Genetic basis of functional traits in low input dairy cattle

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Content outline

1. Estimation of genetic parameters and breeding values for novel functional and conformation traits

2. Evaluation of body condition scoring systems with focus on Brown Swiss Cattle

Estimation of Genetic Parameters for Novel Functional Traits in Brown Swiss Cattle

- **M. Kramer, M. Erbe, B. Bapst, A. Bieber and H. Simianer**

- **Journal of Dairy Science 96:5954 - 5964**

Introduction and aims of the study

- Relevance of functional traits ↑
- Characteristics of many functional traits:
  - low heritability
  - Difficult and/or expensive to measure
  - Some are expressed late in life only

Aims:

- Evaluate utility of data collected by farmers
- Which novel phenotypic traits related to behavior, health, conformation and fertility could be intergrated in modern dairy cattle breeding programs?

Material and Methods

- Phenotypes of 1.799 Brown Swiss Cows
- 40 low-input farms (ø 26 cows, 13 – 56 cows/farm)
- 6 visits for phenotyping from November 2009 until April 2011
- Phenotyping frequency: 2 – 4 samplings/trait and animal
- Pedigree: 4208 animals of interest (phenotyped cows and bulls with high impact on the population)

Material and Methods: Traits

	Scale		Evaluator	Sample per animal
Behavioral Traits				
General temperament	1 - 5	1=very nervous 5= very calm	farmer	≤ 2
Milking temperament	1 - 4	1=very nervous 4=very calm	farmer	≤ 3
Aggressiveness	0/1	0=yes,1=no	farmer	≤ 2
Rank order in herd	1 – 3	1=low rank 2=medium rank 3=high rank	farmer	≤ 2
Conformation Traits				
Udder depth	cm	Distance between udder base and hock	FiBL	≤ 3
Position of labia	0 – 4	see next slide	FiBL	≤ 3
Fertility				
Days to first heat	Day		farmer	≤ 3
Others				
Milking speed	1 – 6	1=very slow, 6=very quick	farmer	≤ 4

Material and Methods:Traits

Position of labia as indicator for urovagina

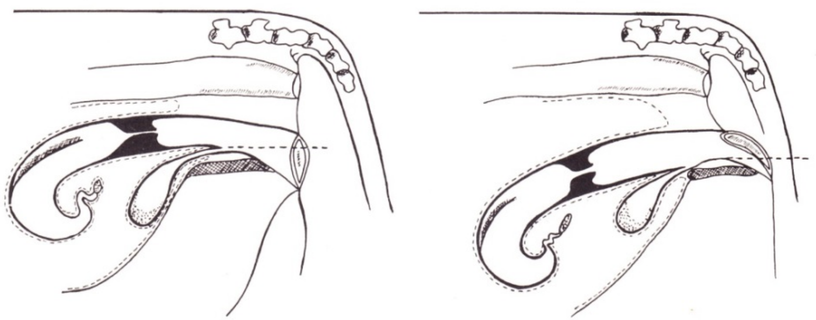
Abb. 243 Physiologische Lage des Genitale. (Zürich)

Abb. 244 Kranialverlagerung des Genitale. Hohlschwanzbildung mit Senkscheide. (Zürich)

Source: Grunert Berchtold (1982)

Scores
0= vertical but oblique labia
1= oblique labia
2= <50% horizontal
3= >50% horizontal
4= sunken vulva

Udder Depth

Model

$$y_{ijklmn} = HYS_{ijk} + AFC_l + Lact_m + b_1 DIM_{ijklmno} + b_2 DIM^2_{ijklmno} + b_3 MkgLact_{ijklmno} + a_n + p_n + e_{ijklmno}$$

y_{ijklmn} dependent variable (e.g. general temperament, milking speed etc.)
HYS_{ijk} fixed effect of herd*year*season of calving (i = 1 - 40, j = 1 - 4, k = 1 - 4)
AFC_l fixed effect of age at first calving in months (≤ 28, 29 – 30, 31 – 32, ≥ 33)
$Lact_m$ fixed effect of lactation number (1, 2, 3, ≥ 4)
$DIM_{ijklmno}$ covariate days in milk
$MkgLact_{ijklmno}$ covariate total milk yield of the lactation in which sampling was done
$b_1 – b_3$ linear regression coefficents for covariates
a_n additiv genetic effect
p_n permanent environment effect of cow
$e_{ijklmno}$ random residual effect

Statistics:

