Genetic Analysis of Female Fertility Traits in Beef Cattle in the Czech Republic

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Abstract

Database of performance testing (so called field test) of 333 thousands of animals of twelve beef breeds and crosses with dairy and dual-purpose breeds was used for analyse. Data from 1995 to 2013 were used. Three female fertility traits were analysed: age at first calving (**AF**), calving interval (**CI**) and lifespan (**LS**). The genetic parameters were estimated by residual maximum likelihood. Multi-trait animal model with relationship matrix with genetic groups based on the breed was used. For estimation (co)variance components there were 40 033 cows with LS, 35 220 cows with AF and 19 833 cows with CI. All three traits showed moderate heritability (0.23 AF, 0.39 CI, 0.27 LS). Genetic correlations between AF and CI as well as between AF and LS were almost zero (- 0.01 and - 0.02 respectively). Genetic correlation between CI and LS was low negative (- 0.07).

Key words: female fertility, maternal trait, genetic parameters, beef cattle

Introduction

In 2000 in the Czech Republic a system for breeding value prediction for field test (calving ease, birth weight, live weight at 120, weaning weight and yearling weight) by a multi-trait animal model with maternal effect was developed (Přibyl *et al.*, 2003). In 2004 the prediction of breeding value for the own growth of bulls at performance-test stations was introduced (Přibylová *et al.*, 2004). Since 2005 a breeding value for the type traits and muscling of young beef cattle has been predicted (Veselá *et al.,* 2005). And in 2011 a system for genetic evaluation for SEUROP carcass traits was developed (Veselá *et al.*, 2011). In beef cattle, whatever the production system, maternal breeding traits appear to be the most economically important traits (Newman *et al.,* 1992; MacNeil *et al.,* 1994; Wolfová *et al.*, 2004). High rates of reproduction in a beef herd are directly related to the profitability of beef production (MacGregor and Casey, 1999). Hence fertility should be included as part of the breeding goal, but the possibilities of actually using reproductive information as a selection tool for breeders are limited. Additionally, reproductive performance is a complex trait that has many components. It is possible to separate the female reproductive complex into subsets that are both relatively easy to measure and have higher heritabilities to be used in genetic improvement (Gutiérrez *et al.,* 2002). Some fertility indicators such as calving interval (CI) or age at first calving (AF) are used as indicator of fertility (Haile-Mariam and Kassa-Mersha, 1994; Tonhati *et al.,* 2000; Goyache and Gutiérrez, 2001; Gutiérrez *et al.*, 2002; Roughsedge *et al.,* 2005). To evaluate production life of cows in beef cattle is often used lifespan (LS) (Roughsedge *et al.*, 2005).

The aim of this study was therefore to analyse 3 female fertility traits (AF, CI, LS), determine environmental effects, obtain model equation for prediction of breeding values and estimate genetic parameters for routine genetic evaluation of female fertility traits in beef cattle in the Czech Republic.

Material and Methods

Data

Database of performance testing (so called field test) of 333 thousands of animals of twelve beef breeds and crosses with dairy and dual-purpose breeds was used for analyse. This database is used for routine genetic evaluation of growth traits of beef cattle in the Czech Republic (Přibyl *et al.*, 2003). However, in the database there are as well included birth dates of animals and numbers of calves per cow, which were information used in our work to analyze female fertility traits. Data from 1995 to 2013 were used.

Definition of traits

Three female fertility traits were analysed. They were age at first calving (**AF**), calving interval (**CI**) and lifespan (**LS**).

Age at first calving was defined as number of days from birth of cow to her first calving. AFs lower than 500 days and higher than 3,5 years were set as missing records.

Only *calving intervals* between first and second calving were used in the analysis. CIs shorter than 290 day and longer than 630 days were set as missing records, following Gutiérrez *et al.* (2002) and Roughsedge *et al.* (2005).

Lifespan was defined as the parity the cow attained or was predicted if data were censored. Cows that had time for calving *n* but not for calving *n + 1* and cows that reached parity five were considered as censored and LS was assigned to reflect parity that was expected to be reached using survival probabilities from parity to parity determined separately for each breed group. The survival probabilities were calculated using dataset of cows first calved between 1995 and 2001 applying the rules by Roughsedge *et al.* (2005). LS for censored data was assigned following Brotherstone *et al.* (1997):

$$LS = n + p_n + p_n \cdot p_{n+1} + p_n \cdot p_{n+1} \cdot p_{n+2} + \ldots$$

where *n* is the known number of parities completed and *p* is the probability of survival from one parity to next.

The full dataset for genetic analysis contained 60 141 cows with LS, 51 954 cows with AF and 28 999 cows with CI. Table 1 shows the basic statistical characteristics of evaluated traits.

