

Polish Simmentals: early predictors of longevity

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Objective

Estimate **genetic correlations between length of productive life and conformation** to identify **early predictors of longevity** in dual-purpose cattle

Material and methods

- 166 Simmental sires
- Genetic correlations based on the correlation between EBVs of 20 conformation traits and functional longevity

Results

- Positive correlations for udder and legs: *udder width (0.25)*, *udder depth (0.11)*, *rear leg set side view (0.27)*, *rear leg set rear view (0.16)*
- Unfavourable correlations for body capacity traits:
moderate values: *body depth (-0.36)*, *chest girth (-0.24)*
smaller values: *stature (-0.15)*, *rump width (-0.16)*, *muscularity of front end (-0.14)*, *rear end muscularity (-0.13)*, *chest width (-0.12)*

Conclusions

- Estimates of genetic correlations low to moderate
- Traits with the largest correlations: **body depth**, **chest girth**, **udder width** and **rear leg set side view** as predictors of longevity
- Cows with smaller body capacity have a lower relative risk of culling



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Förderverein
Bioökonomieforschung e.V.

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Genetic relationships between age at first calving, its underlying traits and survival of Holsteins

67th Annual Meeting of the European Federation of Animal Science

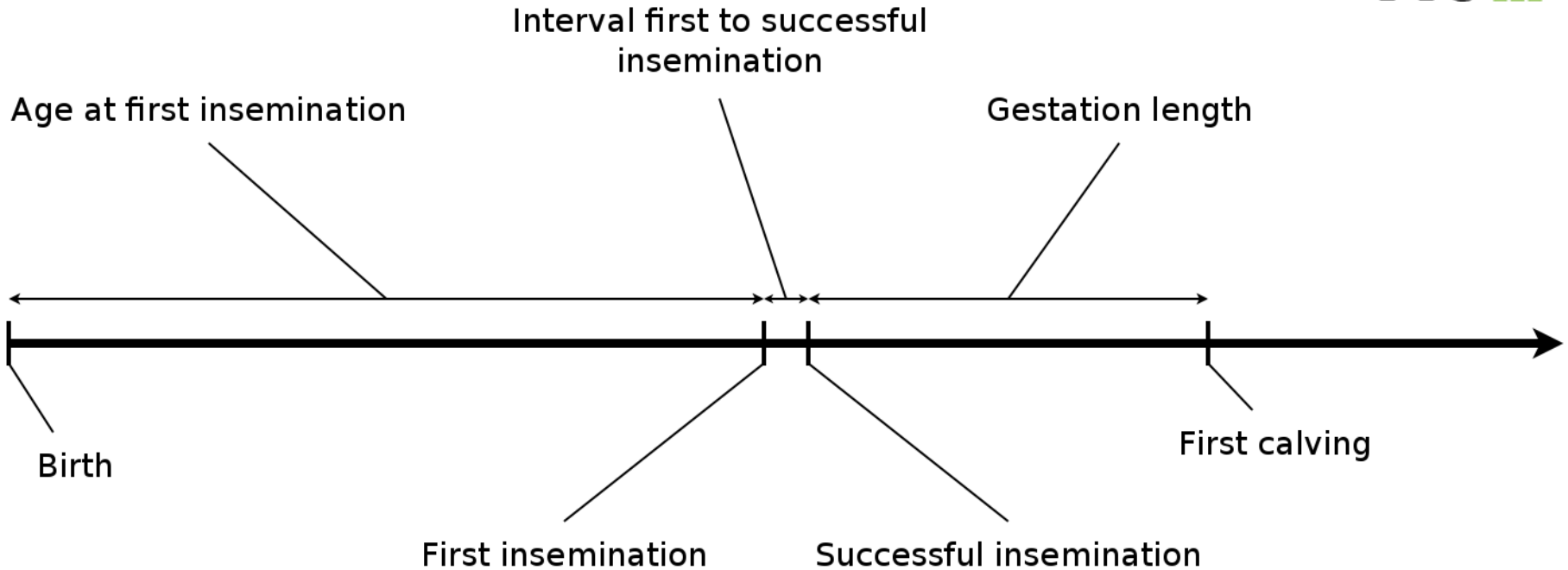
Belfast UK, 29 Aug – 2 Sept 2016

J. Heise^{1,2}, K. F. Stock¹, F. Reinhardt¹, H. Simianer²

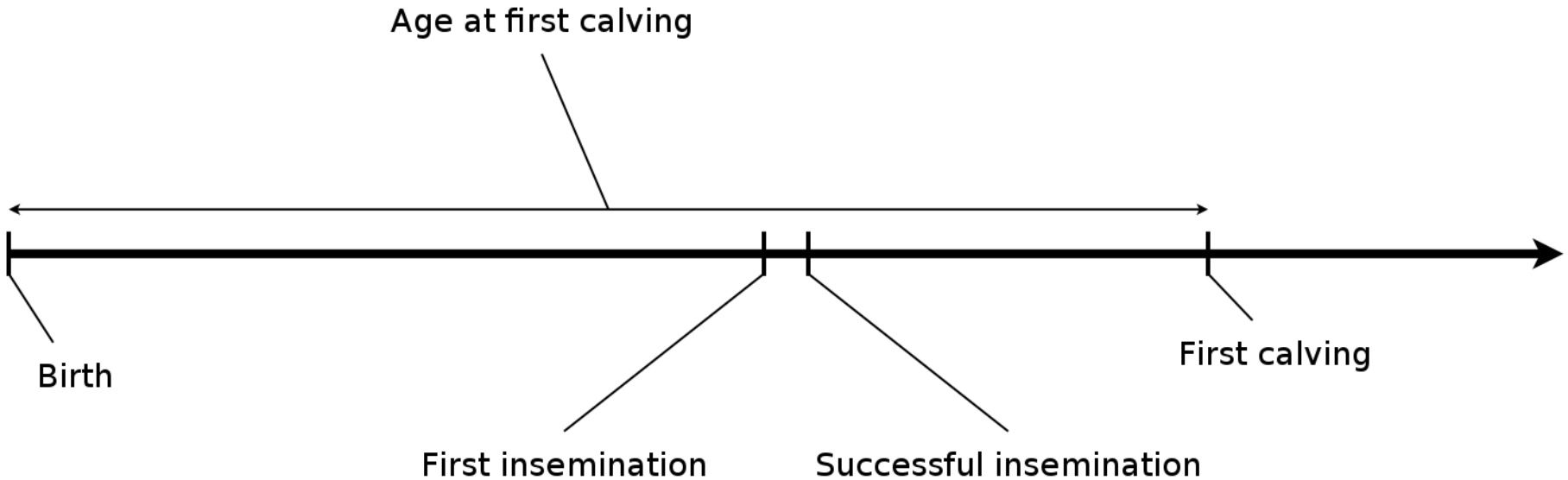
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Motivation



Motivation



Is it appropriate to correct for age at first calving in genetic evaluations of (functional) longevity?



Results & Conclusion

	S1	S2	S3	AFI	FLI	AFC
S1	0.021	0.77**	0.42***	-0.08	-0.15	-0.07
S2	0.03	0.014	0.68***	-0.16*	-0.38**	-0.22*
S3	0.03	0.03	0.027	-0.22*	-0.40*	-0.30*
AFI	-0.02	-0.02	-0.02	0.230	0.18	N. est.
FLI	-0.02	-0.02	-0.03	-0.02	0.006	N. est.
AFC	-0.03	-0.03	-0.04	N. est.	N. est.	0.101

S1: survival 0-49d from 1st calving; **S2:** 50-249d; **S3:** 250d to 2nd calving

Asterisks denote levels of significance, resulting from t-tests on the genetic correlations of the 4 samples (H_0 : genetic correlation is 0): *: $p < 0.05$; **: $p < 0.01$; *** $p < 0.001$

Results suggest that age at first calving should not be correct for in genetic evaluations of (functional) longevity.



Simulations to define the optimum lifetime management for Holstein cows

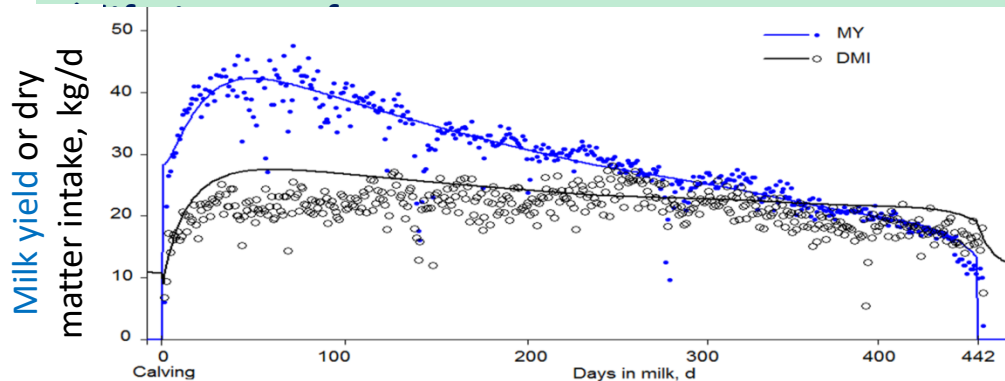
Objectives

Using a lifetime prediction model to determine:

