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Proxies of methane emission based on milk fatty acid profile

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Introduction

- Dairy cows produce methane
- Reduction of methane is a priority
- Breeding:
  - Permanent ☺
  - Cumulative ☺
  - Long-term ☹

Breeding for lower methane production?

- Requires data on a large amount of animals
- Measuring methane is difficult
- Indicator for methane production
  - Milk fatty acid profile

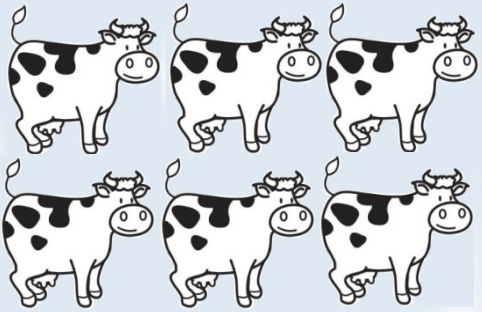
Aim

- Estimate:
    - Phenotypic variation
    - Genetic variation
    - Heritabilities

  of methane yields predicted by three combinations of milk fatty acids

Data set up - Milk Genomics Initiative

1905 Dutch HF cows



Morning milk sample

Milk fat composition

Prediction equations

Methane yield

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Predicted methane yields

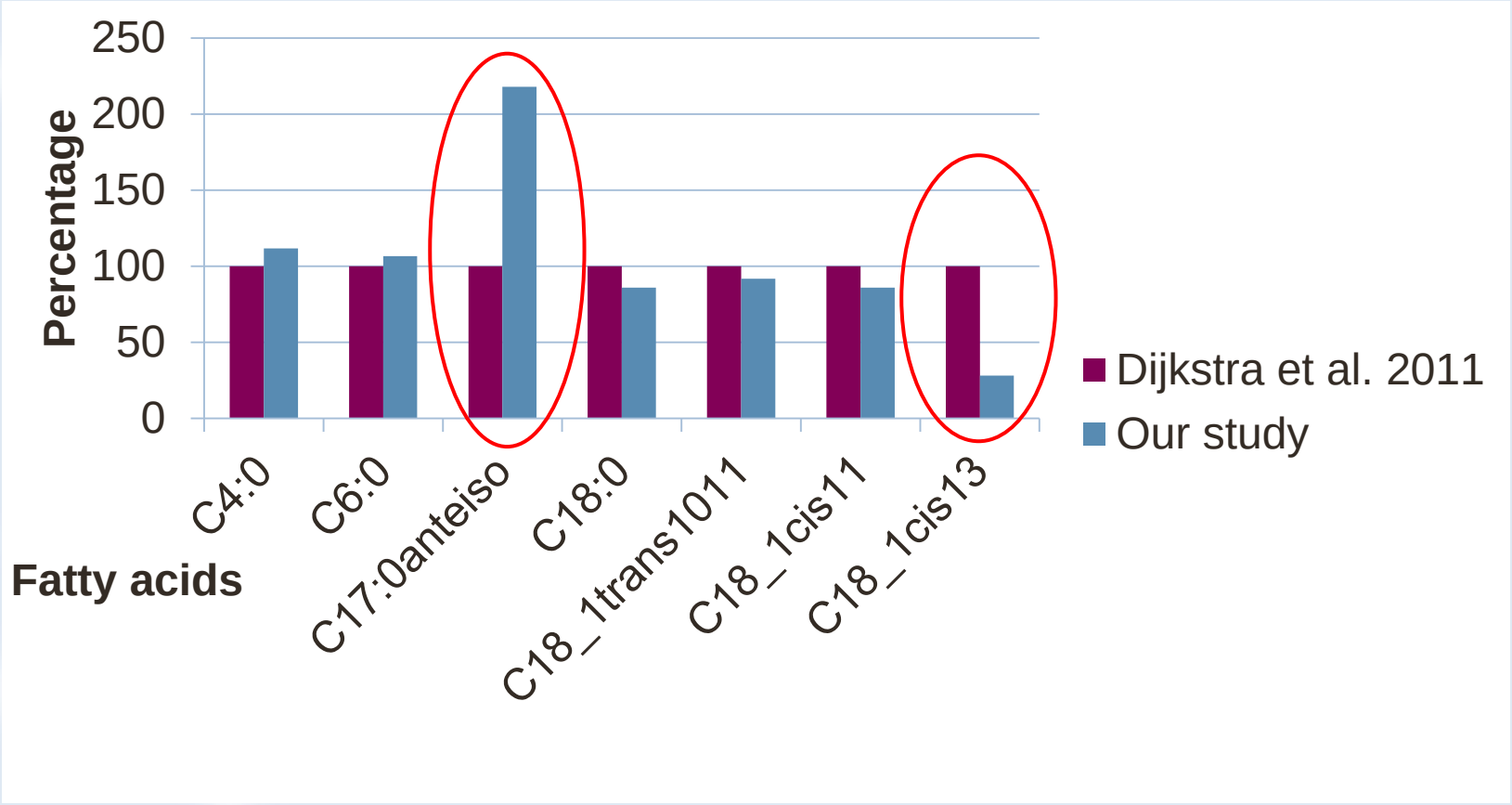
- Based on the study of Dijkstra et al. (2011):