› Proc mixed in SAS (SAS Institute, 2008) to identify significant factors (p< 0.05) by stepwise analysis
› Univariate estimation of genetic parameters were done with ASReml (Gilmour et al., 2009)

Results & Discussion: Behavioral traits

	$h^2 \pm SE$	$w^2 \pm SE$
General temperament	0.38 ± 0.07	0.56 ± 0.03
Milking temperament	0.04 ± 0.04	0.32 ± 0.04
Aggressiveness	0.12 ± 0.08	0.32 ± 0.03
Rank order in herd	0.16 ± 0.06	0.42 ± 0.03

› Relativley high heritabilities compared to literature, though on a low to moderate scale

› Scoring by farmer

→ reflects long term impression, which may reduce random error and contribute to moderate to high repeatabilities

› Big difference in h^2 between general temperament and milking temperament

Results & Discussion: Conformation Traits

	$h^2 \pm SE$	$w^2 \pm SE$
Udder depth	0.42 ± 0.06	0.71 ± 0.02
Position of labia	0.28 ± 0.06	0.33 ± 0.04

Udder depth

- Literature reports heritability of ≈ 0.3 when measured on a discrete scale of 1-9 (Neunschwander et al., 2005), and of ≈ 0.5 when continuous scale is applied (Seykora und McDaniel,1985)

Position of labia

- Estimated for the first time in this study
- moderate heritability
- low repeatability
  - scoring difficulties
    - variability depending on stage of estrus cycle?

Results & Discussion: Milking speed

	$h^2 \pm SE$	$w^2 \pm SE$
Milking speed	0.42 ± 0.06	0.64 ± 0.02

- › High heritability of milking speed given the discret scale
- › Literature:
  - → discrete scale: $h^2 = 0.10 – 0.25$ (Rensing und Ruten, 2005)
  - → continuous scale: $h^2 = 0.28 – 0.48$ (Ilahi und Kadarmideen, 2004)

Possible reasons:

- › Farmers are experienced to use this scale
- › Accurate application by farmers for newly introduced scoring systems (Boettcher et al., 1998)
- › Avoidance of an intermediate score by applying a score of 1-6 (Ilahi und Kadarmideen, 2004)
- › Advantage of smaller herds (Lassen und Mark, 2008)

Results & Discussion : Days to first heat

	h^2 ± SE	w^2 ± SE
Days to first heat	0.02 ± 0.04	0.23 ± 0.05

› Days to first heat practically not heritable

Results: Accuracy of breeding values

Trait	r_{TI} all (4208 animals)	r_{TI} Phenotyped Cows	r_{TI} 30 Bulls with ≥ 10 phenotyped daughters
General temperament	0.49	0.67	0.83
Milking temperament	0.24	0.30	0.47
Aggressiveness	0.27	0.34	0.52
Rank order in herd	0.39	0.51	0.70
Udder depth	0.49	0.68	0.83
Position of labia	0.45	0.62	0.79
Days to first heat	**0.15**	**0.19**	**0.31**
Milking speed	0.53	0.73	0.86

Lowest accuracy: small heritability with high SE of 0.02 ± 0.04

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Milking speed	0.53	0.73	0.86

highest accuracy due to large no. of phenotypes and high heritability

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For most traits the advantage of r_{TI} of bulls is small relative to r_{TI} of EBVs based on phenotyped cows

Our results underline:
The benefit of genomic selection for low heritable traits is expected to outperform the benefit for production traits (König et al., 2009)

Summary

- › Worthwile to invest work into phenotyping of new traits
  - › Reliable applicaton of discrete scales (milking speed)
  - › Application of continuous scales (udder depth)
  - › Poor results for some traits (fertility)
- › position of the labia might be an interesting new trait
  - → further studies required

› Acurracies of EBVs showed: EBVs based on phenotypes of cows are informative, this might be benefical for integration of genomic data of phenotyped cows into genomic breeding programs

Estimation of genetic parameters for indiviual udder quarter milk content traits in Brown Swiss Cattle

- **M. Kramer, M. Erbe, B. Bapst, A. Bieber and H. Simianer**

- **Journal of Dairy Science 96: 5965 - 5976**

Material and Methods

- Milk samples from 1.064 Brown Swiss cows
- 40 farms (ø 26 cows, 13 – 56 cows/farm)
- Milk sampling from period November 2009 until March 2011
- up to 3 milk samples per udder quarter
- sampling close to dry off
- Pedigree consisted of 26.519 animals, going back to the birth year 1908