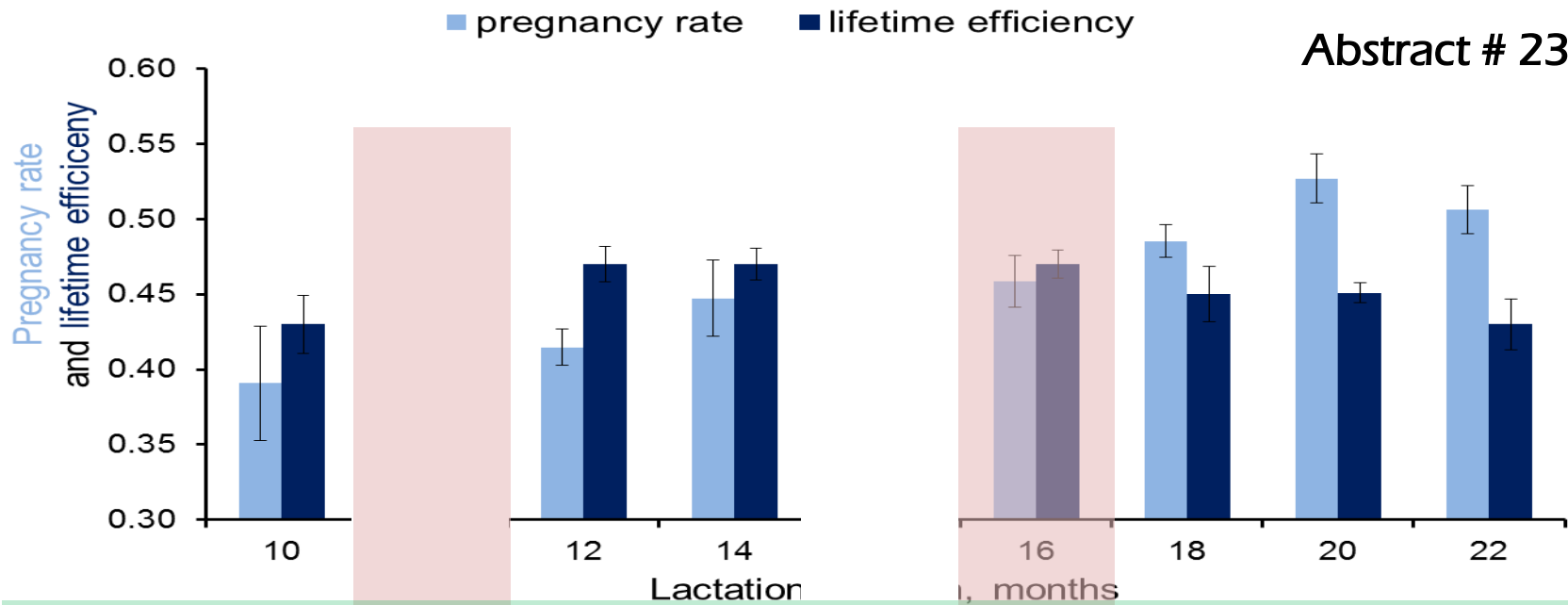
- 1) the optimum duration of a lactation to ↑ lifetime efficiency and pregnancy rate
- 2) if lactation duration should vary with parity to

Lifetime efficiency (MJ/MJ)
= energy in milk / energy intake

GARUNS - a lifetime performance model taking into account the changing physiological priorities of an animal during its life



GARUNS can fit milk yield, dry matter intake, milk components, body weight, and BCS curves of 16 months extended lactation cows



Conclusions

- 1) a 16 mo lactation is the optimum extended lactation length in terms of productive-reproductive performance,
- 2) managing the primiparous cows with a 16 mo extended lactation, followed by 10 mo lactations, ↑ lifetime efficiency to being similar to cows managed for a 16 mo lactation in their entire life.

39.15

Genetic correlations between energy balance and lactation persistency of Holsteins in Japan

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Institute of Livestock and Grassland Science, NARO (NILGS)

Background and Goal

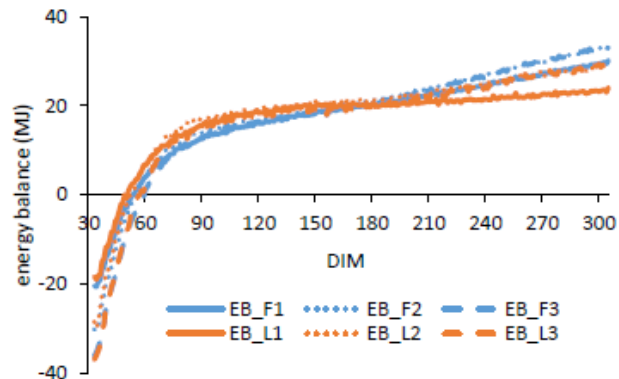
In the early lactation stage...



