/day*	-8.72 x C18:0 + 729	0.88	0.91
Methane3 *g/day*	282 x C8:0 + 11	0.81	0.72
Methane4 *g/day*	16.8 x C16:0 - 77	0.82	0.92

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Kandel et. al., 2015

Milk Mid-Infrared Spectroscopy
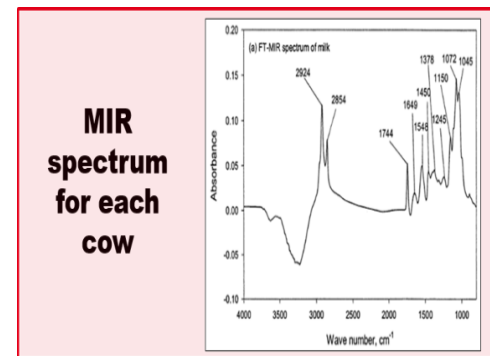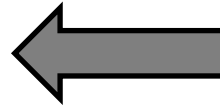
Prediction from milk MIR spectra

Original equation Vanlierde et al., 2015   452 samples

Trait	Mean	SD	R^2C	R^2CV	RMSEP
Methane (g/d)	416	126.4	0.76	0.70	81
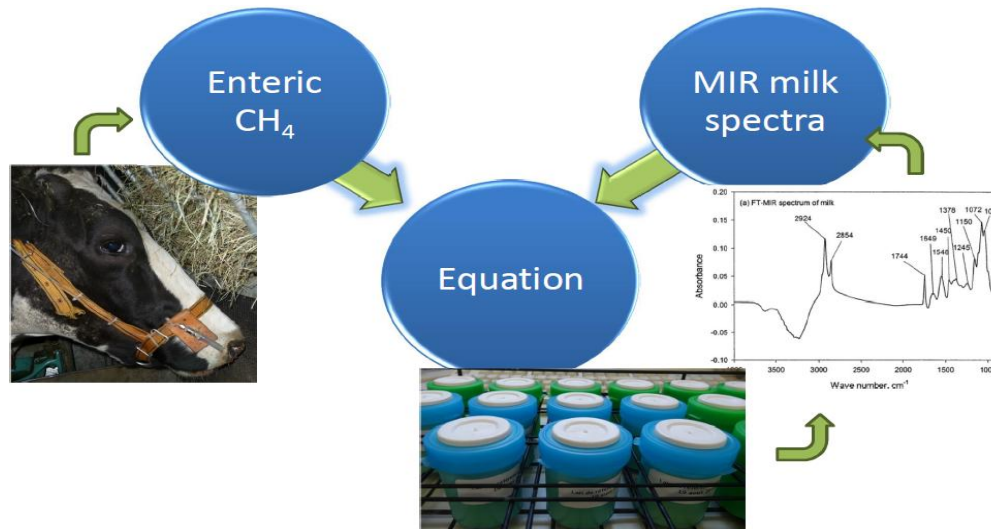
700,000 records
60,000 cows

Vanlierde et al., 2015

Prediction of methane emissions from milk composition

Milk mid-infrared spectrometry:
- Cheap
- **Large number of phenotypes**
- Commercial farms

