Genetic Parameters Of Female Fertility And Udder Conformation Traits In The Czech Holstein Cattle Population

V. Zink*, J. Lassen† and M. Štípková*

Introduction

Female fertility is a complex trait and selection for the traits is therefore very difficult. Due to the economic importance of the trait it is still a hot topic for farmers. Fertility is unfavorably correlated to production traits (Windig *et al.*, 2005) and milk and fat production as well as udder conformation traits are correlated to the culling rate of cows (Weigel *et al.*, 1998). Therefore it is of great importance to make balanced breeding schemes where all traits of economic importance are taken into consideration. It has been found that cows with good udder conformation also have good reproduction (Wall *et al.*, 2005). One opportunity therefore could be to breed for better udder conformation. Good udder conformation is also related to improved longevity (Zavadilová *et al.*, 2009), decreased somatic cell score (SCS), and lower incidence of clinical mastitis (CL) (Rupp and Boichard, 1999). It is likely that cows with good udder conformation are able to have high milk production jointly with good health of the mammary gland and good reproduction performance. The aim of this study was to estimate genetic parameters for selected linear udder type traits and female fertility traits.

Material and methods

For the analyses a total of 59454 animals were available. The analyzed data came from 936 herds. The pedigree included 164125 animals. All data came from the official progeny testing database of the Czech-Moravian Breeders' Corporation. Linear type traits were extracted from October 2005 to February 2009 and the pedigree was traced from November 1994 to November 2006. Fertility traits included days from calving to first service (CF), days open (DO) and days from first to last insemination (FL) in first and second lactation. Numbers of animals for the female fertility traits ranged from 58686 (CF1) to 18915 (FL2). Only animals which had data in the interval from 21 to 180 days for CF and from 40 to 220 for DO were used in the analyses. For linear type traits only first parity cows which were classified from 30 to 210 days after calving were included. Classification of linear type traits was done using the national classification scheme which is modified for the Czech Holstein population according to the official recommendation of the International Holstein-Friesian Federation. The scale for classification ranged from 1 to 9 point with 1 point increments.

^{*} Department of Cattle Breeding, Institute of Animal Science, Přátelství 815, 10400 Prague 10 – Uhříněves, Czech Republic

[†]Department of Genetics and Biotechnology, Danish Institute of Agricultural Sciences, P.O. Box 50, DK-8830 Tjele, Denmark

For estimation of (Co)variance components the DMU software (Madsen and Jensen, 2006) was used, using an AI-REML algorithm (Jensen *et al.*, 1997). Genetic parameters were inferred from a number of bivariate animal models.

For the conformation traits a model containing the following effects was used: $Y = herd + year + season + classifier + days in milk + age at calving + (age at calving)^2 + animal + residual$

There were a total of 936 herds, over 7 years, 4 seasons and 7 classifiers. These were all fixed class variables. Days in milk, age at calving and (age at calving)² were fixed regressions and the animal and residual effect were random effects

For the female fertility traits a model containing the following effects was used: Y = herd + year + season + days in milk + age at calving + (age at $calving)^2 + animal + residual$

Herd, year and season were fixed class variables. Age at calving and (age at calving)² were fixed regressions and the animal and residual effect were random effects. For both conformation traits and female fertility traits the following variance structure of the random effects was assumed.

$$\operatorname{var} \begin{bmatrix} a_{1} \\ a_{2} \\ e_{1} \\ e_{2} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_{\mathbf{a}1}^{2} & \mathbf{A}\sigma_{\mathbf{a}12} & \mathbf{0} & \mathbf{0} \\ \mathbf{A}\sigma_{\mathbf{a}12} & \mathbf{A}\sigma_{\mathbf{a}2}^{2} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{\mathbf{e}1}^{2} & \mathbf{I}\sigma_{\mathbf{e}12} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{\mathbf{e}12} & \mathbf{I}\sigma_{\mathbf{e}2}^{2} \end{bmatrix}$$

where a_1 and a_2 are vectors of the analyzed traits, e_1 and e_2 were unknown random residuals.

Results and discussion

The estimated heritabilities and genetic correlations for the different traits are presented in table 1. All presented heritabilities and genetics correlations were estimated as an average from all bivariate analyses which were done for the trait of interest. Estimated heritabilities for female fertility were low and close to zero. The current estimated heritabilities for reproduction traits are similar with previous studies published by different authors (e. g. Gonzáles-Recio and Alenda (2005); Liu et al. (2008)) as well as heritabilities for udder conformation traits, e. g. Pryce et al. (2000) and Weigel et al. (1998). Heritabilities for the linear type traits ranged from 0.13 for udder width to 0.28 for udder depth. The current results show that all udder traits have moderate heritability and with the exception of the low value for udder width. These estimates show that it is possible to use them for direct selection or as indicator traits with reasonable information for other traits. Estimated genetic correlations between female fertility traits and udder traits ranged from -0.30 between CF1 and udder depth and -0.30 between DO2 and udder depth to 0.27 between DO1 and udder width.