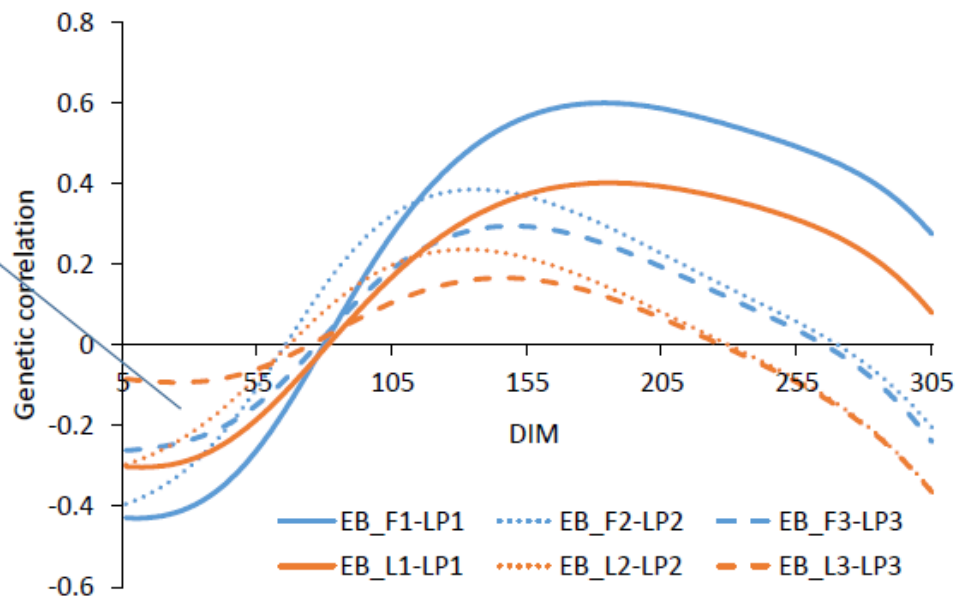
Improving lactation persistency (LP) may be better for energy balance (EB).

The objective of this study was to estimate genetic correlations between EB and LP.

- EB was calculated using the multiple regression equation of Friggens et al. (2007) or Løvendahl et al. (2010).
- LP was defined as the difference in estimated milk yield between 240 and 60 DIM.
- Genetic parameters of EB and LP were estimated using a random regression test-day model.

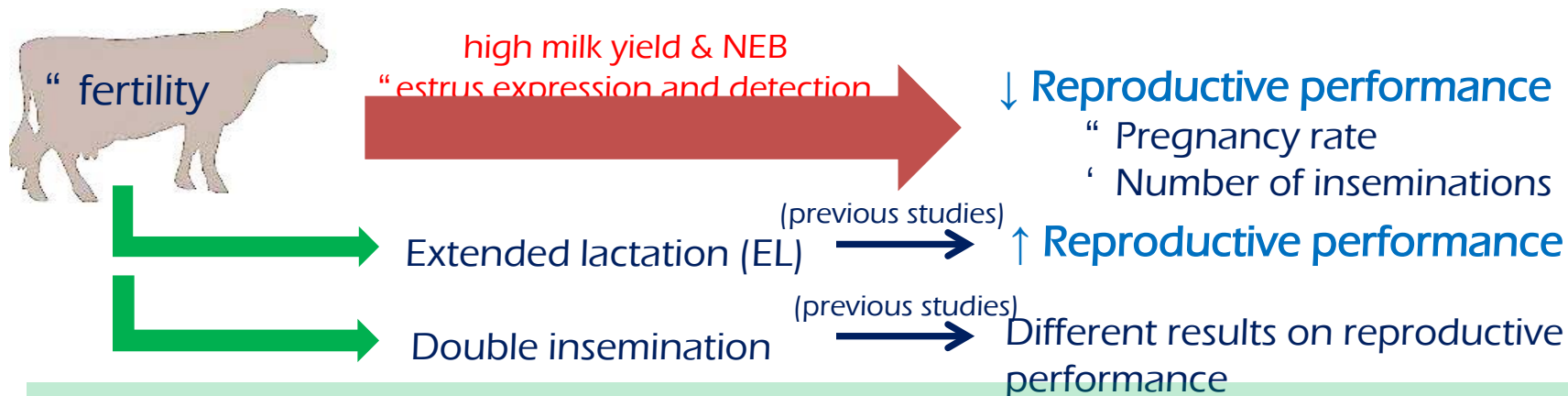


Negative genetic correlation
in the early lactation
stage



Negative genetic correlations were estimated between EB and LP in the early lactation stage, so we need to pay attention for improving EB and LP.

