Genetic parameters for female fertility in Nordic dairy cattle

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Abstract

Nordic Cattle Genetic Evaluation (NCGE) is in the process of updating the fertility model. The fertility traits have low heritabilities; hence the accurate (co)variance components are important for the estimation of breeding values. Multitrait-multilactation sire model with 11 traits was used for analyzing i) non-return rate in 56 days (NRR), ii) interval from the first insemination to the last insemination (IFL), and iii) interval from calving to the first insemination (ICF). The data consisted of Swedish Holstein (N=144,392) and Nordic Red Dairy Cattle (RDC, N=103,653) heifers and cows with three first lactations. The heritabilities in different lactations in both the breeds ranged around 0.01 in NRR, and from 0.01 to 0.04 in IFL. In ICF the heritabilities were 0.06 - 0.07 in Holstein and 0.03 - 0.05 in RDC. The within-trait, across-lactation genetic correlations in cow traits were in general high, they spanned from 0.78 to 0.97 in Holstein and from 0.56 to 0.91 in RDC. Across the traits the correlations in cow traits varied more than within traits; the highest correlations occurred within the lactations. The heifer traits and cow traits correlated from 0.23 to 0.74 within the traits. Across the traits the heifer-cow correlations varied from low to moderate. The results were found logical and can be used as variance parameters for the fertility traits in the model to be updated.

Key words: fertility, genetic correlation, heritability, dairy cattle

Introduction

The breeding values for the fertility traits are evaluated jointly in Sweden, Denmark and Finland by Nordic Cattle Genetic Evaluation (NCGE). NCGE, together with Natural Resources Institute Finland (Luke), is currently in the process of updating the original fertility model (Fogh *et al.*, 2003) for the Nordic dairy cattle.

In May 2015 the sire model was changed to a multitrait multilactation animal model. The current (co)variance components used are revised in the second phase of model updating. The objective of this study was to estimate required variance components for the multitrait multilactation model.

Materials and Methods

Data description

Variance components were estimated for Holstein (HOL) and Nordic Red Dairy Cattle (RDC). The data was obtained from NCGE. The Swedish herds with a minimum of 12 (HOL) or 8 (RDC) first-calvers annually were accepted for data sampling. From these herds we randomly sampled 400 herds from both the breeds. Observations of animals born before 1995 and calved after 2012 were excluded. Fertility records of heifers and the first three parities of cows were used in the analyses. Altogether the HOL data set contained observations from 144,392 HOL females and the RDC data set observations from 103,653 females. The sire model pedigree included 14,111 and 10,397 HOL and RDC sires, respectively.

Traits analyzed were: i) non-return rate in 56 days after the first insemination (NRR0, NRR1, NRR2 and NRR3), ii) interval from the first insemination to the last insemination (IFL0, IFL1, IFL2 and IFL3), and iii) interval from calving to the first insemination (ICF1, ICF2 and ICF3). The numbers in the trait names relate to the different parities. The heifer traits are indicated with 0, and the cow traits with 1, 2 or 3.

NRR is a binary trait, where 0 (or 100) describes that the female did (or did not) return to the heat after 56 days after first service. IFL measures the length of the service period in days and ICF describes the number of days needed for the cow to regain its normal cyclicity after calving.

Statistical Analyses

Variance components were estimated with multitrait multilactation sire model using EM-REML method in MiX99 software (MiX99 Development Team 2015; Matilainen *et al.*, 2012). All the 11 traits were analyzed simultaneously. A separate analysis was conducted for both HOL and RDC. The multitrait model had same model equations for NRR and IFL traits:

$$y_{ijklm} = hy_i + iym_j + iage_k + sire_l + e_m,$$

where

y_{ijklm} is the individual observation

hy_i is herd*birth year for heifer traits, or herd*actual calving year for cow traits;

iym_j is insemination year-month;

$iage_k$ is heifers’ first insemination age;

$sire_l$ is random genetic effect of the sire; and

e_m is the random residual effect.

For ICF traits the insemination year-month effect was replaced by the actual calving year-month effect of the cow.

Results and Discussion

Heifers had higher NRR and lower IFL values compared to cows (Table 1). Differences between breeds were more opposed for interval traits than for NRR.

Table 1. Means and standard deviations by breed. NRR = non-return rate in 56 days [%], IFL = interval from first and last service [day], and ICF = interval from calving to first service [day]. Numbers 0 – 3 refer to the parities.