Enteric CH_4

MIR milk spectra

Equation

Vanlierde el al., 2015

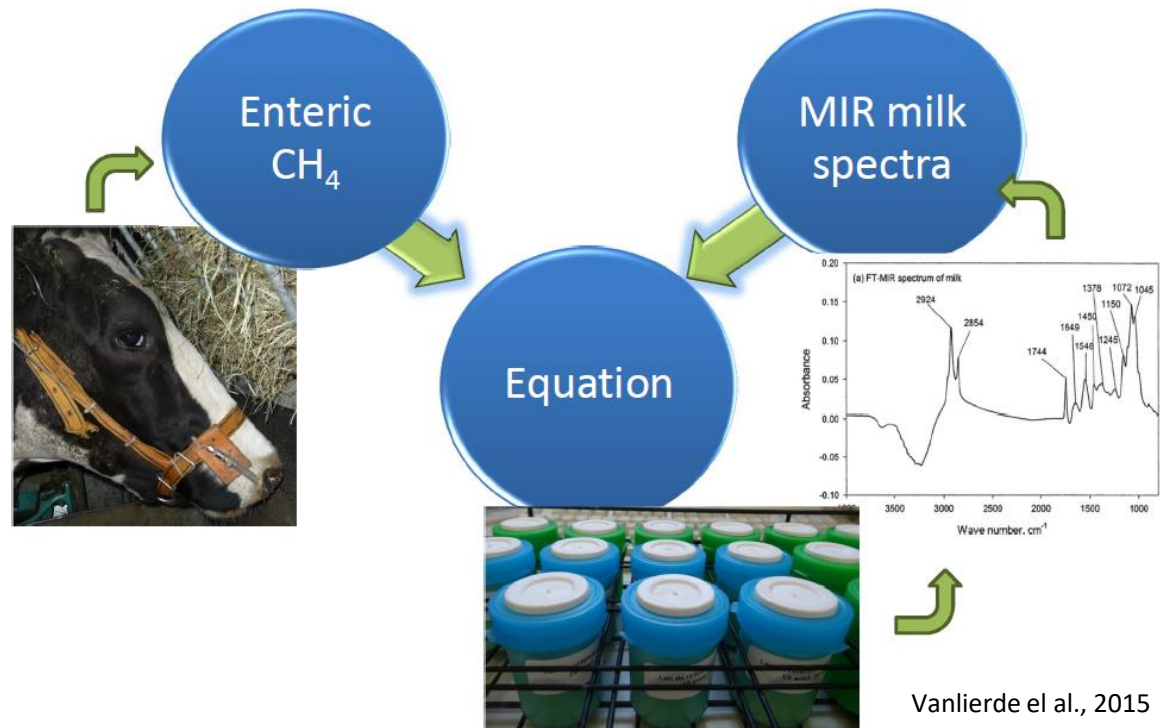# Objectives

Broad objective: genetic evaluation of large scale indirect methane measurements

Specific objectives

- Observations and phenotypic correlations between predicted methane traits and milk production traits

- Genetic parameters of predicted methane traits
- Genetic correlations with production, functional and type traits

- Selection response on methane traits and correlated responses to other traits

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Hypotheses

- MIR predicted methane traits
  - o Heritable
  - o Sufficient genetic variability to rank sires
  - o Possible selection without jeopardizing animal production and efficiency

Estimation of genetic parameters

Phenotype (*P*) = Genotype (*G*) + Environment (*E*)

Heritability $= \dfrac{\sigma^2_G}{\sigma^2_P}$

Genetic correlation: the proportion of variance that two traits share due to genetic cause

Relative genetic change (r)=b'G

b'=proportional index weight
G=genetic correlation between index traits and goal traits

Statistical Model

Methane (g/d) and Log-transformed methane intensity

y=Xβ+Q(Zp+Zu)+e……………………………(model 1)

y=Xβ+Q(Hh+Zp+Zu)+e……………………….(model 2)

β= fixed (herd test day, lactation stage, days in milk) effects
h= random within-herd lactation curve effects
p= permanent environment effect
u=additive genetic effect

Statistical Model

Methane (g/d) and Log-transformed methane intensity

$y=X\beta+Q(Zp+Zu)+e$.............................(model 1)

$y=X\beta+Q(Hh+Zp+Zu)+e$.......................(model 2)

β= fixed (herd test day, lactation stage, days in milk) effects
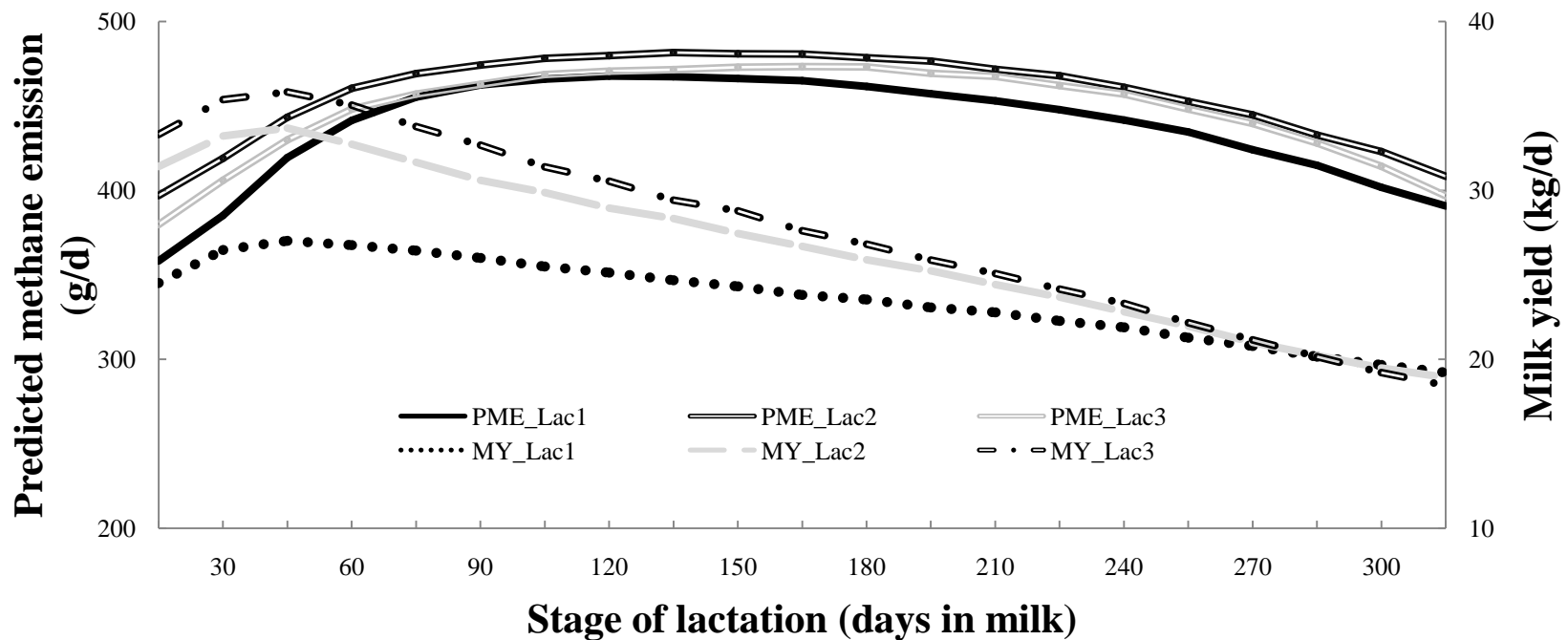h= random within-herd lactation curve effects
p= permanent environment effect
u=additive genetic effect