Material and Methods

- Estimation of genetic parameters and prediction of EBVs with ASReml 3.0
- Multivariate analysis (each quarter defined as different trait): fat, protein and lactose content and SCS
  - Urea content :
  - Univariate analysis for additive genetic variance, permanent environment and residual variance

Results: Mean values for milk composition traits

	Fat (%)	Protein (%)	Lactose (%)	Urea (mg/100 ml)	SCS
FL	3.73^{a}	4.04^{a}	4.56^{a}	21.94^{a}	3.14^{a}
FR	3.73^{a}	4.05^{a}	4.48^{b}	21.71^{a}	3.30^{b}
RL	3.49^{b}	$4.01^{a,b}$	4.61^{c}	22.06^{a}	3.12^{a}
RR	3.51^{b}	3.99^{b}	4.60^{c}	21.88^{a}	3.09^{a}

› Front udder quarters have a significantly higher fat and protein content ($p < 0.05$)

Results: Mean values for milk composition traits

	Fat (%)	Protein (%)	Lactose (%)	Urea (mg/100 ml)	SCS
FL	3.73[a]	4.04[a]	4.56[a]	21.94[a]	3.14[a]
FR	3.73[a]	4.05[a]	4.48[b]	21.71[a]	3.30[b]
RL	3.49[b]	4.01[a,b]	4.61[c]	22.06[a]	3.12[a]
RR	3.51[b]	3.99[b]	4.60[c]	21.88[a]	3.09[a]

- Front udder quarters have a significantly higher fat and protein content ($p < 0.05$)
- Rear udder quarters have a significantly higher lactose content ($p < 0.05$)

Results: Mean values for milk composition traits

	Fat (%)	Protein (%)	Lactose (%)	Urea (mg/100 ml)	SCS
FL	3.73[a]	4.04[a]	4.56[a]	21.94[a]	3.14[a]
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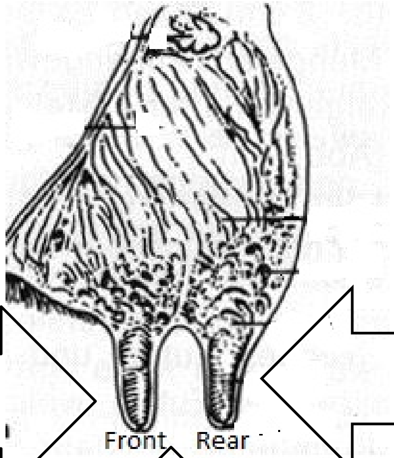
RR	3.51[b]	3.99[b]	4.60[c]	21.88[a]	3.09[a]

- Front udder quarters have a significantly higher fat and protein content ($p < 0.05$)
- Rear udder quarters have a significantly higher lactose content ($p < 0.05$)
- Urea content and SCS do not differ significantly between udder quarters

Heritablitities between udder quarters

Heritability higher in front quarters:

- protein content (Ø 0.21 ± 0.10)
- SCS (Ø 0.16 ± 0.08)



Higher heritability of fat content for rear udder quarters
(Ø 0.10± 0.06)

h^2 comparable in all quarters for:

- urea content (Ø 0.19 ± 0.08)
- Lactose content (Ø 0.08 ± 0.07)

Source figure: K. Wendt et al., 1994

Discussion and Conclusions

- Content of fat , protein and lactose differ significantly between udder quarters and can be regarded as genetically different traits within udder
- No significant difference of SCS and urea content between quarters
- Systematic differences in heritabilities for fat + protein content, but not for urea and lactose content due to the different tissues where the milk constituents are synthetized
- Variance of milk content traits is of limited value as trait to breed for udder health, but helpful trait to detect beginning or subclinical mastitis (health management)

Reliability of Direct Genomic Breeding Values for novel functional traits in Brown Swiss Cattle

- **M. Kramer, M. Erbe, F. Seefried, B. Gredler, B. Bapst, A. Bieber and H. Simianer**

- **Submitted to Journal of Dairy Science**

Aims of the study

- How to integrate novel functional traits into genomic breeding programs?
- How to evaluate the accuracy of direct genomic breeding values for these traits?

