

Genetic Evaluation for Fertility Traits in Polish Holsteins

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Introduction

Improvement of milk production traits has been a main breeding goal in the Polish Holstein cattle population. During the last 20 years, holsteinization and selection have led to an increase of milk yield but have caused unfavourable trends in reproductive performance. Fertility traits are considered very important because of their impact on the economics of dairy cattle breeding. The following consequences of low fertility were listed by Hodel *et al.* (1995): higher insemination costs, decrease of milk and meat production (fewer progeny born), increase in culling rate, and less intensive selection. About 20-30% of all culling has been due to fertility problems (Boichard and Manfredi, 1992; Hoekstra *et al.*, 1994).

The purpose of this paper was to estimate the heritabilities of several fertility traits and the genetic and phenotypic correlations between them.

Material and Methods

The data set contained 42 283 records of cows that were daughters of 1018 sires. The cows calved for the first time in 785 herds and were allocated in 2217 herd-year-season and 1657 herd-year subclasses containing at least 10 contemporaries.

The following fertility measures were calculated for each cow: non-return rate to 56th day (NR56), non-return rate to 72nd day (NR72), age at first service, age at first conception, and age at first calving. Non-return rates were defined as binary traits based on whether or not the cow had a second insemination within 56 (or 72) days after first insemination. Interval fertility measures calculated for each cow in the first three parities were: service period [days] (interval

from first insemination to conception), days of pregnancy [days] (interval from conception to calving), days to first service [days] (interval from calving to first service), days open [days] (interval from calving to conception), calving interval [days] (interval from calving to the next calving).

(Co)variance components of the fertility traits were estimated by restricted maximum likelihood (REML) (Miształ and Perez-Enciso, 1993) with a relationship matrix, based on the following linear model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{ZQg} + \mathbf{Zu} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of observations, $\mathbf{g}$ is the vector of fixed effects of genetic groups, $\mathbf{b}$ is the vector of fixed effects of herd-year of calving and month of calving, $\mathbf{u}$ is the vector of additive animal genetic effects, $\mathbf{e}$ is the vector of residual error, and $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{Q}$ are coincidence matrices. Matrix $\mathbf{G} = \mathbf{A}^{-1} \otimes \mathbf{G}_0$, where $\mathbf{A}^{-1}$ is a numerator relationship matrix and $\mathbf{G}_0$ a genetic (co)variance matrix between traits.

It is assumed that, $E(\mathbf{u}) = \mathbf{0}$, $E(\mathbf{e}) = \mathbf{0}$, $V(\mathbf{u}) = \mathbf{G}$, $V(\mathbf{e}) = \mathbf{R}$, $\text{Cov}(\mathbf{u}, \mathbf{e}) = \mathbf{0}$, and $E(\mathbf{y}) = \mathbf{Xb}$, $V(\mathbf{y}) = \mathbf{ZGZ}' + \mathbf{R}$. Matrix $\mathbf{R} = \mathbf{I} \otimes \mathbf{R}_0$, where $\mathbf{R}_0$ is a residual (co)variance matrix between traits and $\otimes$ is the Kronecker product.

Genetic groups were created according to the rules given by Westell *et al.* (1988). Animals with unknown parents were assigned to genetic groups by birth year and percentage of Holstein-Friesian genes. Five groups for male and eight for female unknown parents were formed.

Variance components for NR56, NR72, age at first service, age at conception and age at calving were estimated using the single trait animal model. Estimated variances were used

as prior values to estimate genetic and residual covariances between the studied traits, using the multitrait animal model. Genetic and phenotypic correlations were computed based on estimated (co)variances. Variance components for service period, days of pregnancy, days open, calving interval and days to first service in the first, second and third parities were estimated using a single-trait animal model. In the next step a multitrait animal model was applied to estimate (co)variances between first-parity-interval fertility measures as well as (co)variances between measures in different parities. Genetic and phenotypic correlations were computed based on estimated (co)variances.

Results and Discussion

One of the most important fertility traits included in total merit indices in many countries is non-return rate. Heritabilities for non-return rates estimated in this paper were very low: 0.012 for NR56 and 0.01 for NR72. The highest heritability was found for age at first service (0.324). Heritabilities for age of conception and age at calving were slightly smaller and amounted to 0.312 and 0.296, respectively. The non-return rate found by Ranberg *et al.* (2003) in a population of heifers in Norway was 74.6%, very similar to NR56 reported in this paper. The heritability of NR56 in the Norwegian population varied from 0.012 to 0.014, depending on the model applied. Heritability of NR56 estimated by Wall *et al.* (2003) in a population of British Holsteins was slightly higher (0.018). Heritability for non-return rate to 90th day estimated by Hodel *et al.* (1995) was lower for heifers (0.011) and higher for cows (0.021).

The calving interval consists of two subintervals: days of pregnancy and days open. The genetic and phenotypic variation of gestation length is quite small and does not depend on management; therefore the number of days open is the main factor affecting the calving interval. The most efficient cows should calve annually, but a short calving interval implies short days open and in consequence a lower yield and shorter lactations. Heritabilities of all interval fertility traits in the first parity were low and ranged

from 0.044 for calving interval to 0.092 for service period (Table 3). Heritabilities of days to first service and days open were similar (0.061 and 0.051, respectively), whereas the heritability of pregnancy days was slightly higher and amounted to 0.074. Heritabilities of all intervals decreased in consecutive parities, and in the third parity were close to zero for days open and days to first service. Higher heritabilities for days of pregnancy (0.062) and service period (0.054) were found in the third parity. The heritabilities of calving interval reported in other papers ranged from 0.01 (Pryce *et al.*, 2001) to 0.086 (Veerkamp *et al.*, 2001). Olori *et al.* (2003) published an estimate of 0.04, what was similar to the heritability in Polish Black-and-White cattle. Pryce *et al.* (2002) and Wall *et al.* (2003) obtained slightly smaller heritabilities (0.025 and 0.033, respectively). Heritabilities for days open have ranged from 0.03 (Abdallah and McDaniel, 2000) to 0.066 (Veerkamp *et al.*, 2001), not significantly differing from the estimate published in this paper.