Model 2 fits better and 10 percent of variance was attributed to random within-herd lactation curve effects

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MIR methane prediction (g/day)

Lactation	First	Second	Third
Methane (g/d)	433 ± 80	453 ± 78	444 ± 76

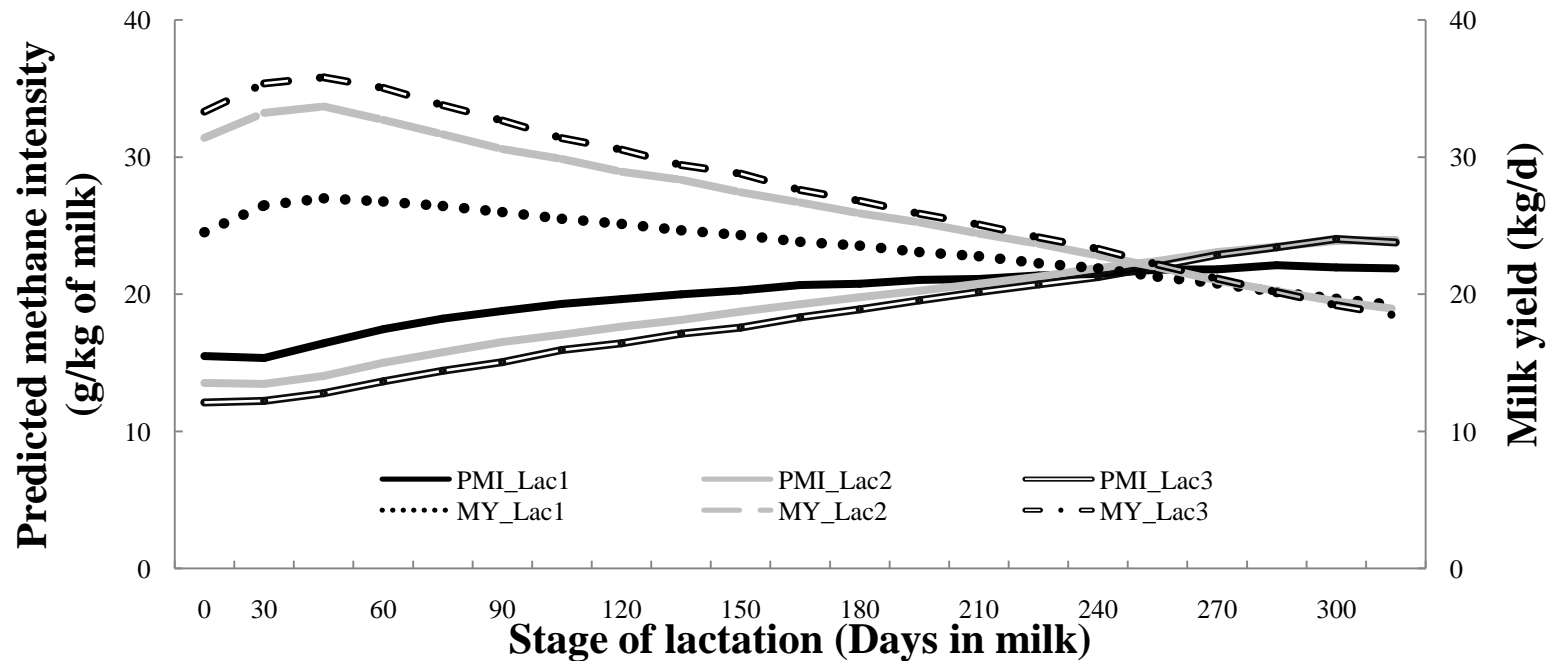Kandel et al., 2017a

Comparison with published literature
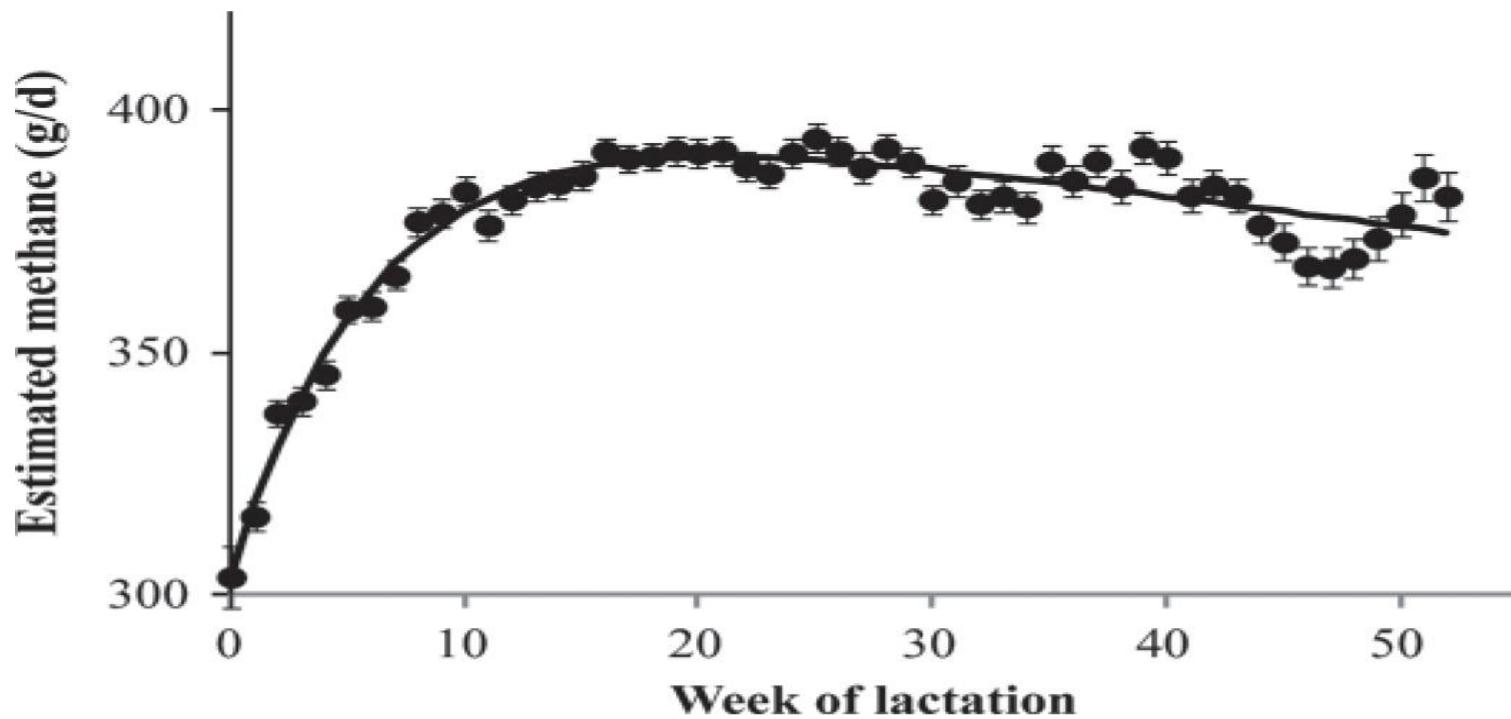
Gransworthy et al., 2012

© 2012 American Dairy Science Association

MIR methane intensity (g/kg of milk)

Lactation	First	Second	Third
Methane intensity (g/kg of milk)	19.8 ± 6.8	18.8 ± 7.6	17.7 ± 7.1

Kandel et al., 2017a

Heritability and correlations of MIR predicted methane traits with milk traits

Heritability (diagonal), phenotypic correlations (below diagonals) and genetic correlations (above diagonals)

Traits	PME	LMI	Milk yield	Fat yield	Protein yield
PME	**0.25**	0.71	-0.19	0.11	-0.05
LMI	0.47	**0.18**	-0.68	-0.21	-0.66
Milk yield	-0.07	-0.68	**0.16**	0.79	0.92
Fat yield	-0.01	-0.43	0.79	**0.13**	0.82
Protein yield	-0.02	-0.55	0.92	0.82	**0.14**

PME=predicted methane emission (g/d), LMI=Log transformed methane intensity (g/kg of milk)

