

## GENETIC ANALYSIS OF FERTILITY DISEASE TRAITS AND THEIR RELATIONSHIP TO REPRODUCTION TRAITS IN DAIRY CATTLE

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### INTRODUCTION

From both an economic and an animal welfare point of view the functional traits are of great importance (Christensen, 1998), but genetic improvement of dairy cows is mainly focused on increasing milk production (Hoekstra *et al.*, 1994). There was however an observed decline in pregnancy rates over the last 20 years (Royal *et al.*, 2000), there was also an increase of services per conception and days open (Washburn *et al.*, 2002) within this time. One reason may be an unfavourable genetic relationship between milk production traits and reproductive performance, which is reported in several studies (e.g. Roxström *et al.*, 2001 ; Veerkamp *et al.*, 2001). There is also an antagonistic association between production and reproductive disorders (e.g. Fleischer *et al.*, 2001 ; Hooijer *et al.*, 2001). Selection based primarily on production traits may therefore increase the incidence of fertility related diseases and will reduce reproductive performance. There are only few reports on the genetic relationship between fertility disorders and reproductive performance. The objective of this study is to estimate heritabilities for fertility disease categories. Genetic correlations between fertility disease categories and reproduction traits were also analysed.

### MATERIAL AND METHODS

**Research project:** Records of reproduction traits and fertility disorders were obtained from three commercial farms with 3600 German Holstein cows in the time from beginning of February 1997 to the end of April 2001. These farms are integrated in a project for further development of performance testing in dairy cattle. Compared to conventional testing programmes data recording is more frequent and expected to be more precise, especially for functional traits.

**Data recording:** Data on reproduction (inseminations, results of pregnancy tests) and disease occurrence were registered daily by the farm staff and veterinarians of the three farms. Pregnancy tests were done 6 weeks after insemination by rectal palpation. These data were promptly stored on record sheets or in computer based management programmes. The farms were visited every two or three weeks to take backups of the management program data. At these visits there was the possibility to discuss non plausible data and to correct it in time.

**Trait definition:** Four reproduction traits and four fertility disorder categories were defined. **Reproduction traits** were non-return-rate at day 90 based on first insemination (NR90), interval from calving to first insemination in days (ICF), conception rate after first insemination (CRF) and conception rate for all inseminations (CRA). For CRF and CRA a success (trait value: 1) was recorded if the cow had a positive pregnancy result in the time from 30 to 60 days after insemination. Inseminations with a negative pregnancy diagnosis within the time from 30 to 60 days after insemination were considered as a failure (trait value:

0) and inseminations without a positive pregnancy check but a following insemination got the same trait value. Inseminations without any further information were excluded.

The **disease traits** were defined as presence or absence of several fertility disorders and therefore treated as all-or-none traits. Only the first diagnosis per lactation of each disease category was considered. The first trait included retained placenta and all cases requiring veterinary treatment at calving or up to ten days after calving (RP), the second one included all cases of metritis, endometritis and pyometra (ME), the third trait, termed ovarian diseases (OD), included cystic ovarians, anestrus and hormonal treatments because of ovarian problems. A general reproductive health trait (ALL) measured the occurrence of the first three traits. The disease traits were analysed separately for first parity and for all parities. First diagnosis of a disease after the 200-th day of lactation was not considered. The data set contained 13.809 lactations of 7.856 cows of all parities. Number of sires was 775, with ten daughters on average.

**Statistical analyses:** Variance components were estimated with an animal threshold model with two categories for fertility diseases. Genetic correlations between the reproduction traits and the fertility diseases were estimated in bivariate analyses with linear models.

Using a Bayesian approach the estimation of variance components for fertility diseases was done with the Gibbs sampling algorithm implemented in the LMMG\_TH program, a threshold model derivative of LMMG (Reinsch, 1996), as a single-trait estimation. Mean values of the posterior distributions are reported as parameter estimates. For each trait 120.000 cycles were generated and the result of each cycle retained. Convergence was determined by visual inspection. The results of the first 20.000 iterations were discarded (burn-in) and the results of the remaining 100.000 iterations were used for calculation of variance component estimates. The following basic threshold model was used for first parity:

$$\pi_{ij} = \Phi (HYS_i + c_1x + c_2x^2 + a_j)$$

where  $\pi_{ij}$  is the expected probability for occurrence of fertility disease,  $\Phi$  is the cumulative probability function of standard normal distribution,  $HYS_i$  is the fixed effect of  $i$ -th Herd-Year-Season-class of calving (35 classes),  $c_1$ ,  $c_2$  are the linear and quadratic regression coefficients on the lactation length  $x$  and  $a_j$  is the genetic effect of the animal  $j$ .

Some model modifications have been done for RP. There was no correction on lactation length, because of natural outcome of RP in time of calving. Also a fixed effect of age of calving divided into five classes was included.