Due to the biology of the linear type traits it can be problematic to interpret some of the genetic correlations. For two of the udder conformation traits (fore udder attachment and udder depth) with intermediate optimum we found correlations statistically significant from zero. Negative genetic correlations of these traits show that animals which tend to have extremely strong and tight fore udder attachment have less days from calving to first insemination in first and second lactation and shorter DO1. Also it shows that animals with shallower udder have shorter CF1 and less days open in first and second lactation. Dal Zatto et al. (2007) presented negative genetics correlation (-0.21) between calving interval (CI) and udder depth (i. e. animals with shallower udder conformation have shorter CI). For all estimated genetic correlations between traits which were significantly different from zero the udder conformation trait has an extreme biological optimum. Positive genetic correlations were estimated between udder width and all analyzed traits, though only between udder width and CF1, DO1 and DO2 the correlations were statistically significant. These results show that cows with more width udder have more days from calving to first insemination as well as longer DO1 and DO2. This might also correspond to the fact that body width has an unfavorable genetic correlation to female fertility. For the general udder conformation score only one genetic correlation was found to be statistically significant (CF1). This corresponds with the results presented in the study by Dal Zotto et al. (2007).

Table 1: Heritability estimates (h^2) and genetic correlations between conformation traits in first lactation and fertility traits in first (1) and second (2) lactation (CF – days from calving to first insemination, DO – days open, FL – days from first to last insemination). All estimates are with corresponding standard errors.

Traits		CF1	DO1	FL1	CF2	DO2	FL2
	h^2	0.04	0.03	0.01	0.03	0.02	0.01
		± 0.01	± 0.004	± 0.003	± 0.01	± 0.01	± 0.01
Fore udder	0.22	-0.29	-0.21	-0.02	-0.24	-0.13	0.05
attachment	± 0.01	± 0.06	± 0.08	± 0.10	± 0.10	± 0.13	± 0.16
Front teat	0.26	-0.07	-0.07	-0.03	-0.02	0.11	0.16
placement	± 0.01	± 0.06	± 0.07	± 0.10	± 0.10	± 0.12	± 0.15
Teat length	0.26	0.02	0.06	0.03	-0.01	0.15	0.15
	± 0.01	± 0.06	± 0.07	± 0.10	± 0.10	± 0.12	± 0.15
Udder depth	0.28	-0.30	-0.25	-0.02	0.19	-0.30	-0.26
	± 0.01	± 0.06	± 0.07	± 0.10	± 0.10	± 0.12	± 0.16
Rear udder	0.20	-0.003	0.05	0.07	0.07	-0.03	-0.11
height	± 0.01	± 0.07	± 0.08	± 0.10	± 0.10	± 0.13	± 0.17
Central	0.19	-0.04	-0.02	-0.01	-0.02	-0.04	-0.05
ligament	± 0.01	± 0.07	$\pm v0.08$	± 0.10	± 0.10	± 0.13	± 0.16
Rear teat	0.27	-0.05	0.01	0.05	0.06	0.07	0.03
placement	± 0.01	± 0.06	± 0.07	± 0.10	± 0.10	± 0.12	± 0.15
Udder width	0.13	0.18	0.27	0.18	0.13	0.26	0.25
	± 0.01	± 0.07	± 0.08	± 0.11	± 0.11	± 0.13	± 0.16
Udder	0.22	-0.20	-0.14	-0.01	-0.11	-0.12	-0.07
	± 0.01	± 0.06	± 0.08	± 0.10	± 0.10	± 0.13	± 0.16

Very low correlations between the two traits teat length and rear udder height and CI were reported by Pryce *et al.* (2000). This corresponds to our results for DO1 for these two udder conformation traits. Calving interval and days open are traits that are very similar. We estimated genetic correlations between central ligament and all the female fertility traits. These were all negative and close to zero ranging from -0.01 to -0.05 which does not correspond to the results presented by Wall *et al.* (2005), for CI and CF. However, a similar result was found for non-return rate 56 days from insemination (-0.09).

Conclusion

Good udder conformation is not important only because of its relation to mastitis problems. Information about udder conformation could also support genetic evaluation for reproduction traits in Czech Holstein. This study suggests that data on udder conformation could be used as a part of the genetic evaluation for female fertility and thereby help to improve the level of female fertility within the Czech Holstein population.

Acknowledgments

This study was supported by project NAZV QH91270.

References

Dal Zotto, R., De Marchi, M., Dalvit, C. et al. (2007). J. Dairy Sci., 90:5737-5743

Gonzáles-Recio, O., and Alenda, R. (2005). J. Dairy Sci., 88:3282-3289

Jensen, J., Mäntysaari, E. A., Madsen, P. et al. (1997). J. Ind. Soc. Agric. Stat. 49:215-236.

Liu, Z., Jaitner, J., Reinhardt, F. et al. (2008). J. Dairy Sci., 91:4333-4343

Madsen, P. and J. Jensen. 2006. DMU: DJF, Foulum, Denmark

Pryce, J. E., Coffey, M. P., Brotherstone, S. (2000). J. Dairy Sci., 83:2664-2671

Rupp, R. and Boichard, D. (1999). J. Dairy Sci., 82:2198-2204

Wall, E., White, I. M. S., Coffey, M. P. et al. (2005). J. Dairy Sci., 88:1521-1528

Weigel, K. A., Lawlor, T. J., JR., Vanraden, P. M. et al. (1998). J. Dairy Sci., 81:2040-2044

Windig, J. J., Calus, M. P. L., Veerkamp, R. F. (2005). J. Dairy Sci., 88:335-347

Zavadilová, L., Němcová, E., Štípková, M. et al. (2009). Czech J. Anim. Sci., 54:387-394