

Estimation of genetic parameters for female fertility traits in the Czech Holstein population

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Summary

Genetic parameters for the days open and calving interval in the Czech Holstein population were estimated using a single trait animal model. The fertility traits were days open and calving interval. The heritability estimate was 0.038 for days open and 0.034 for calving interval. Variances of random permanent effects were higher than those of additive genetic effects in these traits in mature cows. Repeatability (w^2) was 0.087 and 0.090 for days open and calving interval, respectively.

Keywords: dairy cattle, breeding value, days open, calving interval

Introduction

Female fertility is one of the major factors that affect the profitability of milk production in dairy cattle. Poor fertility parameters increase the cost of milk production through a higher culling rate, cost of fertility treatments, and number of inseminations, and longer calving intervals. A long-term selection for yield traits has led to the decreased reproductive performance in high-yielding breeds owing to the negative genetic correlation between reproduction and milk production traits (Yamazaki *et al.*, 2014; Zink *et al.*, 2012) and owing to the reduced or absence of emphasis on reproduction in dairy cattle selection schemes. Therefore, it is necessary to incorporate fertility into selection programs to slow the deterioration or to improve fertility in dairy cattle. Recently, novel fertility traits have been incorporated into selection schemes over the world. The most frequent traits are calving interval, calving to first service interval, days open, variates of non-return rates, days from first insemination to conception, the number of inseminations per conception, age at first calving, and age at first service (Kadarmideen *et al.* 2000, Jamrozik *et al.*, 2005, Liu *et al.*, 2008, Zink *et al.*, 2012, Guo *et al.* 2014). The estimates of genetic parameters for fertility traits are usually low (below 10%).

In the Czech Republic, the only evaluated fertility trait is the conception rate, where the insemination effect is evaluated after approximately 3 months from after the artificial insemination (AI) is performed. Data are collected by AI service technicians via insemination and rectal examination for pregnancy. Since 1995, inseminations have been evaluated using a linear model. The prediction of breeding values runs separately for cows and heifers. Breeding values for male (AI bull) and female fertility (inseminated cow/heifer) are predicted. Fertility has a weighting of 0.12 in the total merit index (SIH) in the Czech Republic (Plemdat, 2016). Despite the inclusion of fertility traits in the total merit index, fertility has experienced a negative trend over the past few years.

The aim of this study was to estimate the genetic parameters for selected cow fertility traits in the Czech Holstein population as a step toward the incorporation of novel fertility traits into routine genetic evaluations.

Material and methods

Data were obtained from the Czech Moravian Breeding Corporation. Insemination data are routinely collected in the Czech Republic. The database of insemination records, milk production records, and pedigree have been used for the derivation of all fertility traits. The data of days open (DO) and calving interval (CI) were derived from these databases. DO is incorporated into the breeding objectives of Holstein in the Czech Republic, but has not been genetically evaluated. Genetic evaluation of non-return rate should be better but in our database there are no suitable data for this.

Only data collected since 2005 were included. The traits had specific editing condition according to extreme values, the number of observations in each herd-year-month/season, the number of sires in each herd-year-month/season, the number of herds in which the bull was used, and the number of inseminations per bull to ensure the connectivity of the records, the predictability of the effects, and to reduce the computational demands. The data collected on the first 10 lactations were included in the estimation.

A pedigree file containing animals with data and five generations of ancestors was created. The animals in the last generation and animals with unknown parents were assigned to phantom parent groups, created according to year and country of birth. The numbers of animals in the pedigree file and the numbers of HYSB and HYMC are listed in Table 1.

In the first step, the analysis of variance was conducted using the General Linear Model (GLM) procedure of SAS 9.4 to identify the effects that should be included in the models for genetic parameter estimation. Significant effects ($p < 0.05$) were included. The Bayesian approach in the DMU RJMC (Madsen and Jensen, 2013) module was used to estimate the variance components. A specific single trait animal model in simplified scalar notation was used for the estimation of genetic parameters, as follows:

$$Y = \text{HYSB} + \text{HYMC} + L + \text{CE} + \text{AGE} + \text{AGE}^2 + A + \text{PE} + E$$

where Y is the dependent variable, HYSB is the fixed effect of herd-year-season of birth, HYC is herd-year-month of calving, L is the fixed effect of lactation number, CE is the fixed effect of the last calving ease, AGE is regression at the age at first insemination in heifers with respect to the age at first calving in cows, A is the random animal effect, PE is the random permanent environmental effect, and E is the random residual effect.

Results and discussion

Basic descriptive statistics of all fertility traits and results of performance editing are presented in Table 1.