The following basic threshold model was used for all parities:

$$\pi_{ijkl} = \Phi (HYS_i + L_j + c_1x + c_2x^2 + pc_k + a_i)$$

additional to the first parity model  $L_j$  is the  $j$ -th fixed effect of the parity of the cow (3 classes) and  $pc_k$  is the permanent environmental effect of cow  $k$ .

The fixed effect of parity contained three classes, lactations three and higher were grouped together. Because of repeated data of cows in several parities a permanent environmental component of the cow has been analysed, except for ME. These models were also used for the covariance estimation.

Data from all parities were included for covariance estimation between fertility diseases and reproduction traits. For a Bayesian analysis with linear models the program MTGSAM (Van Tassell and Van Vleck, 1996) was used. The model for reproduction traits was:

$$y_{ijkl} = \mu + HYM_i + pc_j + a_k + e_{ijkl}$$

where  $y_{ijk}$  is the trait,  $\mu$  is the general mean,  $HYS_i$  is the fixed effect of  $i$ -th Herd-Year-Month-class of insemination (106 classes),  $pc_j$  is the permanent environmental effect of the cow  $j$ ,  $a_k$  is the genetic effect of the animal  $k$  and  $e_{ijkl}$  is the residual. For NR90 and CRF the interval between calving and first insemination within lactation was additionally included. For CRA insemination sire was added as a permanent environmental effect, because of repeated inseminations with sperm from the same bull. The model for CRA additionally comprised insemination number (1, 2,  $\geq 3$ ), and an interaction between interval from calving to insemination with parity number, and for ICF parity was additionally included as a second fixed effect.

## RESULTS AND DISCUSSION

Observed disease frequencies were higher than in the literature (table 1). Literature values for RP are in the range of 4 (Schomaker, 2001) to 6 percent (Ouweltjes *et al.*, 1996) and for OD of 8 (Hooijer *et al.*, 2001) to 12 percent (Pösö and Mäntysaari, 1996). One cause of this large range is probably the varying definition of these traits. The heritability estimates are also higher than literature reports (e.g. Pösö and Mäntysaari, 1996; Wassmuth *et al.*, 2000). First parity estimates for heritabilities were higher or equal compared to estimates for all parities combined. This result is similar to results of Uribe *et al.* (1995), who analysed cystic ovarian diseases. The highest heritability was estimated for OD.

**Table 1. Mean frequencies (%), heritabilities ( $h^2$ ) and proportion of permanent environmental variance ( $p^2$ ) of fertility disease traits for first and all lactations**

Trait	First lactation		All lactations		
	mean	$h^2$ (s.e.)	mean	$h^2$ (s.e.)	$p^2$ (s.e.)
RP	15,4	0,08 (0,04)	15,0	0,09 (0,03)	0,09 (0,04)
ME	18,3	0,09 (0,05)	14,9	0,06 (0,03)	-
OD	19,4	0,12 (0,05)	21,6	0,12 (0,03)	0,14 (0,05)
ALL	41,3	0,14 (0,04)	41,3	0,09 (0,02)	0,10 (0,03)

RP = retained placenta, ME = metritis, OD = ovarian disease, ALL = general reproductive health trait

The estimated genetic correlations between reproduction traits and fertility diseases are low with high standard errors except for ICF (table 2). Pösö and Mäntysaari (1996) supposed that such high standard errors reveal difficulties involved in estimating genetic correlations between binary coded traits of low heritability. Nevertheless, the correlations show that there is a generally unfavourable genetic relationship between fertility disorders and reproduction traits. The highest correlations exist between ICF and OD, and ICF and all diseases.

**Table 2. Genetic correlations between fertility disease categories and reproduction traits**

	NR90	CRF	ICF	CRA
RP	-0,05 (0,22)	-0,15 (0,22)	0,25 (0,17)	-0,02 (0,20)
ME	-0,15 (0,16)	0,18 (0,17)	0,17 (0,13)	-0,22 (0,15)
OD	-0,12 (0,18)	-0,23 (0,17)	0,58 (0,09)	-0,11 (0,17)
ALL	-0,12 (0,18)	-0,16 (0,18)	0,48 (0,11)	-0,01 (0,16)

RP = retained placenta, ME = metritis, OD = ovarian disease, ALL = general reproductive health trait, NR90 = non-return-rate at day 90, ICF = interval calving first insemination, CRF = conception rate first insemination, CRA = conception rate all inseminations

### CONCLUSION

The mean frequencies of the general reproductive health trait showed that 41 percent of all lactating cows had to be treated at least one time because of fertility diseases. Heritabilities for fertility disease traits especially for OD showed a clear genetic determination for this traits. The genetic correlations suggest that there is a possibility for better reproductive performance by selection against fertility disorders.

### ACKNOWLEDGEMENTS

Financial support was provided by Federal Ministry of Consumer Protection, Food and Agriculture (Berlin, Germany) and NOG Nord-Ost Genetic GmbH & Co. KG (Verden, Germany).

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