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Kandel et al., 2017a

Heritability and correlations of MIR predicted methane traits with milk traits

Heritability (diagonal), phenotypic correlations (below diagonals) and genetic correlations (above diagonals)
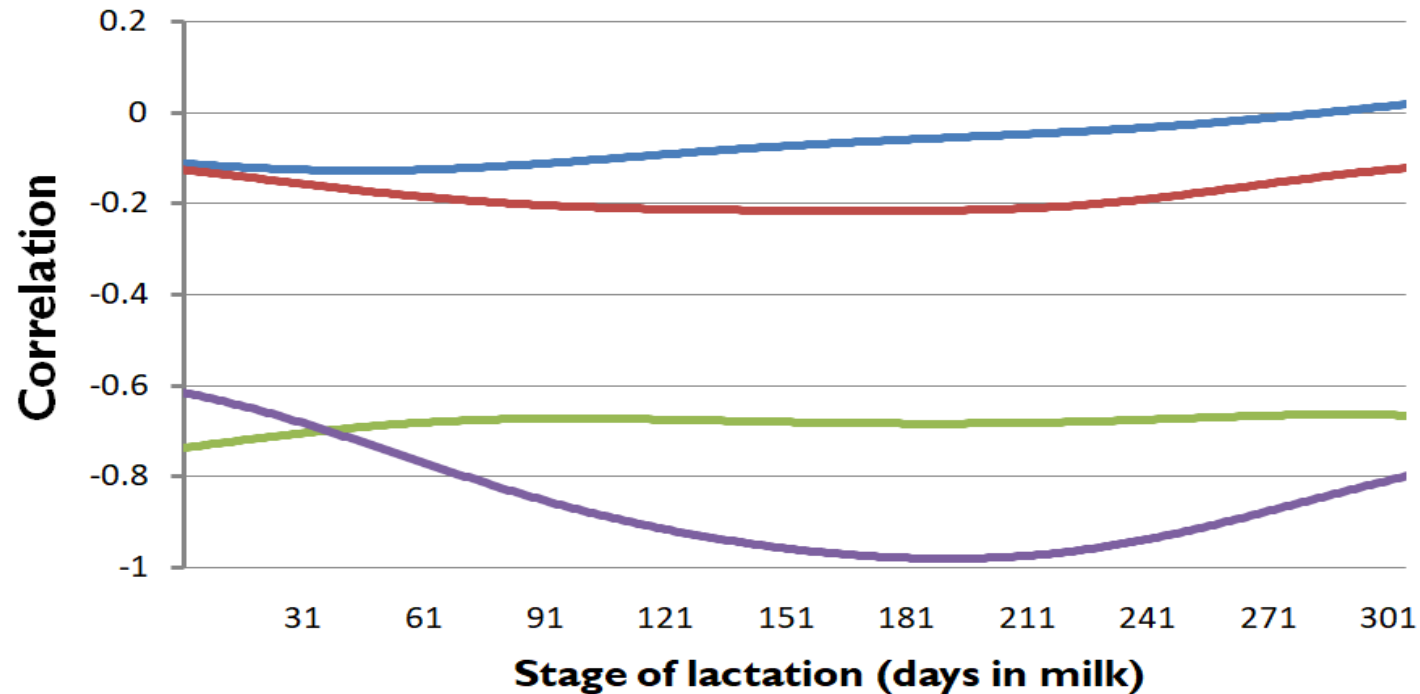
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PME=predicted methane emission (g/d), LMI=Log transformed methane intensity (g/kg of milk)

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Kandel et al., 2017a

Heritability throughout lactation (PME)
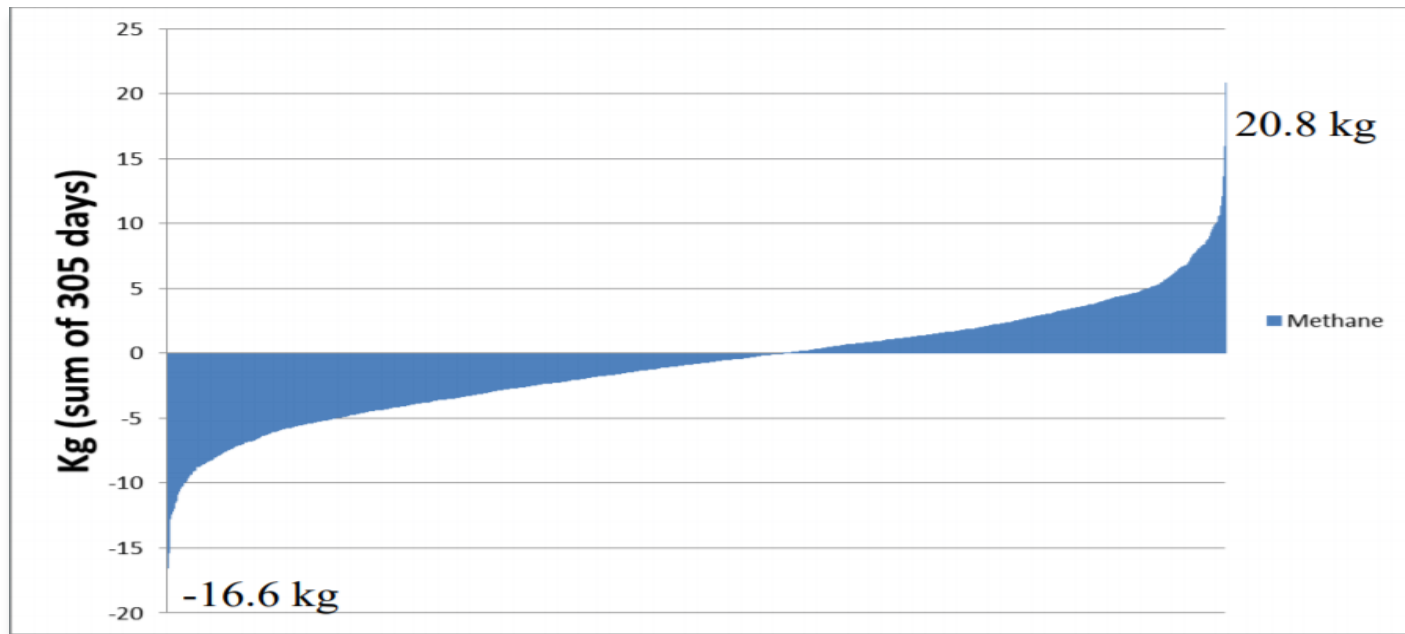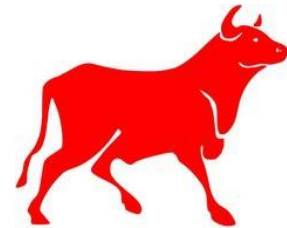