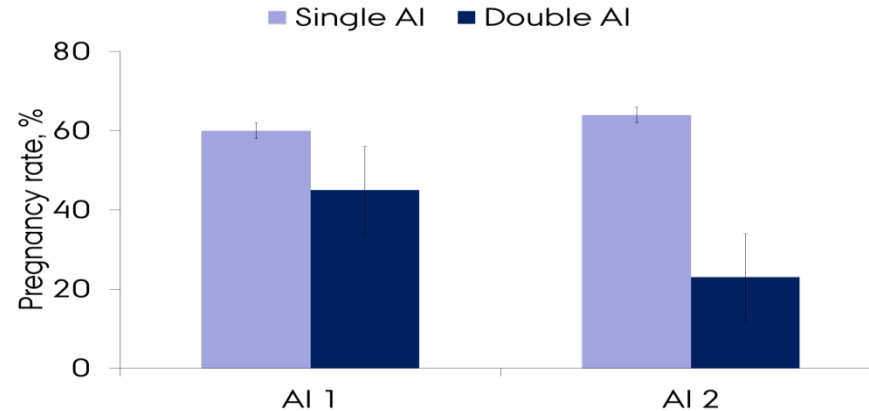
Voluntarily delayed rebreeding and double insemination effects on pregnancy rates of Holstein cows



Hypotheses

- 1) Delaying rebreeding to 8 months will ‘ mounting behavior and estrus detection, and ‘ pregnancy rate (PR)
- 2) The use of a double AI technique around estrus will ‘ PR

Compare early rebreeding (2 months) with late rebreeding (8 months)
Mounting behavior	+
Pregnancy rate (PR)	=
Number of inseminations	=



Conclusions

- 1) Delaying rebreeding increased mounting behavior but did not increase PR
- 2) The double artificial insemination (AI) had a negative effect on PR

HERD DYNAMICS AND ECONOMICS OF DIFFERENT STRATEGIES FOR MANAGING A HERD FOR EXTENDED LACTATION

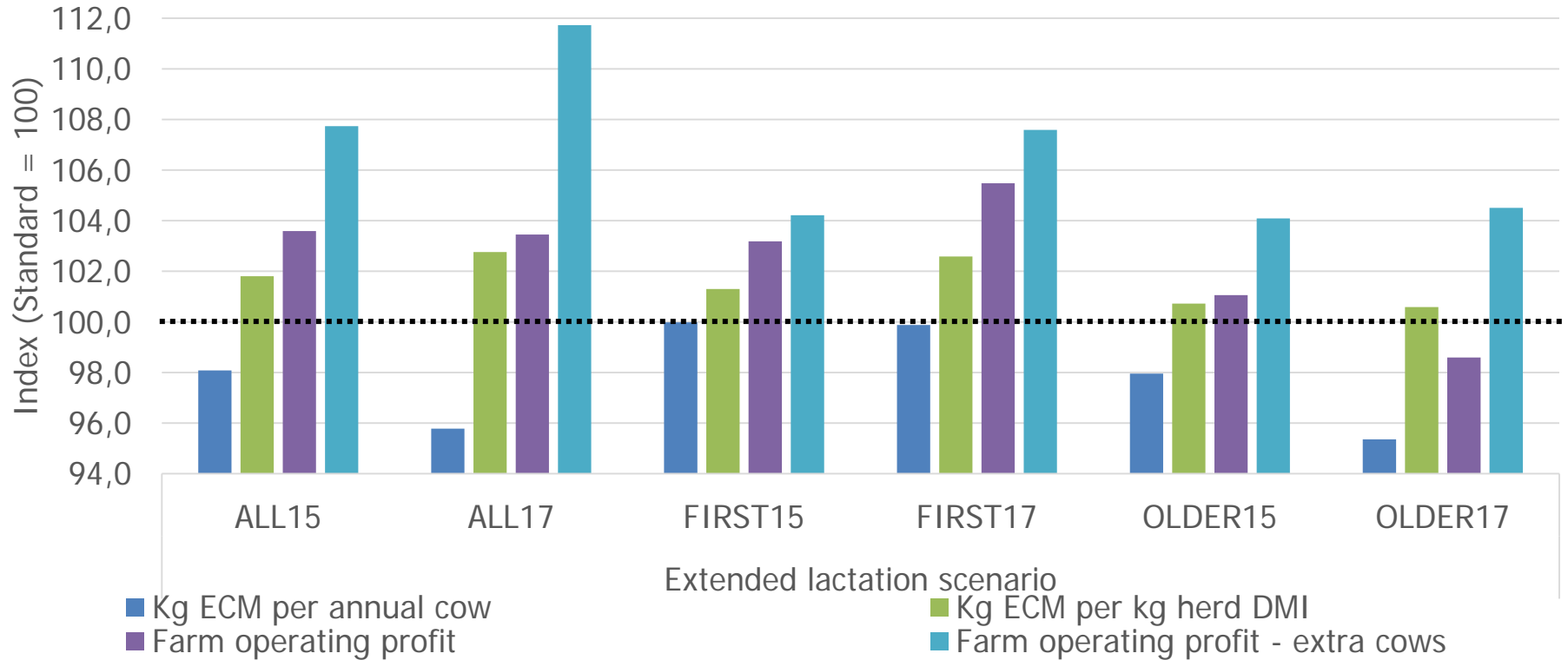
J. O. Lehmann, L. Mogensen, S. Østergaard,
J. F. Ettema & T. Kristensen

