

Genetic approaches for methane mitigation strategies

Jan Lassen, G.F. Difford, L. M. Kristensen, L. Zetouni & P. Løvendahl

Center for Quantitative Genetics and Genomics

Århus University



Why is genetics a PART of the solution?

- > No economic value for farmer
- > Effect of selection is permanent and cumulative.
- > Progress for traits with low heritability
- > Mastitis: 5% best vs 5% worst -10 treatments dif/100 cows



Measuring methane for genetic analysis

- > A well defined trait...
- > Methane / day
- > Methane / output
- > Methane / input
- > Residual methane

> Selection trait vs breeding goal trait



Measuring methane for genetic analysis

> Precise measurements in large numbers

- > Respiratory chambers are "Golden Standard"
- > Greenfeed
- > Snapshot methods
- > SF₆ methods
- > "All models/methods are wrong but some are usefull"



Geneticists vs Nutritionists

- > Acceptance by both disciplines
- > Accurate, repeatable measures
- > Same ranking of animals between methods



Sheep/Beef vs Dairy cattle

- > Data from commercial farms are inevitable
- > No training can be allowed
- > Hard to individualise cows for long periods
- > Expensive to have staff to handle equipment
- > Useful phenotype for the farmer









Laser





Good and bad

> High capacity

> Spot samples

- > Non-invasive
- > Small investment

- > No control of breath
- > Quantification is a challenge



Quantifying methane production

- > Measure methane and carbon dioxide concentrations
- > Heat producing units (HPU) = 5.6 *live weight^{0,75} + 22*FPCM + 1.6*10⁻⁵*days carried calf
- > CH4_LITERS = CH4_RATIO*180*24*HPU
- > Highly influenced by milk production
- > Ignoring variation in CO₂ production



Danish data

Trait	Units	#	Mean	SD	Min	Max
CH4_RATIO		3121	0.087	0.012	0.043	0.109
CH4_LITERS	L/ day	1745	381	41.2	283	548
CH4_MILK	L/kg/day	1745	10.41	1.34	8.43	13.7
FPCM	L/ day	3121	36.6	7.9	19.2	62.7
Weight	Kg	1745	647	68.4	467	890



Results

Trait	CH4_RATIO	CH4_LITERS	CH4_MILK	FPCM	Weight
CH4_RATIO	0.16	0.83	0.23	0.37	-0.16
CH4_LITERS	0.18	0.21	0.07	0.43	-0.18
CH4_MILK	0.21	0.11	0.21	0.15	-0.10
FPCM	0.04	0.12	0.21	0.27	-0.10
Weight	-0.12	-0.05	-0.05	0.04	0.35



Genomic prediction and GWAS

> 1739 Holstein cows

> Illumina 50 K SNP beadchip



Genome wide association study



Manhattan Plot - CH4

Chromosome

From G Sahana



Genomic prediction

- > Five-fold cross validation procedure
- > Whole data randomly into five subsets
- > Reliability = $(r_{ebv,y_c})^2/h^2$
- > Regression of y_c on estimated breeding values



Genomic prediction

Model Validation set

Reliability Regression

BLUP	0.171	1.025
GBLUP	0.175	1.002
GBLU _w	0.183	1.003







Milk as predictor

> Milk is measured routinely

> Milk spectra is available in many countries

> Many very optimistic results predicting phenotypes from milk spectras: Feed efficiency (McPharland et al 2014), Methane emission (Dehareng et al., 2012)



Design description

- > 340 genotyped Holstein cows
- > 3 herds
- > Similar feeding regime
- > Milk spectra from sample from morning milking
- > Methane using CO₂ method



Predicted vs measured methane



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Fatty acids

>Methane / Kg Milk >Pedigree based >SNP based

C18:1

(Correlations	Correlations
	pedigree	genomic
C6	-0.65	-0.71
C8	-0.80	-0.60
C10	-0.82	-0.51
C12	-0.63	-0.17
C13	-0.66	0.57
C14	0.09	0.13
C15	0.40	0.50
C16	-0.05	0.23
C17	0.39	0.28
C18	0.18	-0.06
C18:1trans11	-0.70	0.03
C18:2n6cis	0.33	0.22
Fat	0.59	0.11
Protein	0.78	0.46
Mean se	0.61	0.43
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Milk as predictor

> Not as optimistic as other studies

> Less accurate methane measurements - but many

> Room to learn and understand more on underlying biology



RUMEN MICROBIOME



Host microbiome interaction

- > 1000 cows genotyped and phenotyped
- > Milk, rumen samples
- > Methane measurements
- > 16s analysis of bacteria and archcea



Heritability estimates of bacteria





International collaboration

- > Comparison and validation of methods
- > Integration of methods for analysis across countries
- > Estimation of genetic and genomic parameters
- > Correlation to other traits

> METHAGENE, ICAR, RUMINOMICS and ASGGN



Black box biology

- > Cross validations
- > Independent data
- > What is causal and what is just by chance?





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Conclusion

> Methane emission is under some genetic control

> Selection for increased milk yield will also increase methane production

> Our results on milk data is not as positive as other studies



Conclusion

> The rumen content is under some host genetic control

> International collaboration is needed an initiated

> There is still a lot to do...



Job openings at QGG - post docs

> Genomic prediction models for new phenotypes in dairy cattle

> Genetic and genomic relationship between methane, feed efficiency and cost reducing traits

> Welcome phd-students