

Development of Genetic Evaluations for Fertility Traits in Austrian and German Dairy Cattle

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Introduction

As reported in many countries decreased reproductive performance is the main reason for involuntary culling of dairy cows in Austria and Germany (ADR, 2005; ZuchtData, 2006). Low reproductive performance of dairy cows results in additional insemination costs and costs for veterinary treatments and prolonged calving intervals. Hence, a high fertility is of great importance with regard to economic efficiency of cattle breeding. To improve the joint genetic evaluation for fertility in Austria and Germany the project 'Development of genetic evaluations for fertility traits in cattle' was implemented in November 2004. Overall aims are the increase of economic efficiency and a longterm genetic improvement of fertility.

Genetic evaluation for fertility is carried out in Germany since 1994 and in Austria since 1995. Since 2002 genetic evaluations for all traits are performed jointly in Simmental and Brown Swiss in Austria and Germany. Currently the non-return rate 90 is considered of genetic evaluation for fertility in the joint breeding value estimation in Austria and Germany (Fuerst and Egger-Danner, 2002). However, as fertility is a very complex trait (Thaller, 1998) the non-return rate 90 demonstrates only one single aspect of fertility. It is aimed to develop a fertility index combining several fertility traits. Traits analysed are non-return rate 56 and 90, days to first service, days open, interval between first and last insemination, interval between two subsequent inseminations, calving interval and number of inseminations. As fertility is influenced by many different factors body condition score, milk yield, milk urea nitrogen and fat:protein-ratio are considered as auxiliary traits. To account for fertility at different age heifer and cow fertility are considered to be

genetically separate traits. It is supposed that farmers prefer high yielding cows, they are given more chances to conceive, get a better feeding and a better management. To handle problems caused by preferential treatment an effect of milk yield will be included in the analysis. It will also be examined whether survival analysis results in a more accurate genetic evaluation for interval traits compared to linear models. Additionally to consider male fertility the relationship between semen quality and fertility (Gredler *et al.*, 2005) and the effect of semen batch on male fertility will be analysed, also taking into account the effect of semen dilution on fertility. A first analysis was carried out examining the relationship between the auxiliary traits body condition score (BCS), milk yield (Mkg), milk urea nitrogen (MUN), fat:protein-ratio (F:P) and days open (DO).

Data

BCS has been partly recorded during the routine milk recording in Lower Austria since October 2004. BCS is scaled from 1 (very thin) to 5 (very fat) with an increment of 0.25 according to the body condition scoring chart by Edmonson *et al.* (1989). So far 53,800 BCS records of 8,767 Simmental (Fleckvieh) dual purpose cows are available. To investigate the relationship between BCS and DO, BCS and milk records within the interval of ± 20 days to the date of first insemination were used. Data were restricted to the BCS and milk record being closest to the date of first insemination. In total 3,611 Simmental cows with BCS and milk records from 351 herds were analysed. DO were calculated as number of days between calving and last insemination in a given lactation. Mkg and MUN were routinely assessed during milk recording and F:P was computed from milk fat and protein percentages of each milk record. Data were

excluded from the analysis if DO were outside the range of 20 to 365 days and if MUN was greater than 60 mg/100 ml milk.

Statistical analysis

All statistical analyses were performed using SAS Version 8.0 (SAS Institute Inc., 1999). To analyse the impact of various environmental effects on DO, BCS, Mkg, MUN and F:P the procedure GLM was applied. Heritabilities and genetic correlations of all traits were estimated by REML using VCE4 (Groeneveld, 1994). For genetic parameter estimation bivariate analyses were run based on an animal model. The pedigree file consisted of 16,116 animals. The following statistical models were applied:

$$\begin{aligned} \text{DO: } y_{ijkl} &= \mu + \text{HMC}_i + L_j + \beta_1 \text{ac} + a_k + e_{ijkl} \\ \text{BCS: } y_{ijklm} &= \mu + \text{HM}_i + L_j + C_k + \beta_1 \text{dm} + \beta_2 (\text{dm})^2 + a_l + e_{ijklm} \\ \text{Mkg, MUN, F:P: } y_{ijkl} &= \mu + \text{HM}_i + L_j + \beta_1 \text{dm} + \beta_2 (\text{dm})^2 + a_k + e_{ijkl} \end{aligned}$$

where y = individual observation for DO, BCS, Mkg, MUN and F:P,
 μ = the overall mean,
 HM_i = fixed effect of i^{th} herd-month interaction of test-day of BCS classification and milk recording ($n = 1,736$),
 HMC_i = fixed effect of i^{th} herd-month interaction of calving ($n = 2,126$),
 L_j = fixed effect of the j^{th} parity ($j = 1$ to $7+$),
 C_k = fixed effect of k^{th} BCS classifier ($k = 1$ to 11),
 β_1 and β_2 = linear and quadratic regression coefficients,
 dm = continuous effect of days in milk after calving (linear and quadratic);

ac = continuous effect of calving age in month,
 a = random additive genetic effect of animal and
 e = residual error term.

As only one record for DO, BCS, Mkg, MUN and F:P was considered per cow, no random permanent environmental effect was considered in the model. Fixed effects were regarded significant with P -values < 0.05 .