Kandel et al., 2017a
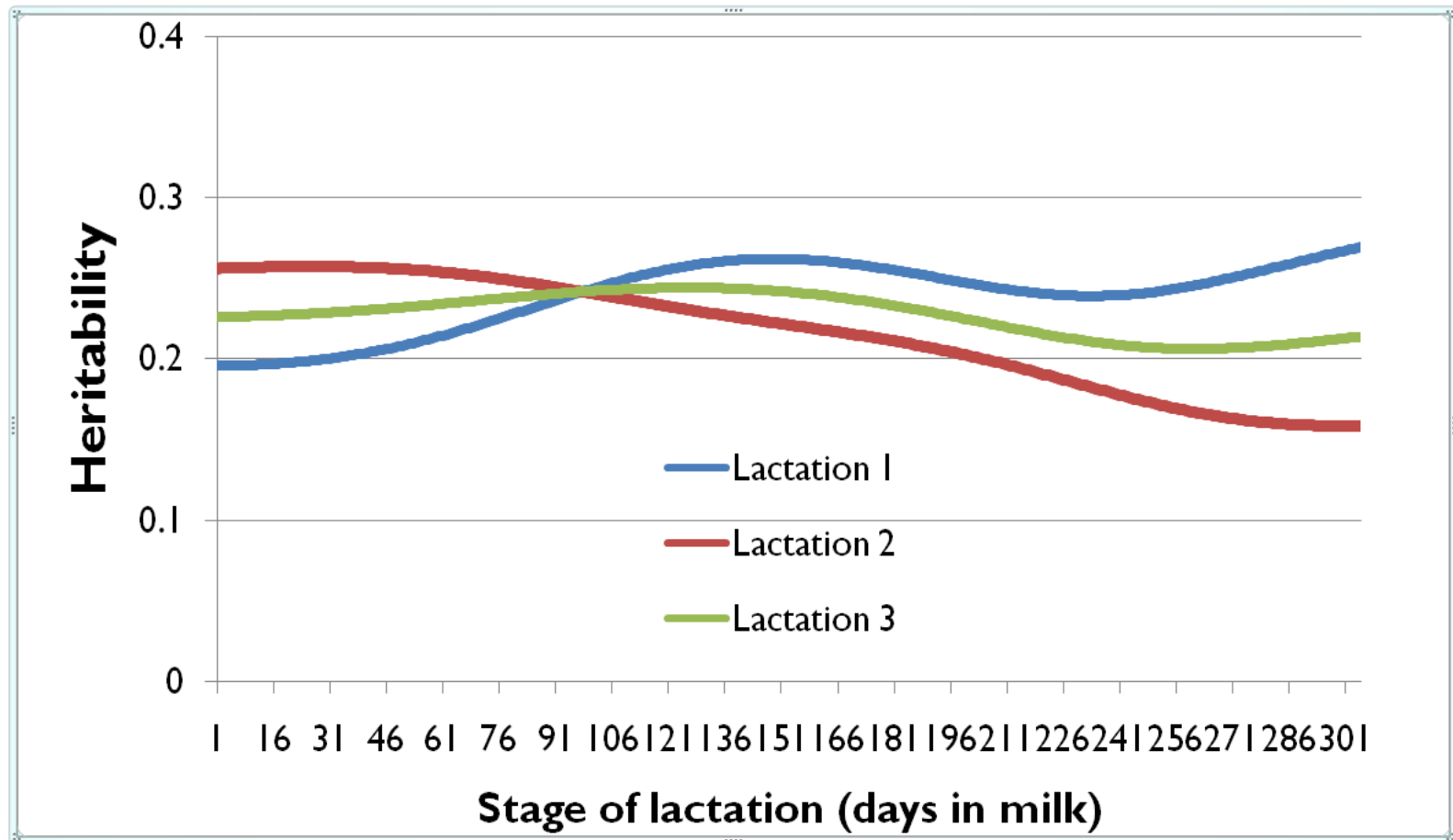
Dynamic evolution throughout lactation between methane traits and milk yield

