New Genetic Evaluation of Fertility in Swiss Brown Swiss

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Abstract

A new five-trait fertility model was developed for Brown Swiss cattle in Switzerland. The current model considers non-return-rate 56 in cows and days to first service only. The new model includes traits measured in heifers and cows. The traits evaluated were non-return-rate 56 and interval between first and last insemination in heifers and cows and days to first service. Estimated heritabilities were low for all traits and ranged from 0.015 to 0.063. Breeding values were estimated using a multi-trait animal model. The reliability of fertility breeding values could be improved through incorporation of heifer data and new traits.

Key words: fertility, fitness, genetic evaluation, Brown Swiss cattle

Introduction

Poor reproductive performance is the main reason for involuntary culling in Brown Swiss cattle in Switzerland. 28 % of all cullings are due to impaired fertility (Alder, 2011). In the last decade many countries have improved genetic evaluations for fertility (e.g. Fuerst and Gredler, 2009; Liu *et al.,* 2007).

In Switzerland, breeding values for female fertility were implemented in 2003. The traits currently used in genetic evaluations are non-return-rate 56 in cows (NRC) and days to first service (DFS) (Schnyder and Stricker, 2002). Heritabilities used in the genetic evaluation are 0.012 and 0.039 for NRC and DFS, respectively. The genetic correlation used between NRC and DFS is 0.16. Breeding values are officially published if the reliability of breeding values for DFS exceeds 65 %. No breeding values for male fertility exist. However, direct NRC corrected for main environmental factors are published by the AI centre Swissgenetics (Schmitz-Hsu, 2013).

To account for the complexity of reproductive performance a combination of different fertility traits should be considered in genetic evaluations. The international genetic evaluation of fertility at Interbull allows for five trait groups: trait 1 - maiden heifer's ability to conceive, trait 2 - lactating cow's ability to recycle, trait 3 and trait 4 - lactating cow's ability to conceive expressed as a rate and interval trait, respectively, and trait 5 - lactating cow's interval between calving and conception (Jorjani, 2007a and 2007b). The objective of this study was to develop a new genetic evaluation of fertility in Swiss Brown Swiss cattle based on the trait definition of fertility at Interbull and to compare the reliability of fertility breeding values based on the current and new model.

Material and Methods

Estimation of genetic parameters

A bivariate linear animal model was used to estimate heritabilities and genetic correlations for five different female fertility traits using REMLF90 (Misztal, 2002). Traits analysed were non-return-rate in heifers (NRH) and NRC, DFS, interval between first and last insemination in heifers (IFLH) and cows (IFLC). Two data sets consisting of 44,126 (13,531 heifer and 30,595 cow inseminations) and 88,444 (27,352 heifer and 61,092 cow inseminations) insemination records were used for genetic parameter estimation. Extensive data quality checks were carried out. For NRH and NRC only information on inseminations > 56 days prior to the evaluation date was included. Lower and upper bounds for age at first service were 245 days and 915 days, respectively. Days to first service were required to be within the range of 30 and 200 days. The IFL had to be within 0 and 300 days. Schnyder and Stricker (2002) provide a full list of data validation criteria.

The following model was applied:

$$Y_{ijklmnopqrs} = HY_i + MYI_j + MYC_k + LACT_l + AGE_m + SS_n + IY_o + CODE_p + a_q + p_r + e_{ijklmnopqrs}$$

where

$y_{ijklmnopqrs}$ = phenotypic observation for NRH, NRC, DFS, IFLH, IFLC

HY_i = random effect of herd*year of insemination (all traits)

MYI_j = fixed effect of month*year of insemination (NRH, NRC, IFLH)

MYC_k = fixed effect of month*year of calving (DFS, IFLC)

$LACT_l$ = fixed effect of age at calving within lactation (NRC, DFS, IFLC)

AGE_m = fixed effect of class of age at first service (NRH, IFLH)

SS_n = random effect of service sire*semen batch (NRH, NRC)

IY_o = random effect of inseminator*year (NRH, NRC)

$CODE_p$ = fixed effect of sampling code (testbull or proven bull; NRH, NRC)

a_q = random additive genetic effect of animal (all traits)

p_r = random permanent environmental effect (NRC, DFS, IFLC)

$e_{ijklmnopqrs}$ = random residual effect (all traits)

For the effect of lactation cows in first lactation were grouped according to age at first calving (AFC): lactation 1a (AFC ≤ 27 months), lactation 1b (27 months < AFC ≤ 32 months) lactation 1c (> 32 months). Lactations ≥ 6 were merged to form one group.