Objective

To investigate the effect of different lactation management strategies on herd dynamics and economics.

Scenario	Which cows?	Calving interval	
		Prim	Mult
STANDARD	All	13	13
ALL15	All	15	15
ALL17	All	17	17
FIRST15	Primiparous	15	13
FIRST17	Primiparous	17	13
OLDER15	Multiparous	13	15
OLDER17	Multiparous	13	17

EXTENDED LACTATION COMPARED WITH STANDARD



Effect of curve traits and Age of first calving on productive life of Holstein primiparous Walloon cows

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Longevity, productive life, or lifespan of dairy cattle defined as the time from first calving to culling, death or sale, is an important and ambiguous trait resulting from many factors.

Aim

Linking cow's longevity to lactation curve characteristics and age of first calving.

Data

❖ Lactation curve traits for milk provided by the Walloon Breeding Association

❖ 20.766 primiparous Holstein cows calvings from 2003 to 2014

❖ 395 herds (> 50cows)

Model

Linear model :

$$LPL_{ijkmpnoq} = \mu + H_i + CY_j + CS_k + AFC_m + M305_p + \beta_1 PS_n + \beta_2 PK_o + \beta_3 DIM_q + e_{ijkmpnoq}$$

$LPL_{ijkmpnoq}$: length of productive life, μ overall mean

H_i , CY_j , CS_k and AFC_m fixed effects of i^{th} herd, j^{th} year of calving, k^{th} calving season and age at first calving ($AFC=C1$ to $C10$)

$M305_p$, PS_n , PK_o , DIM_q fixed effects of Milk Yield adjusted to 305 days ($M305d=L1$ to $L4$), persistency, peak and days in milk.

β_1 , β_2 , β_3 Regression coefficients, e residual effect with $e_{ijkmpnoq} \sim N(0, \sigma_e^2)$.



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Results and discussion

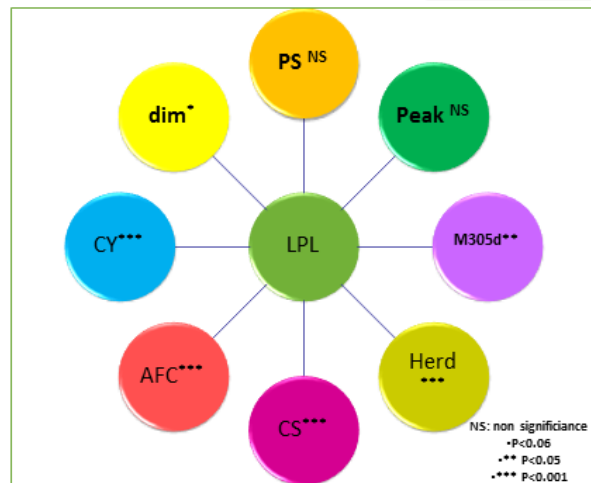


Figure 1: Effect of traits of interest on LPL.

the least favorable season

❖ Higher longevity
→ voluntary culling of low producing cows and of involuntary culling for reasons such as diseases for very high producing cows.

❖ later calvings (> 28 month) linked to lower LPL.

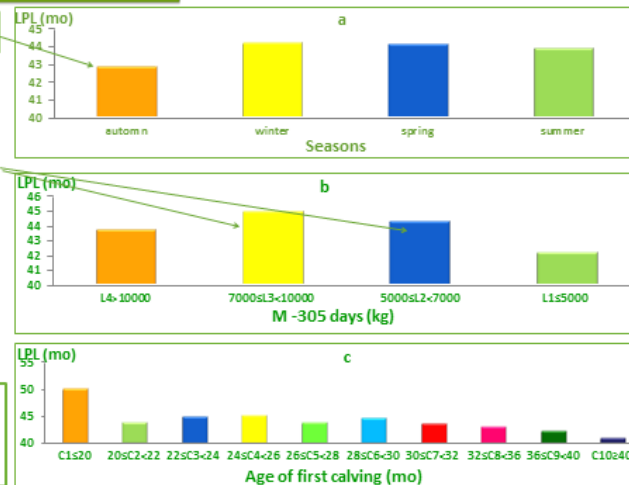


Figure 2: Lsmeans of LPL by season (a), M-305d (b) and by age of first calving (c).