	Mean		St.dev	
Trait	HOL	RDC	HOL	RDC
NRR0	76.1	75.1	42.7	43.3
NRR1	64.7	61.7	47.8	48.6
NRR2	62.0	61.6	48.6	48.7
NRR3	62.3	61.5	48.5	48.7
IFL0	18.5	16.1	36.5	32.0
IFL1	47.9	40.8	65.9	58.6
IFL2	53.0	42.1	67.2	58.9
IFL3	52.4	43.6	66.1	59.7
ICF1	90.6	83.4	35.4	29.9
ICF2	89.4	80.6	34.9	29.0
ICF3	89.6	80.8	34.8	29.1

Heritabilities of the studied traits in both the breeds were low (Table 2) and in the range of heritabilities reported by Liu *et al.* (2008) and reviewed by Berry *et al.* (2014). The heritabilities were at their lowest in the heifer traits and at their highest in the later parities, a pattern which was also reported by Liu *et al.* (2008). NRR is a binary trait and therefore the heritability estimates were expected to be lower than those in the interval traits (Falconer and Mackay, 1996). As reviewed by Berry *et al.* (2014), also here ICF had the highest heritability among the traits. In general, the heritabilities were similar in both the breeds. However, RDC had lower heritabilities in ICF than HOL. RDC is a more heterogeneous breed compared to HOL, which may explain the differences between the breeds.

Table 2. Heritabilities by breed. NRR = non-return rate in 56 days, IFL = interval from first and last service, and ICF = interval from calving to first service. Numbers 0 – 3 refer to the parities.

trait	HOL	RDC
NRR0	0.01	0.01
NRR1	0.01	0.01
NRR2	0.01	0.01
NRR3	0.01	0.01
IFL0	0.01	0.01
IFL1	0.04	0.02
IFL2	0.04	0.03
IFL3	0.04	0.05
ICF1	0.06	0.03
ICF2	0.06	0.03
ICF3	0.07	0.04

Genetic correlations within the traits. Genetic correlations were low for NRR (Table 3) and higher for ICF (Table 5). Genetic correlations between cow traits were high but not unity. In RDC the correlations were a bit lower, but the pattern of the correlations was similar as in HOL.

Table 3. The genetic correlations across parities in non-return rate in 56 days (NRR) in Holstein.

	NRR1	NRR2	NRR3
NRR0	0.74	0.68	0.44
NRR1		0.88	0.78
NRR2			0.87

For NRR, Liu et al. (2008) reported a heifer-cow correlation of 0.63, which is lower than we found for HOL. The lowest genetic correlations were estimated between heifer and cow traits in IFL (Table 4). This is in line with findings of Liu et al. (2008), where the heifer-cow correlation was estimated to be 0.48. Roxström *et al.* (2001) reported a heifer–cow correlation of 0.65 from Swedish Red and White Dairy Cattle.

Table 4. The genetic correlations across parities in interval from first to last service (IFL) in Holstein.

	IFL1	IFL2	IFL3
IFL0	0.47	0.40	0.43
IFL1		0.97	0.93
IFL2			0.91

The genetic correlations were high in ICF (Table 5). Roxström *et al.* (2001) reported similar correlation for the first and second parity; for the second and third parity their correlation was unity.

Table 5. The genetic correlations across parities in interval from calving to first service (ICF) in Holstein.

	ICF2	ICF3
ICF1	0.91	0.87
ICF2		0.96

The correlations between heifer and cow traits were 0.4 – 0.7, which indicates that the heifer traits should be considered genetically different from cow traits as Pryce *et al.* (2004) suggested. Also the correlations between different parities in cow traits suggest keeping the parities as separate traits in the model.

Genetic correlations across the traits ranged widely. Between heifer traits (NRR0 and IFL0) correlation was high negative (Table 6). The correlations between heifer and first-parity traits ranged from low to moderate. Between NRR and ICF the correlation was low or moderate and unfavorable: shortening of ICF seems to lead to lower NRR. However, the low estimates had high standard errors (results not shown). Berry *et al.*, (2014) reviewed that the average correlation between NRR and ICF was low and negative, although there were some positive correlations in the range of studies in their review. Liu *et al*. (2008) and Fuerst and Gredler (2009) found a high, negative correlation in their studies. Between interval traits the correlations were positive and of the range reviewed by Berry *et al.* (2014) and Liu *et al*. (2008), indicating that an early service after calving correlates with shorter service period. In RDC the correlations were in general lower but with a similar structure as in HOL.

Table 6. The genetic correlations across the traits in heifers and first-parity cows in Holstein. NRR = non-return rate in 56 days, IFL = interval from first and last service, and ICF = interval from calving to first service.

	IFL0	NRR1	IFL1	ICF1
NRR0	-0.75	0.74	-0.30	0.10
IFL0		-0.57	0.47	0.15
NRR1			-0.52	0.29
IFL1				0.50

Phenotypic correlations were in general low. Between the heifers and 1st parity cows; 1st and 2nd parity cows; and 2nd and 3rd parity cows the phenotypic correlations for NRR were 0.02, 0.03 and 0.03, respectively. In the same order for IFL the estimates were 0.03, 0.09 and 0.10. And for ICF the correlations across 1st and 2nd; and 2nd and 3rd parity were 0.13 and 0.15.

Conclusions

The estimated heritabilities were in general low. The genetic correlation estimates ranged from moderate to high within traits (across parities). However, the correlations indicate that parities should be modeled as different traits. The correlation structure was similar for both the breeds, although in RDC the correlations were in general lower.

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