Table 1. Basic statistical characteristics of evaluated traits.

	Records	Mean	SD	Min	Max
AF	51 954	973.5	167.1	500	1277
CI	28 999	389.6	57.7	290	630
LS	60 141	4.07	2.57	1	8.63

To ensure an appropriate data structure for the parameter estimation, some extra edits were applied. Minimum size of HYS had to be at last 5 cows, each cow had to have at last 4 half-sisters by the same sire and each sire had to have daughters at last in 3 HYS. Based on these edits, in order to estimate (co)variance components, there were 40 033 cows with LS, 35 220 cows with AF and 19 833 cows with CI.

Statistical methods

The significant environmental fixed effects were determined using MIXED and GLM procedure in SAS analytical software and are summarized in table 2.

Table 2. Environmental fixed effects in model equation.

Environmental effect	AF	CI	LS
Heterosis coefficient (L)	FR	FR	FR
Age of dam (classes)	F		
Calving ease at first calving		F	F
Age at first calving (LQ)		FR	FR
Month of first calving		F	
Herd birth		F	
HYS birth	F		
HYS first calving		F	

F = fixed effect, FR = fixed regression, L =linear, Q = quadratic, HYS = herd – year - season

The genetic parameters were estimated by residual maximum likelihood using AIREMLF90 program (Misztal *et al.*, 2002). Multi-trait animal model with relationship matrix with genetic groups based on the breed was used.

Results

Results for the variance components and related genetic parameters are reported in table 3.

Table 3. Estimates of genetic (σ^2_G), environmental error (σ^2_E), phenotypic (σ^2_P) variances, standard deviation of estimation (SD σ^2_G and SD σ^2_E) and heritability coefficients.

	AF	CI	LS
σ^2_G	2 328.6	871.9	1.13
σ^2_E	7 822.0	1 355.8	3.08
σ^2_P	10 150.6	2 227.7	4.21
h^2	0.23	0.39	0.27
SD σ^2_G	128.8	42.9	0.05
SD σ^2_E	160.1	59.6	0.06

The heritability estimate for AF was moderate 0.23. This results is in line with coefficient of heritability 0.235 reported by Gutiérrez *et al.* (2002) and 0.27 reported by Goyache and Gutiérrez (2001) in Asturiana de los Valles, 0.17 in Simmental, 0.26 in Limousine and 0.22 in Aberdeen Angus reported by Roughsedge *et al.* (2005) and 0.28 in Aberdeen Angus reported by Bormann *et al.* (2010). The heritability estimate for CI (0.39) was higher than the heritability coefficients reported in other studies for beef cattle. Gutiérrez (2007) reported heritability 0.12, Roughsedge *et al.* (2005) 0.04 to 0.13, Yagüe *et al.* (2009) 0.085 and Mercadante (2000) 0.08 to 0.26 in Nellore cattle. In our work we analyzed only first calving intervals. The literature shows that genetic correlations between different subsequent calving intervals are not equal to one (Haile-Mariam *et al.,* 2003; Olori *et al.,* 2003) and therefore should be taken into account as different traits. Heritability coefficient for LS was 0.27. Roughsedge *et al.* (2005) reported heritabilities for LS in beef catte in the range 0.04 to 0.13.

Table 4. Genetic correlation matrix.

	AF	CI	LS
AF		- 0.01	- 0.02
CI			- 0.07
LS			

Table 4 shows the genetic correlation matrix. Genetic correlations between the female fertility traits differed only slightly. All genetic correlations were very low negative. Correlations between AF and CI as well as between AF and LS were almost zero (- 0.01 and - 0.02 respectively). Genetic correlation between CI and LS was low negative (- 0.07). Genetic correlations reported in the literature vary from negative to positive (Bourdon and Brinks, 1983; Haile-Mariam and Kassa-Mersha, 1994; MacGregor and Casey, 1999; Tonhati *et al.,* 2000; Braga Lobo, 1998; Guttiérez *et al.*, 2002). Rougsedge *et al.* (2005) reported genetic correlation between CI and AF - 0.71 to - 0.07, between CI and LS - 0.34 to 0.31 and between AF and LS - 0.06 to 0.24.

Conclusion

The data of performance testing of beef cattle appears to be suitable for genetic evaluation of female fertility traits in the Czech Republic. Three female fertility traits were selected: age at first calving, calving interval and lifespan. All of these traits showed moderate heritability and therefore could be improved by selection. Multi-trait animal model is recommended for genetic evaluation of the AF and CI. Although this model appears suitable even for genetic evaluation of LS, there should be in the further work also analyzed the suitability of other approaches (for example survival analysis).

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