Breeding value estimation

All first inseminations and natural services since January 1994 are used for genetic evaluation. Based on data of the routine genetic evaluation of August 2009 three different genetic evaluations were compared: (1) current genetic evaluation for DFS and NRC using a bivariate animal model; (2) same data as in (1) with new genetic parameters for DFS and NRC estimated in this study were applied in the bivariate model; (3) multiple

trait animal model for five fertility traits using genetic parameters estimated in this study. In model (3) heifer data were included for the first time. Breeding values were estimated using BLUPF90 (Misztal, 2008). The same model as described above for the genetic parameter estimation was used to estimate breeding values. Data validation was performed using the same criteria as described above and in Schnyder and Stricker (2002). The three models for genetic evaluation of fertility were evaluated by comparing the reliabilities of DFS and NRC based on the three models. Data characteristics of the genetic evaluations are shown in Table 1.

Table 1. Data characteristics of the genetic evaluations.

Data characteristics	
No. records August 2013	3,228,306
No. records 5-trait model	4,190,225
No. heifer records	1,041,918
No. cow records	3,148,307
Mean NRH (%)	78.3
Mean IFLH (days)	24.6
Mean DFS (days)	74.9
Mean NRC (%)	68.4
Mean IFLC (days)	33.7

Results and Discussion

Genetic parameters

Heritabilities and genetic correlations for all five fertility traits are shown in Table 1. As expected, heritabilities were low ranging from 0.015 for IFLH to 0.063 for DFS. Heritabilities and genetic correlations between NRC and DFS were higher than the estimates currently used in routine genetic evaluation (see description above). Heritabilities are similar to results reported by Fuerst and Gredler (2009) and Gredler (2008) who estimated genetic parameters for fertility traits in Austrian and German Brown Swiss cattle. Genetic correlations between traits measured in heifers and cows were moderate: 0.48 and 0.49 for NR and IFL, respectively. Given these moderate correlations, fertility traits measured in heifers and cows represent genetically different traits and both should be considered in genetic evaluations. These results are in agreement with other studies (e.g. Gredler *et al.*, 2007).

Table 2. Heritabilities (diagonal) and genetic correlations (off-diagonal).

Trait	NRH	IFLH	NRC	IFLC	DFS
NRH	**0.016**				
IFLH	-0.51	**0.015**			
NRC	0.48	-0.51	**0.018**		
IFLC	-0.42	0.49	-0.62	**0.041**	
DFS	0.41	0.28	0.38	0.22	**0.063**

Genetic correlations between traits measured in heifers and cows were moderate: 0.48 and 0.49 for NR and IFL, respectively. Given these moderate correlations, fertility traits measured in heifers and cows represent genetically different traits and both should be considered in genetic evaluations. These results are in agreement with other studies (e.g. Gredler *et al.,* 2007).

Breeding value estimation

The number of insemination records clearly increased by incorporating the heifer data into the genetic evaluation. Figure1 shows the distribution of number of daughters per bull in the current model (Routine August 2013) and the new model including heifer data exemplarily for bulls born in 2007. The average number of daughters per bull in the routine run August 2013 was 13.4. Including heifer data in the new model leads to an increase of the average number of daughters of 33.1.
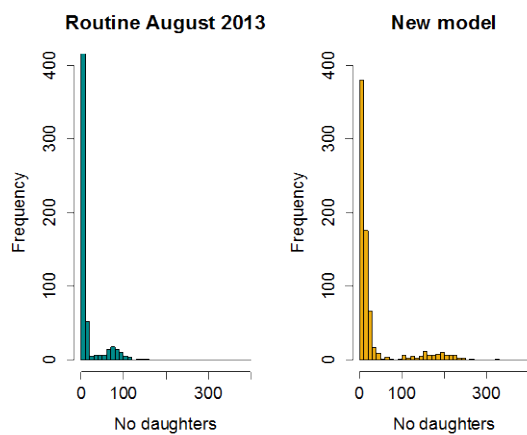

Figure 1. Histogram of number of daughters of bulls born in 2007 based on the routine genetic evaluation in August 2013 and the new five trait model.