Material

Genotypic data

- 777k genotypes of 1.126 animals
  - (partly imputed from 54 k chip using FImpute (Sagolzaei et al., 2011)

→ 930 phenotyped cows

→ 196 bulls with at least 1 phenotyped daughter

Phenotypic data

› De-regressed proofs (DRPF) were used as quasi phenotypes (Garrick et al., 2009)

Method

- Variance component estimation for the complete data set using ASReml (Gilmour et al., 2009)

Problem:

- accuracy of genomic breeding values (r_{DGV}= $r_{DGV,DRPF}/r_{EBV}$) often overestimated when assuming that $r_{DGV,DRPF}$= $r_{DGV,EBV}$, because of an overlap of testing and training sets in cross-validation (Amer and Banos, 2010)

Solution:

- Correcting for this bias by fitting a model, according to method of Wellmann et al. (2013) for estimating r_{DGV}
- random cross validation with 10 replicates

Results: Accuracy of genomic breeding values

Trait	$r_{DGV,DRPF}$	h^2	n EBV	r_{EBV}	$r_{DGV,DRPF} / r_{EBV}$ (Common approach)	r_{DGV} (Approach of Wellmann et al.)
General temperament	0.63	0.38	2.312	0.66	0.95	0.37
Milking temperament	0.73	0.04	2.259	0.30	>1	0.20
Aggressiveness	0.69	0.12	2.309	0.34	>1	0.19
Rank order in herd	0.65	0.16	2.304	0.51	>1	0.27
Milking speed	0.69	0.42	4.540	0.72	0.96	0.48
Udder depth	0.71	0.42	2.195	0.66	>1	0.45
Position of labia	0.66	0.28	2.232	0.61	>1	0.36
Days to first heat	0.74	0.02	1.678	0.18	>1	0.12

› overestimation of accuracy of DGV with common approach due to high values of $r_{DGV,DRPF}$ and low but highly variable values for r_{EBV}

› r_{DGV} and r_{EBV} are dependent on h^2 and size of training set (e.g. milking speed vs. days to firs heat)

Summary

- Overestimation of accuracy of genomic breeding values can be avoided applying the method of Wellmann et al. (2013) to cattle data

Evaluation of different body condition scoring systems in Brown Swiss Cattle

- **A. Isensee, A. Bieber, F. Leiber, V. Maurer and P. Klocke**

Introduction

- Body condition /body fat reserves vary through lacation cycle
- Amount of fat mobilization post calving influences productivity, health and reproduction → monitoring the energetic status of the cow is useful (Bewley and Schutz, 2008)

Aims of the study

- How great is the subjective impact of the evaluator on the BCS given?
- Which scoring method leads to a better estimate of body fat thickness?

Material and Methods

Data collection:

- Period: 6 weeks during November and Dezember 2009
- 1112 cows on 40 low -input farms in Switzerland
  - Ø herd size : 26 cows (13-56 cows/herd)
  - Ø milk yield : 6634 kg (5268 – 8557 kg)

Traits:

Body Condition Score

- Scaling system: 2 to 5 with intervals of 0.25

Validation method: ultrasound measurement of the backfat thickness (BFT) (Staufenbiel et al., 1992)

Scoring methods

Independent BCS (iBCS)

- Based on a matrix of all relevant body regions
- each body region evaluated independently and subsequently integrated into the decision tree structure
- Goal: minimize subjective impact

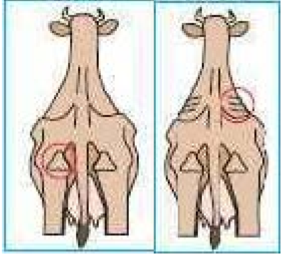
Dependent BCS (dBCS)

- Flowchart with decision-tree structure (Ferguson et al., 1994, modified by Ivemeyer et al., 2006)
- Allows the subjective impression of the whole cow to be taken into account

Statistics: Linear regression models in R (Version 2.15)

Preliminary Results and Discussion

- Inconsistency of scores between the two methods:
- iBCS= deficiencies in assessing the pin bone and transverse processes



- Breed: Brown Swiss show a diverse deposit of muscles (Mösenfechtel et al., 2000) ⟶ quantity of fat apposition harder to assess than in Holstein cows
  - fatter appearance without palpable fat appositions → probably due to their higher muscle deposit

Preliminary Results and Discussion

- dBCS was able to explain BFT best compared to iBCS
- albeit its subjective part dBCS reflects the amount of subcutaneous adipose tissue the best
- Training of assessors is a prerequisite for valid BCS results (Kristensen et al., 2006)

Outlook

- Estimation of genetic parameters for BCS and BFT
- Composite Genomic breeding values

Thank you for your attention

Acknowledgements

The authors gratefully acknowledge co-funding from the European Commission, under the Seventh Framework Program for Research and Technological Development, for the Collaborative Project LowInputBreeds (grant agreement no. 222623).