Methane = 24.6
+ 8.74 x C17:0anteiso
– 1.97 x C18:1trans10+11
– 9.09 x C18:1cis11
+ 5.07 x C18:1cis13

(R^2 = 0.73)

Dijkstra et al. 2011
Animal Feed Science and Technology
Vol. 166-167, pages 590 -595

Predicted methane yields 2



Predicted methane yields 2

- FA that were present in similar concentrations between our dataset and dataset Dijkstra et al. (2011):

Methane-Sim = 28.6
– 1.13 x C4:0
+ 0.36 x C18:0
– 2.57 x C18:1trans10+11
– 9.29 x C18:1cis11

(R^2 = 0.70)

Predicted methane yields 3

- FA that were present in our dataset with at minimum concentration of 1 g/100 g of fat:

Methane-Quant = 27.1
– 3.04 x C4:0
+ 2.71 x C6:0
– 1.63 x C18:1trans10+11

(R^2 = 0.63)

Estimating genetic parameters

Y = μ + fixed environmental effects + **animal** + **herd** + e

- **animal** = additive genetic relationships (4 generations)
- **herd** = 398 herds

Animal model used in ASReml 2.0 (Gilmour et al., 2006)

- Phenotypic variance (σ^2_p) =
  Animal variance (σ^2_{Animal})
  + Herd variance (σ^2_{Herd})
  + Error variance (σ^2_{Error})

Genetic and phenotypic parameters

- Heritability: $h^2 = \frac{\sigma^2_{Animal}}{(\sigma^2_{Animal} + \sigma^2_{Error})}$