Conclusion

- ❖ LPL was affected by herd → management and culling decisions
- ❖ The lack of significance for the regressions of PK and PS on LPL should be considered a preliminary result for two reasons:
 - 1) the simultaneous presence of other correlated effects as milk yield in the model and
 - 2) the use of a linear regression when non-linear relationship are more likely (intermediate optimum).

Lost in transition – a reaction norm model to breed cows that can better cope with metabolic stress

The Problem

In the transition phase in early lactation, dairy cows have higher energy requirements than can be satisfied by feed intake (Fig. 1).

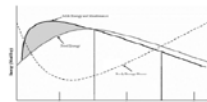


Figure 1: Discrepancy of energy requirements for maintenance and milk production and energy intake in the early lactation!

We hypothesize, that some cows are genetically less well suited to cope with this metabolic stress than others, leading to adverse follow-up effects on longevity. Robust cows thus will remain unaffected by a metabolic load, while non-robust cows will react with a reduced fitness (Fig. 2). We use a reaction norm sire model to test whether this robustness has a genetic component.

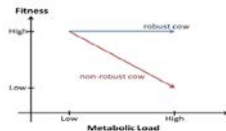


Figure 2: Robust cows stay unaffected by an increased metabolic challenge, while non-robust cows react with reduced fitness

Animals, Data and Methods

- ~38 million test day records of ~1.4 million Brown Swiss dairy cows were available
- only bulls with ≥ 10 daughters that were born before 2011 and had an exit record were used
- 4,983 bulls and 579,004 daughters, 30,842 animals in pedigree

Challenge variables: accumulated milk yield or accumulated fat:protein ratio for the first 3 lact days, precorrected

Response variable: functional longevity from Survival Kit 5.0 (log pseudo records)

Reaction norm sire model:

$$y_{ij} = \mu + \beta x_{ij} + s_i + b_i x_{ij} + \epsilon_{ij} \quad \begin{pmatrix} s_i \\ b_i \end{pmatrix} \sim \begin{pmatrix} 0, A\sigma^2 & \sigma_{sb} \\ \sigma_{sb} & \sigma_b^2 \end{pmatrix}$$

y_{ij} response variable of daughter j of sire i
 x_{ij} challenge variable of daughter j of sire i
 μ fixed regression constant
 β fixed regression coefficient
 s_i random effect of sire i
 b_i random regression coefficient of sire i
 $\epsilon_{ij} \sim (0, \frac{\sigma^2}{w_{ij}})$ random residual error
 w_{ij} weights reflecting reliability of survival pseudo records
 A additive-genetic numerator relationship matrix

Models were fitted using **ASReml 3.0**^[1], random components were tested using a **likelihood ratio test** for hierarchical sub-models, standard errors and confidence bands for estimated parameters were obtained by adapted **bootstrap** procedures.^[2]

Conclusions

The results of this study show that the ability to cope with metabolic stress in the transition phase clearly has a genetic component.

The suggested reaction norm sire model can be used to identify bulls that inherit an improved ability to handle metabolic stress without adverse effects on longevity and thus resulting breeding values can be the basis to select for metabolically more robust dairy cows.

Results

- All estimated (co-)variance components were significantly different from 0 (Fig. 3), and the models accounting for σ_{sb} provided a significantly better fit compared to reduced models.
- Daughter groups of different bulls differed substantially in their ability to cope with metabolic stress (Fig. 4).
- Heritabilities of the response variable under high challenge are substantially increased (Fig. 5)
- Robustness to metabolic stress thus has a genetic component

Figure 3: Empirical bootstrap distribution of estimated (co-)variance components with the fat:protein ratio as challenge variable. The red vertical lines depict the estimates obtained from the original data.