Average DO was 124.26 days and average CI was 400.08 days. The length of both is strongly influenced by herd management. These fertility traits are at a lower level than is desirable, which is associated with economic loss; therefore, genetic evaluation and selection are important. A little higher heritability was found in DO compared with CI. Van Raden *et al.* (2004) estimated that DO heritability was 0.03, with an upper limit of 305 days. As the upper limit of DO decreases, heritability increases. As heritability for DO is higher than heritability for the calving interval and has a higher genetic variability, it is preferable for routine breeding (Table 2). Heritability for CI (0.034) obtained in the present study was lower than that obtained by Haile-Mariam *et al.* (2003) (0.09), but this was estimated from routine

data. Lower heritability (0.01, 0.022, and 0.024) was presented by Pryce *et al.* (2001), Kadarmideen *et al.* (2000), and Kadarmideen *et al.* (2003), respectively.

Our estimated heritability for DO corresponds with heritability (0.03) estimated by Zink *et al.* (2012) in first-parity Czech Holstein cattle. Liu *et al.* (2008) estimated heritability for DO as 0.026 using multiple trait models. DO and CI are overlapping traits with a high genetic correlation. Guo *et al.* (2014) presented a genetic correlation of 0.99 between DO and CI, while Zaabza *et al.* (2016) reported the correlation as 0.81. Breeding with CI as the selection objective could lead to better fertility, but breeding for DO appears to be preferable. Moreover, DO has a higher heritability and genetic variance, so we can expect higher genetic progress. DO and CI are both strongly influenced by the decisions of the farmer. In high-yielding cows, early pregnancy can negatively influence milk yield, so many farmers postpone the first service after calving. In large balanced herds, with systematic management, this could be mathematically accounted for in the herd-year-season effect; however, in small herds, it is not effective.

For both traits evaluated in mature cows, the permanent environmental effect of the cow conferred a higher variance than the additive genetic effect, but the permanent environmental effect of the cow is not included in prediction of breeding values for conception rate at present in the Czech Republic. Repeatability of DO and CI was 0.087 and 0.090, respectively.

Table 1. Structure and descriptive statistic of input data after editing

| Trait | No of Record | No of sires | PED | HYSB | HYMC | MIN (days) | MAX (days) | MEAN (days) | S.D. (days) |
|-------|--------------|-------------|------------|--------|--------|------------|------------|-------------|-------------|
| DO | 599 901 | 4 385 | 709 287 | 11 515 | 26 025 | 20 | 300 | 124.26 | 60.20 |
| CI | 480 022 | 5 669 | 698 881 | 14 626 | 33 161 | 300 | 600 | 400.08 | 58.74 |

DO – days open, CI – calving interval, HYSB - number of herd-year-season of birth, HYMC – number of herd-year-month of calving, PED – number of animals in pedigree file, σ^2_P – phenotypic variance, MIN – minimal value, MAX – maximal value

Table 2. Estimated genetic and nongenetic parameters

| Trait | σ^2_G | σ^2_{PE} | σ^2_E | h^2 | w^2 |
|-------|---------------|-----------------|----------------|-------|-------|
| DO | 128.39 ± 5.94 | 170.09 ± 7.39 | 3117.43 ± 8.06 | 0.038 | 0.087 |
| CI | 108.91 ± 5.68 | 181.08 ± 8.34 | 2935.45 ± 9.14 | 0.034 | 0.090 |

σ^2_G – genetic variance with standard error, σ^2_{PE} - variance of random permanent effect with standard error, σ^2_E - residual variance with standard error, h^2 – heritability, w^2 – repeatability

Conclusion

Genetic parameters for days open and calving interval in the Czech Holstein population were estimated using single trait animal model and Bayesian approach. Heritability and repeatability estimates were low, but in accordance with previous studies. The genetic parameters of the present study will be implemented in the routine genetic evaluation of fertility traits in the Czech Republic.

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ANSWERS FOR REVIEWER

- 1) **How do you account for heifers - with the traits CI and DO you can only account for information where a calving is available.**

My fault, corrected.

- 2) Why to use two traits which are influenced a lot by management - for DO there is the affect that the farmer may decide that they start later with first insemination; CI depends on culling a lot - if a cow is culled earlier, this one will not have a calving intervall - why not use e.g. Non-Return-Rate**

These traits are influenced by management a lot but they have a genetic background too. Commonly, calving interval is considered to be an economically important trait. Non-Return-Rate will be better but in our database there weren't a suitable data. Farmers don't have a unified time to pregnancy detection and it is reason why data have not been recorded yet.

- 3) Reason for use of a single trait animal model - why not multitrait.**

A single trait animal model was used because it is routinely used in dairy cattle genetic evaluation for all of traits in Czech Republic.

- 4) Why not to use another traits like NNR - it could be also assessed at heifers.**

Suitable data are not available.

- 5) The genetic correlation would have been also of interest in this study.**

Yes, but for now we have finished just single trait animal model, next approaches will follows. We start with single trait animal model.

- 6) Looking on the data about 20% don't calve again - no information for CI available - how much is due to fertility problems and how much due to other reasons for culling.**

In our database, reason for culling is not recorded so these informations are not available.

- 7) can't follow the argumentation on premature calving - but agree that DO is preferable**

Corrected.

Thank you for your comments.