Relations among ages at first insemination, conception and calving are shown in Table 4. The largest genetic correlation was found between age at first service and age at calving (0.98). The correlation between age at first service and age at conception was slightly smaller (0.96).

The genetic correlation between NR56 and NR72 was high (0.80) whereas the correlations between non-return rates and the remaining traits were low. The highest and negative correlation was found for NR72 and age at conception (-0.11). A positive correlation was obtained for NR56 and age at first service (0.10).

Genetic and phenotypic correlations among interval reproductive measures are shown in Table 5. The highest correlation was found between calving interval and days open (0.99). Days to first service was highly correlated genetically with days open (0.74) and calving interval (0.72). Moderate genetic correlations were obtained for service period with days open (0.32) and with calving interval (0.35). Phenotypic correlations were moderate or low except for the correlation between calving interval and days open (0.99). The phenotypic correlation between days to first

service and days open was 0.39, and between days to first service and calving interval was 0.39. All remaining correlations were close to zero.

A large and positive genetic correlation was found between service period and age at first service (0.72) (Table 6). Service period was also correlated with age at conception (0.90) and age at calving (0.90). Other intervals were moderately genetically correlated with age at first service, age at conception and age at calving; the correlation between days open and age at first insemination was 0.44, and all remaining correlations were less than 0.35. Phenotypic correlations were close to zero except for the correlations of service period, which ranged from 0.53 with age at calving to 0.64 with age at conception.

In future, the fertility index containing both fertility measures and type traits will be constructed. The largest genetic correlations of calving interval and days open were found with rear leg set (0.187 and 0.241, respectively) whereas NR56 showed strong relations to body depth, chest width and rump width (-0.125, -0.264, -0.282).

Conclusion

Heritabilities of fertility measures were low but within the range of results published by other authors. Fertility traits with higher heritabilities and correlated with some type and production traits could be used to construct a fertility index.

Acknowledgment

Supported by the State Committee for Scientific research, Grant No. P06D 03827

Table 1. Means and standard deviations for fertility measures.

Trait	N	$\bar{x}$	SD
Age at first service	42 283	537.6	75.5
Age at conception	42 283	556.8	79.0
Age at calving	42 283	835.8	83.2
NR56	42 283	0.73	0.39
NR72	42 283	0.69	0.42
Service period	42 283	27.5	53.8
Pregnancy days	42 283	278.0	5.6
Days open	25 013	132.1	77.1
Calving interval	25 013	409.8	77.4
Days to first service	25 013	79.3	35.2

Table 2. Heritabilities of heifer fertility traits.

Trait	$\bar{x}$	SD	h^2	s.e.
Non return rate to 56. day	0.73	0.39	0.012	0.009
Non return rate to 72. day	0.69	0.42	0.010	0.009
Age at first service	537.6	75.5	0.324	0.033
Age of conception	556.8	79.0	0.312	0.021
Age at calving	835.8	83.2	0.296	0.019

Table 3. Heritabilities of interval fertility traits in first (h_1^2), second (h_2^2) and third (h_3^2) parities (standard errors of heritabilities in brackets).

Trait	h_1^2	h_2^2	h_3^2
Service period	0.092 (0.038)	0.086 (0.041)	0.054 (0.035)
Days of pregnancy	0.074 (0.004)	0.071 (0.004)	0.062 (0.003)
Days open	0.051 (0.008)	0.045 (0.007)	0.043 (0.007)
Calving interval	0.044 (0.009)	0.041 (0.009)	0.002 (0.005)
Days to first service	0.061 (0.011)	0.053 (0.010)	0.003 (0.008)

Table 4. Genetic (above diagonal) and phenotypic (below diagonal) correlations of fertility traits.

No.	Trait	1.	2.	3.	4.	5.
1.	Non return rate to 56 day		0.80	0.10	0.05	-0.11
2.	Non return rate to 72 day	0.48		-0.05	-0.08	-0.05
3.	Age at first service	0.12	-0.02		0.96	0.98
4.	Age at conception	-0.12	-0.02	0.78		0.98
5.	Age at calving	-0.20	-0.08	0.80	0.98	

Estimated SE for r_g ranged from 0.05 to 0.15

Table 5. Genetic (above diagonal) and phenotypic (below diagonal) correlations of interval fertility measures in first parity.

No.	Trait	1.	2.	3.	4.	5.
1.	Service period		0.26	0.32	0.35	0.09
2.	Days of pregnancy	0.04		-0.02	0.07	-0.05
3.	Days open	0.03	0.00		0.99	0.74
4.	Calving interval	0.04	0.01	0.99		0.72
5.	Days to first service	0.01	-0.02	0.39	0.39	

Table 6. Genetic (r_g) and phenotypic (r_p) correlations between interval fertility measures in first parity and heifer fertility traits.

Trait	Age at first service		Age at conception		Age at calving	
	r_g	r_p	r_g	r_p	r_g	r_p
Service period	0.72	0.54	0.90	0.64	0.90	0.53
Days of pregnancy	0.20	0.04	0.30	0.06	0.23	0.12
Days open	0.44	0.03	0.32	0.06	0.15	0.04
Calving intervals	0.30	0.03	0.34	0.06	0.12	0.04
Days to first service	0.21	0.06	0.23	0.06	0.18	0.06

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