The reliability of breeding values for NRC and DFS increased when using new genetic parameters (model 2) and the new five-trait model (model 3) compared to the current genetic evaluation. Figure 2 and 3 show the distribution of reliabilities of breeding values for NRC and DFS estimated with the three different models for bulls born in 2006 (n=815), 2007 (n=752), and 2008 (n=443). For NRC the average increase in reliability by using the five-trait model was 11.4 %, 11.3 %, and 10.7 % for bulls born in 2006, 2007, and 2008, respectively. For DFS, the average increase was 7.3 %, 9.4 %, and 9.2 % for bulls born in 2006, 2007, and 2008, respectively. Pryce (2013) reported similar improvements in first proof reliabilities of fertility of 5 % by using a multi-trait model compared to a single trait model in Australian Holstein cattle.
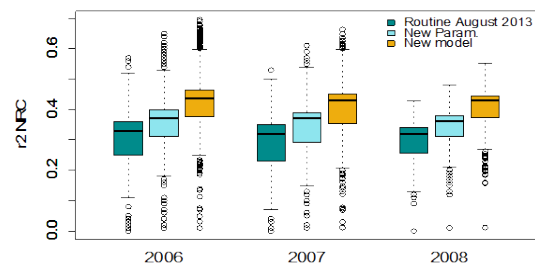

Figure 2. Reliability (r2) distribution for NRC of bulls born in 2006, 2007 and 2008 for three different models.
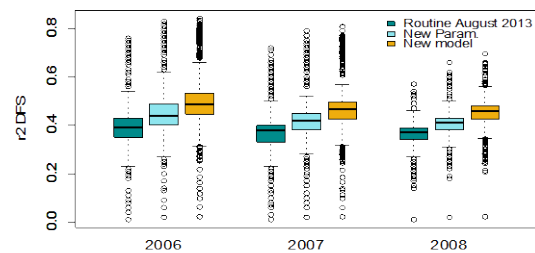

Figure 3. Reliability (r2) distribution for DFS of bulls born in 2006, 2007 and 2008 for three different models.
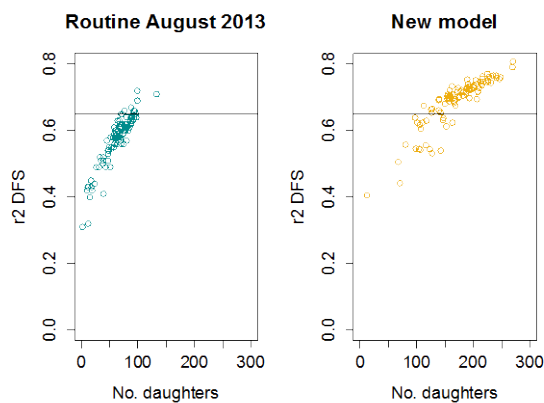
Figure 4. Number of daughters plotted against the reliability of DFS for bulls with first crop daughters born in 2007. The horizontal line marks the reliability threshold of 65 % for official publication.

Figure 4 reports the relationship between number of daughters and the reliability of breeding values for DFS for bulls with first crop daughters born in 2007 (n=99). In the routine genetic evaluation of August 2013 12.1 % of all bulls pass the official publication criteria of 65 % reliability for DFS. Using the new five-trait fertility model and including heifer data 78.8 % of all bulls pass the publication criteria.

Conclusions and further steps

The current genetic evaluation of fertility in Brown Swiss cattle considers NRC and DFS only. A five-trait fertility model was developed to account for the complexity of reproductive performance. Heritabilities of all fertility traits were low ranging between 1.5 % and 6.3 %. Moderate genetic correlations were found between heifer and cow fertility and should therefore be considered as genetically different traits. Including heifer data increased the information per bull. The new five-trait model leads to higher reliabilities of breeding values for NRC and DFS. Further steps will include fine-tuning of data editing and effect definitions used in the model. Since the reliability threshold of 65 % for official publication is rather high, new publication criteria will be considered. It will be evaluated whether the five fertility traits will be combined in a fertility index or published as single traits.

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