Environmental impact of milk production can be reduced using indicator traits and genomic selection

Helen Hansen Axelsson
PhD student at the Dept. of Animal Breeding and Genetics,

SLU
Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

Background

- Increasing awareness of milk production's environmental impact
- Little attention on specific design of breeding programs to reduce this impact
- World wide implementation of genomic selection

Aim of the study

Study possible breeding strategies in a medium sized dairy cattle breed 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 → New trait

Current breeding goal traits

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

	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

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 (ΔG) in euros and the genetic response in milk production (ΔG_{MP}), functional traits (ΔG_{FT}) and environmental impact (ΔG_{EI}) in genetic standard deviation units

Scenario	ΔG	ΔG_{MP}	ΔG_{FT}	ΔG_{EI}
No IT	49.5	0.256	0.180	-0.161
STAY	51.4	0.259	0.184	-0.180
STAT	49.4	0.260	0.180	-0.160
LW	49.4	0.253	0.176	-0.168
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 (ΔG) in euros and the genetic response in milk production (ΔG_{MP}), functional traits (ΔG_{FT}) and environmental impact (ΔG_{EI}) in genetic standard deviation units

Scenario	Accuracy	ΔG	ΔG_{MP}	ΔG_{FT}	ΔG_{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

Thank you for your attention!

Contact: Helen.Hansen@slu.se
Coauthors: Freddy Fikse, Morten Kargo, Anders Christian Sørensen, Kjell Johansson, Karl-Johan Petersson and Lotta Rydhmer

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Results from simulation

The rate of inbreeding per generation in percentage (ΔF_G) and the generation interval in years (L)

Scenario	ΔF_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