Kandel et al., 2017a

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Sire ranking based on estimated breeding values
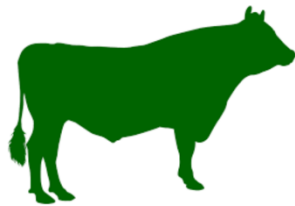
Current Walloon selection index
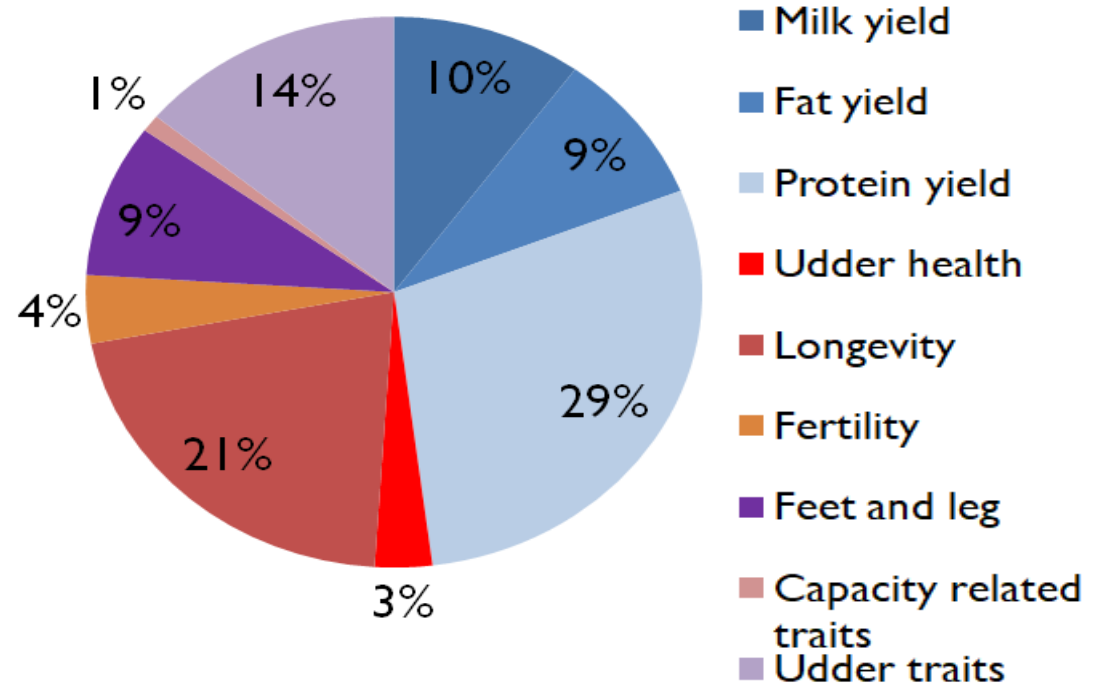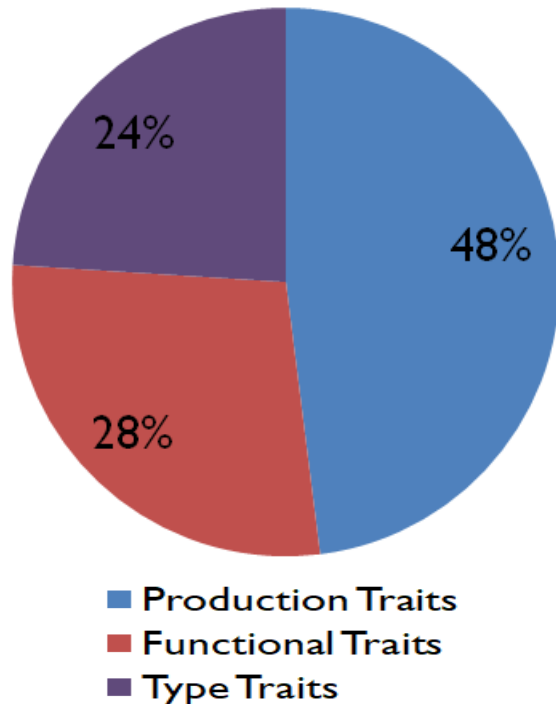
Production Traits
Functional Traits
Type Traits

Milk yield
Fat yield
Protein yield
Udder health
Longevity
Fertility
Feet and leg
Capacity related traits
Udder traits

Relative genetic change (r)=b'G
b'=proportional index weight
G=genetic correlation between index traits and goal traits

Vanderick et al., 2015

Modified Walloon selection index
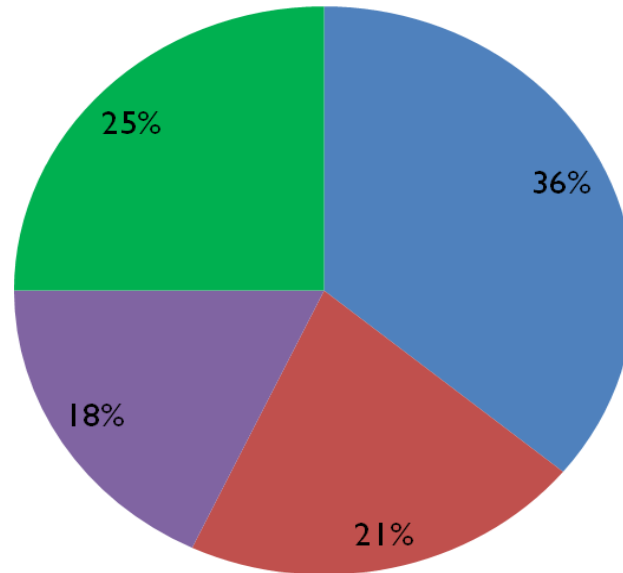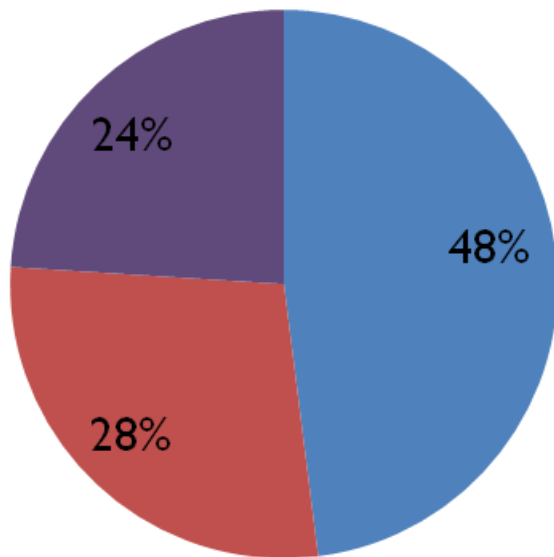
Legend:
- ■ Production Traits
- ■ Functional Traits
- ■ Type Traits
- ■ Environment Traits

