

# Should we change the cow's genes?

**Helen Hansen Axelsson**

**PhD student at the Dept. of Animal Breeding and Genetics, SLU**



Sveriges lantbruksuniversitet  
Swedish University of Agricultural Sciences

Published paper in **Applied and Environmental Microbiology** 2012  
(Danielsson et al.)

*Methanogenic population and CH<sub>4</sub> production in Swedish dairy cows fed different levels of forage*

- Methanogenic population similar to cows on other geographical locations
- Number of methanogens is not correlated to CH<sub>4</sub> produced
- CH<sub>4</sub> production seems to be correlated with a certain group of methanogenic species
- Large individual variations
- Diet has no effect on population structure of methanogenic species

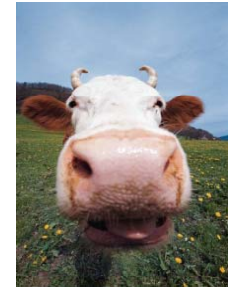
**Yes, we should change the cow's genes!**

# Background

How could we do it?



- Little attention on specific design of breeding programs to reduce environmental impact
- Complicated traits difficult to use in breeding schemes with progeny testing
- World wide implementation of genomic selection



# Aim of the study

Develop a good breeding strategy for dairy cattle where the best males and females are genotyped in order to reduce the environmental impact of milk production





# Our hypothesis

- New 'environmental traits' can be recorded in a few selected herds
- Phenotype information of these traits can be used in breeding programs with genomic selection for genetic evaluation of cattle



# Breeding goal

Three traits in the breeding goal:

- Milk production (MP) €83\*
- Functional trait (FT) €82
- Environmental impact (EI) €-83

} Current  
breeding  
goal traits

➔ New trait

## EI- greenhouse gas emissions

\* *gsdu- genetic standard deviation unit*



# Experimental design

- No records or genotype data for EI
- Records and genotype information for indicator traits correlated to EI
- Favorable correlations between EI, MP and FT



# Indicator traits for EI

- Three categories of indicator traits:
  - 1) Stayability and stature → all herds
  - 2) Live weight and the gas concentration in the breath of the cow → AMS herd
  - 3) Residual feed intake and methane measured in respiration chamber → few selected herds





# Heritabilities and accuracies



	$h^2$	Accuracy
Stayability, STAY	0.02	0.67
Stature, STAT	0.40	0.72
Live weight, LW	0.30	0.70
Gases in the breath, BRH	0.20	0.69
Residual feed intake, RFI	0.35	0.46
Methane, METH	0.25	0.40



# Genetic correlations

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	$r_g$ EI
Stayability, STAY	-0.30
Stature, STAT	0.10
Live weight, LW	0.20
Gases in the breath, BRH	0.50
Residual feed intake, RFI	0.60
Methane, METH	0.80

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# Scenarios

7 scenarios were analyzed:

The first scenario included no indicator trait (No IT)

6 scenarios with indicator traits were STAY, STAT, LW, BRH, RFI and METH



# Method

- Stochastic simulation program ADAM (Pedersen et al., 2009)
- Pseudo-genomic selection: direct genomic values were used for milk production, functional trait and indicator traits with a heritability of 0.99
- Results were averaged over 15 years





# Results from simulation



The annual genetic gain ( $\Delta G$ ) in euros and the genetic response in milk production ( $\Delta G_{MP}$ ), functional traits ( $\Delta G_{FT}$ ) and environmental impact ( $\Delta G_{EI}$ ) in genetic standard deviation units

Scenario	$\Delta G$	$\Delta G_{MP}$	$\Delta G_{FT}$	$\Delta G_{EI}$
No IT	49.5	0.256	0.180	-0.161
STAY	51.4	0.259	0.184	-0.180
BRH	53.0	0.249	0.178	-0.215
RFI	52.7	0.257	0.168	-0.213
METH	54.5	0.243	0.176	-0.241



# Results for METH

The annual genetic gain ( $\Delta G$ ) in euros and the genetic response in milk production ( $\Delta G_{MP}$ ), functional traits ( $\Delta G_{FT}$ ) and environmental impact ( $\Delta G_{EI}$ ) in genetic standard deviation units

Scenario	Accuracy	$\Delta G$	$\Delta G_{MP}$	$\Delta G_{FT}$	$\Delta G_{EI}$
No IT		49.5	0.256	0.180	-0.161
METH	0.40	54.5	0.243	0.176	-0.241
METH	0.10	52.3	0.244	0.180	-0.211



# Conclusions

Breeding goals with milk production and functional traits are beneficial for the environment as they result in larger genetic gain in reduced GHG emissions



# Conclusions

- Genetic gain in EI enhanced 30-55% by including EI in breeding goal using phenotypic and genomic data of correlated indicator traits
- No significant reduction in genetic gain for milk production and functional traits





# Should we change the cow's genes or the rumen microbes?

- Yes, we should change the cow's genes and that will probably change the rumen environment and thereby the microbes
- What characterize the good host?
- Can we select for better hosts?



# Thank you for your attention!



Contact: [Helen.Hansen@slu.se](mailto:Helen.Hansen@slu.se)

Coauthors: Freddy Fikse, Morten Cargo, Anders Christian Sørensen, Kjell Johansson and Lotta Rydhmer

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# Results from simulation

The rate of inbreeding per generation in percentage ( $\Delta F_G$ ) and the generation interval in years (L)

Scenario	$\Delta F_G$	L
No IT	0.71	2.54
STAY	0.69	2.53
STAT	0.76	2.56
LW	0.76	2.56
BRH	0.72	2.53
RFI	0.74	2.55
METH	0.73	2.57





# Genetic correlations



	$r_g$ EI	$r_g$ MP	$r_g$ FT
Stayability, STAY	-0.30	0.20	0.20
Stature, STAT	0.10	0.35	0.10
Live weight, LW	0.20	0.20	0.10
Gases in the breath, BRH	0.50	-0.10	-0.10
Residual feed intake, RFI	0.60	-0.45	0.20
Methane, METH	0.80	-0.20	-0.20



# Next step

- Economic analysis of all tested scenarios
- Investigate which scenarios result in the largest total genetic improvement per invested money