Results and discussion

In Table 1 arithmetic means and standard deviations of DO, BCS, Mkg, MUN and F:P are presented. Mean of BCS was 3.28 with a standard deviation of 0.44. The distribution of BCS is given in Figure 1 which shows that BCS of 3.0, 3.25 and 3.5 have the highest frequency. Since the Simmental breed is a dual purpose breed in Austria, obtained means of BCS were obviously higher than for Holsteins in earlier studies (e.g. Pryce *et al.*, 2001; Kadarmideen and Wegmann, 2003).

Estimated heritabilities with their standard errors for all traits are shown in Table 2. Heritability for BCS was 0.44. Lower results were found by Pryce *et al.* (2001), who estimated heritabilities of 0.28 and 0.27 for BCS one week and 10 weeks after calving, respectively. Heritabilities of 0.26 and 0.29-0.58 are reported by Kadarmideen (2004) and Berry *et al.* (2003), respectively. As expected, the estimated heritability of 0.06 for DO was low. Slightly lower heritabilities of 0.04 and 0.05 were calculated by Dechow *et al.* (2004) and Mitchell *et al.* (2005), respectively.

Table 1. Number of observations (N), arithmetic means (Mean), standard deviations (SD) as well as minimum (MIN) and maximum (MAX) values for days open (DO), body condition score (BCS), milk kg (Mkg), milk urea nitrogen (MUN) and fat:protein-ratio (F:P)

	N	Mean	SD	MIN	MAX
DO	3,611	106.6	58.5	20	359
BCS	3,611	3.28	0.44	1.2	5
Mkg	3,611	25.7	6.9	7.2	58.4
MUN	3,611	18.3	8.9	1	60
F:P	3,611	1.26	0.23	0.53	2.57

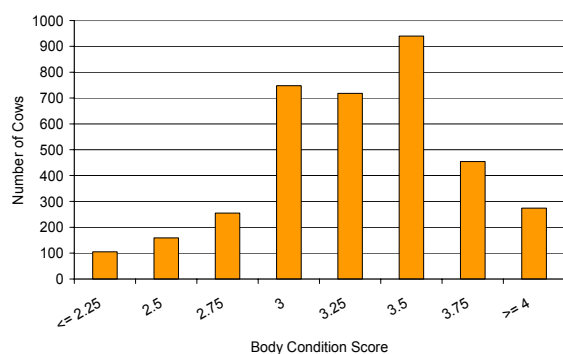


Figure 1. Distribution of body condition score.

For MUN the estimated heritability was 0.20. Comparable heritability results were found by Mitchell *et al.* (2005). Wood *et al.* (2003) calculated higher heritabilities for MUN of 0.44, 0.59 and 0.48 in first, second and third lactation, respectively. For Mkg and F:P heritabilities of 0.15 and 0.16 were estimated, respectively.

Phenotypic and genetic correlations are reported in Table 2. A favourable genetic relationship between BCS and DO was found. The estimated genetic correlation was -0.12

indicating that cows with better body condition show shorter DO. A higher genetic correlation of -0.30 was found by Dechow *et al.* (2004). An obvious high genetic correlation of 0.74 was estimated between DO and Mkg showing that higher Mkg may lead to increased DO. An unexpected genetic correlation of -0.31 was estimated between DO and MUN. A possible reason could be that MUN represents a so called ‘optimum-trait’ with an optimum in the range of 15 to 30 mg/100ml milk. Reasonable genetic correlations between DO and MUN of 0.21 and 0.41 in first and second lactation, respectively, were found by Mitchell *et al.* (2005). Between DO and F:P the genetic correlation was -0.01. Between BCS and MUN and F:P low positive genetic correlations were calculated, whereas between BCS and Mkg an unfavourable relationship was observed. All Pearson correlation coefficients for phenotypic values were close to zero. Due to the low number of animals included in the analyses standard errors of estimated genetic correlations were very high. Therefore results ought to be carefully interpreted.

Table 2. Heritabilities (bold), genetic correlations (above diagonal) with their standard errors and Pearson correlation coefficients for phenotypic values (below diagonal) between days open (DO), body condition score (BCS), milk kg (Mkg), milk urea nitrogen (MUN) and fat:protein-ratio (F:P).

	DO	BCS	Mkg	MUN	F:P
DO	0.06±0.03	-0.12±0.24	0.74±0.15	-0.31±0.23	-0.01±0.22
BCS	-0.03	0.44±0.05	-0.93±0.03	0.16±0.12	0.21±0.09
Mkg	-0.05	-0.01	0.15±0.04	0.11±0.17	0.52±0.19
MUN	-0.01	0.01	0.13	0.20±0.04	0.25±0.16
F:P	0.01	-0.07	0.01	0.07	0.16±0.05

Conclusions

Estimated heritabilities of DO, BCS, Mkg, MUN and F:P were 0.06, 0.44, 0.15, 0.20 and 0.16, respectively. Results found in this study confirm that substantial genetic variation exists for BCS, MUN and F:P. Genetic relationships between traits show that BCS, Mkg, MUN and F:P may be used for prediction of fertility in cattle. However, in order to obtain more reliable estimates for genetic correlations, a higher number of animals should be considered. Further research, especially including fertility measures such as non-return rate and calving interval, is necessary to justify

the usefulness of BCS and production data as indicators for fertility in Austrian Simmental cattle.

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