Approximate genetic correlations

Calculated from estimated breeding values

Traits	PME	LMI
Fertility	0.17	0.36
Body condition score	-0.02	0.20
Longevity	0.22	0.06
Udder Health	0.22	0.08

PME=predicted methane emission (g/d), LMI=Log transformed methane intensity (g/kg of milk)

Kandel et al., 2017b

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Expected genetic changes

Selection scenario	PME	Milk yield	Fat yield	Protein yield
Current Index	1.9%	16.6%	17.2%	22.2%
25% PME	-5.9%	15.0%	5.7%	11.3%

PME= Predicted methane emission (g/d)

Kandel et al., 2017b

Expected genetic changes

Selection scenario	PME	Fertility	BCS	Udder health	Longevity
Current Index	1.9%	-3.3%	-7.9%	15.9%	27.8%
25% PME	-5.9%	-3.8%	-10.9%	13.0%	22.3%

PME= Predicted methane emission (g/d)
BCS= Body condition score

Kandel et al., 2017b

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Expected genetic changes

Selection scenario	LMI	Milk yield	Fat yield	Protein yield
Current Index	-14.5%	16.6%	17.2%	22.2%
25% LMI	-23.8%	29.4%	16.2%	28.4%

LMI= Log-transformed methane intensity (g/kg of milk)

Kandel et al., 2017b

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Expected genetic changes

Selection scenario	LMI	Fertility	BCS	Udder health	Longevity
Current Index	-14.5%	-3.3%	-7.9%	15.9%	27.8%
25% LMI	-23.8%	-10.2%	-12.8%	12.5%	22.6%

LMI= Log-transformed methane intensity (g/kg of milk)
BCS= Body condition score

Australian Balance Performance Index

Methane intensity decrease by 0.6 percent per year

Reduction of methane was quantified at 1.5 kg/cow/year

(Pryce and Bell, 2017)

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Confirmation of hypothesis

- MIR predicted methane traits
  - Heritable ✔
  - Sufficient genetic variability to rank sires ✔
  - Possible selection without jeopardizing animal production and efficiency ✔

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Conclusions

- Dynamic relationships between methane traits and milk production, energy balance related traits throughout lactation

- Impacts :
  - PME (g/d) ↑ and LMI (g/kg of milk) ↓ with the current Walloon selection index
  - Based on approximate genetic correlations, potential negative effects on fertility, udder health and longevity

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Future research

- Validation of the MIR predicted phenotypes through genetic correlations between predicted and direct traits

- Estimation of direct genetic correlations between MIR methane predictions and functional, type traits

- Some of these animals are also genotyped

  o Genome wide association study to pinpoint the chromosomal regions

  o Prime example of difficult to measure traits in dairy cows and to be benefitted from genomic selection

Acknowledgements

Supervisors:

    H Soyeurt, N Gengler

Thesis Committee Members:

    Y Beckers, Y Brostaux, E Froidmont (CRA-W)
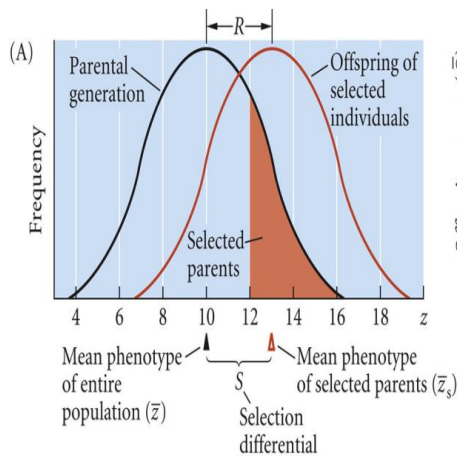
Co-authors:

    ML Vanrobays, S Vanderick, A Vanlierde, F Dehareng

Jury Members:

    L Willems, Y de Haas

Genetic relationships between methane-related traits and milk composition in lactating dairy cows

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Jan 2018