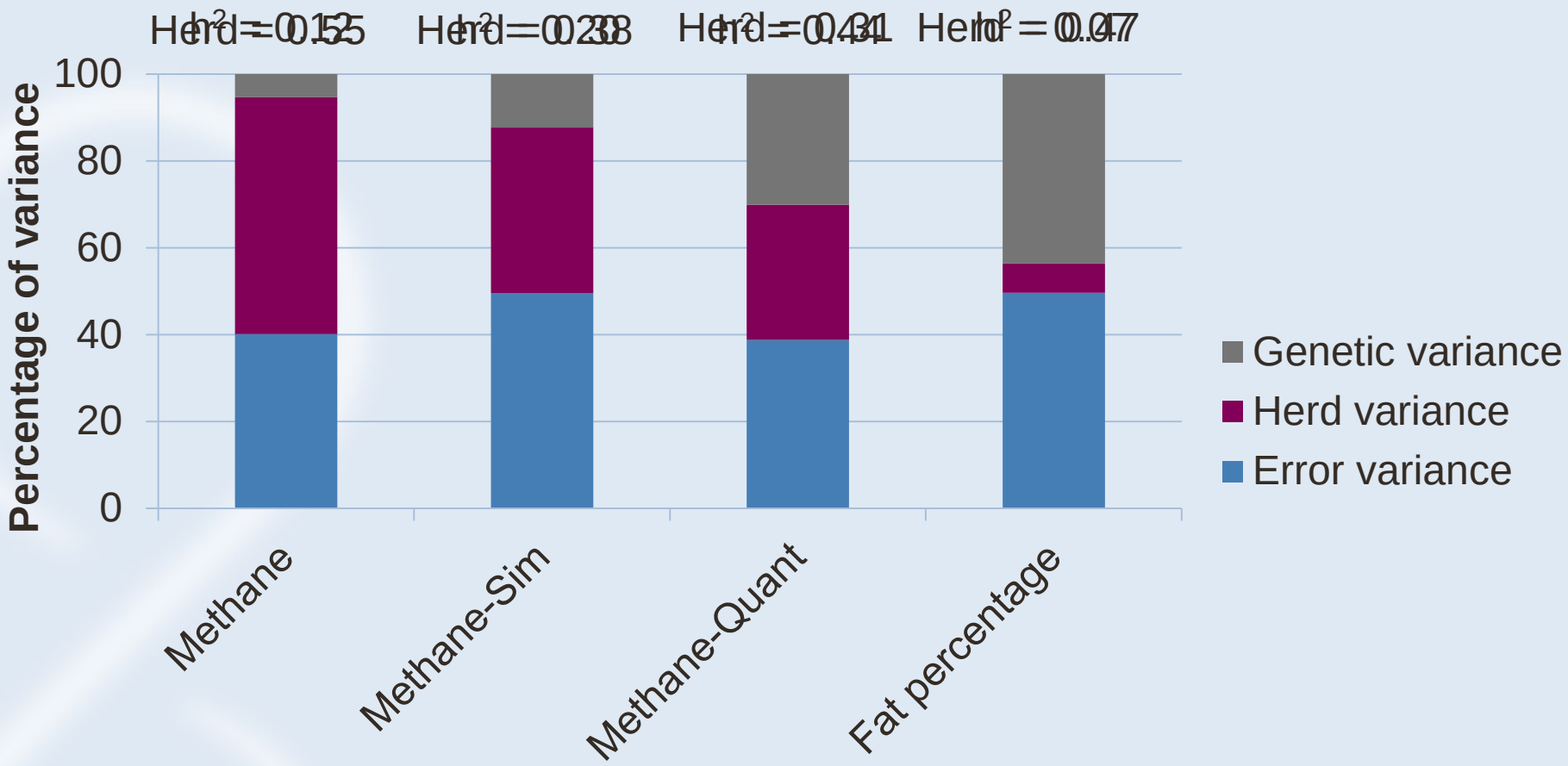
- Herd effect: $Herd = \frac{\sigma^2_{Herd}}{(\sigma^2_{Animal} + \sigma^2_{Herd} + \sigma^2_{Error})}$

Animal variance (σ^2_{Animal})
Herd variance (σ^2_{Herd})
Error variance (σ^2_{Error})

Results – descriptive statistics

Predicted methane yields (in g/kg DMI)	Mean
Methane	23.6
Methane-Sim	21.3
Methane-Quant	20.9

Heritability and Herd effect



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Correlations between predicted methane yields

- Bivariate model with same effects in model as in univariate model:

Trait	Methane r_{gen}	Methane-Sim r_{gen}
Methane-Sim	0.73	--
Methane-Quant	-0.23	0.06

Conclusions

- Predicted methane yield is a heritable trait
- Herd has a large effect on predicted methane yield
- Methane and Methane-Sim explain different part of methane yield than Methane-Quant
    - One or multiple proxies necessary?

Questions???
Thank you for your attention

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Van Engelen et al. (2015)
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