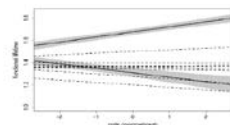
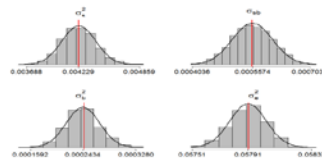


Figure 4: Estimated regression curves of ten randomly chosen bulls and the bulls with the highest and lowest slope for the regression (with bootstrap-based 95% confidence bands)

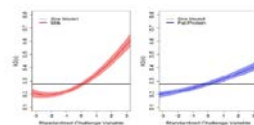


Figure 5: Estimated heritability functions (with bootstrap-based 95% confidence bands) from the reaction norm sire model as a function of the challenge variable milk yield (left) and fat:protein ratio (right) compared to sire model h^2 (black line)

References and Acknowledgements

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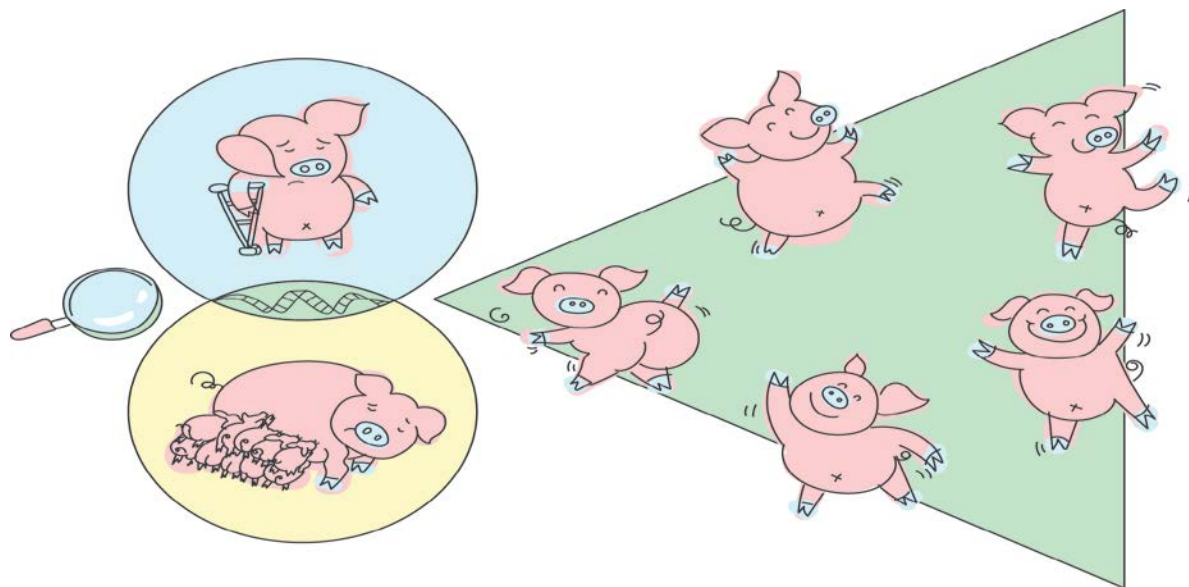
We thank Braunvieh Schweiz and Qualitas for providing the data. This study was supported by a grant of the Swiss Commission for Technology and Innovation CTI (project no. 13048.2 PFLS-LS) and Swissgenetics, Zollikofen, Switzerland.



GOOD LEG MEANS GOOD STAYABILITY OF THE SOWS

AND GENOME-WIDE ASSOCIATION STUDY (GWAS) FOR LEG CONFORMATION

T. H. Le, E. Norberg, G. Sahana, P. Madsen, O. F. Christensen, B. Nielsen, K. Nilsson, N. Lundeheim



1. Introduction



1. Estimate **heritability and genetic correlations** of conformation and longevity in Swedish and Danish pigs
2. Identify **genomic variants** affecting conformation in Danish pigs

2. Material and methods



LONGEVITY

Stayability to 2nd or 3rd parity,
lifetime piglet production

*Linear / linear
threshold model*

DMU



CONFORMATION (B+@, 5 months, 100 kg)
Movement, Toes, Standing-under, Front leg,
Back, Rear leg, Overall

GWAS AND META-ANALYSES

- *Mixed linear model, software GCTA*
- *Multiple traits within breed, approximate test statistic*
- *Across breeds, software METAL*

3. Results

❖ Genetic parameters

- Low to moderate heritabilities for conformation traits
- Favorable correlation between conformation and longevity

❖ GWAS and meta-analyses

- Genes affecting conformation: related to bone and skeleton development , muscle and fat metabolism (*LRPPRC*, *WRAP73*, *VRTN*, *PPARD*) and growth (*GF2BP2*, *GH1*, *CCND2*, *MSH2*)
- Meta-analyses
 - ✓ Multi-trait within breed suggested QTLs with possible pleiotropic effect
 - ✓ Across breeds detected novel candidate genes *SOS2*, *TRIM24* and *ELMO1*

4. Conclusion

BETTER LEG CONFORMATION – LONGER STAY

→ possible to **improve longevity through conformation**

Conformation is complex, partly controlled by genes involved in **development and growth**

Meta-analyses **increased power** to detect QTLs