H. Simianer[1], N. T. Ha[1,2], J.J. Gross[2], U. Schnyder[3], F. Schmitz-Hsu[4], R.M. Bruckmaier[2]

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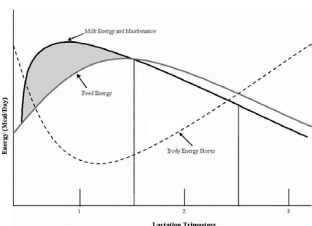**CiBreed**
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Lost in transition – a reaction norm model to breed cows that can better cope with metabolic stress

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[1]

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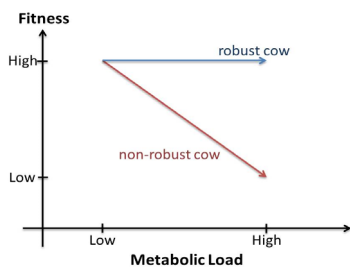
Figure 2: Robust cows stay unaffected by an increased metabolic challenge, while non-robust cows react with reduced fitness

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 579,994 daughters, 30,842 animals in pedigree

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

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

Reaction norm sire model:

$$y_{ij} = \mu + \beta x_{ij} + s_i + b_i x_{ij} + \epsilon_{ij} \qquad \binom{s}{b} \sim \left(0, A \otimes \begin{pmatrix} \sigma_s^2 & \sigma_{sb} \\ \sigma_{sb} & \sigma_b^2 \end{pmatrix}\right)$$

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*
$\epsilon_{ij} \sim (0, \frac{\sigma_e^2}{w_{ij}})$	*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**[2], 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.[3]

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.
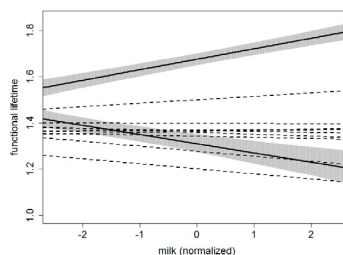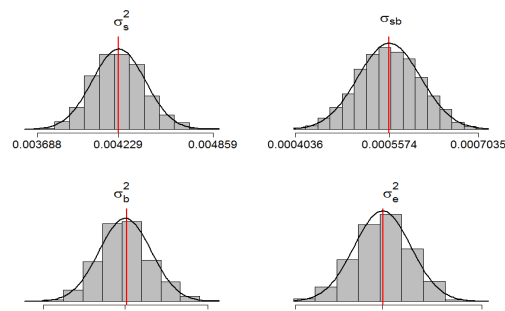
Figure 4: Estimated regression curves of ten randomly chosen bulls and the bulls with the highest and lowest slope for the regression (with bootstrap-based 95% confidence bands)
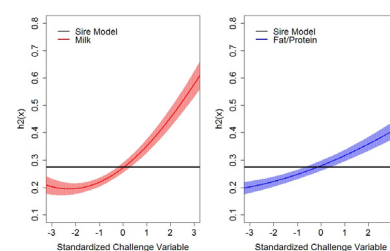
Figure 5: Estimated heritabilitiy functions (with bootstrap-based 95% confidence bands) from the reaction norm sire model as a function of the challenge variable milk yield (left) and fat/protein ratio (right) compared to sire model h^2 (black line)

References and Acknowledgements

[1] Mendenhall, K. (ed.) 2009. The organic dairy handbook: a comprehensive guide for the transition and beyond. Northeast Organic Farming Assoc. of New York, Cobleskill, NY.

[2] Gilmour, A.R., B.J. Gogel, B.R. Cullis, R. Thompson, and D. Butler. 2009. ASReml user guide, release 3.0.

[3] Thai, H.-T., F. Mentré, N.H.G. Holford, C. Veyrat-Follet, and E. Comets. 2013. A comparison of bootstrap approaches for estimating uncertainty of parameters in linear mixed-effects models. *Pharm. Stat.* 12:129–140.