Genetic Evaluation of Fertility Traits of Dairy Cattle Using a Multiple Trait Model

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Abstract

A multiple trait model is applied to five fertility traits: interval first to last inseminations and non-return rate to 56 days of virgin heifer, interval calving to first insemination, non-return rate to 56 days and interval first to last inseminations. Using the two interval traits of cows as components, breeding values of days open are derived posterior to solving mixed model equations of this multiple trait animal model. Fertility traits of later lactations are treated as repeated measurements. Genetic parameters were estimated with residual maximum likelihood method. Mixed model equations of the genetic evaluation model are solved with preconditioned conjugate gradients algorithm and iteration on data technique. Reliability values of estimated breeding values are approximated with the multi-trait effective daughter contribution method. Daughter yield deviations and associated effective daughter contribution are calculated with a multiple trait approach. This model has been applied to insemination data of dairy breeds in Germany and validated with various statistical methods, including Interbull's genetic trend validation method III.

1. Introduction

In past decades successful selection on milk production traits in dairy cattle has led to decline in female fertility due to unfavourable, correlated selection response (Jorjani 2006). In order to improve or at least stop the deterioration trend in fertility, more emphasis on fertility traits in selection is necessary (de Jong 2005; Jamrozik *et al.*, 2005; VanRaden *et al.*, 2004; Wall *et al.*, 2005). Germany has a complete database for nationwide storing and evaluating all breeding and fertility data for a long time. A routine genetic evaluation for female and male fertility has been applied to non-return rate (NR) to 90 days since the early 80’s. Because the current single trait genetic evaluation model doesn’t consider some important fertility traits, such as interval from calving to first insemination and interval from first to last inseminations, a more up-to-date statistical model is required for accurately evaluating fertility of female and male animals. The objective of this study was to develop a genetic evaluation system with a multiple trait model for fertility traits.

2. Materials and Methods

2.1. Data

A total of five fertility traits were selected for routine genetic evaluations, two of them for virgin heifers: non-return rate to 56 days (NRh) and interval from first to last inseminations (FLh), and three traits for cow fertility: interval calving to first insemination (CF), non-return rate to 56 days (NRc) and interval first to last inseminations (FLc). As a combined trait, days open (DO) was derived from their respective component traits (Jamorzik *et al.*, 2005).

Insemination records of virgin heifers and cows in first to six lactations were selected for the fertility genetic evaluation. Virgin heifers must be born from 1994 onwards and cows must first calve in 1995 or later. Female animals from all farms enrolled in milk recording programmes were considered in the evaluation, including those not in the herdbook system. Inseminations of both AI and non-AI bulls were evaluated. Values of the fertility traits must fall in defined ranges. Insemination records were compared to calving information of following lactation, if available. FL was only calculated, if a subsequent calving was available. In addition to the plausibility checks within service period of animal, data on herd-year level were also examined. If the NR rate on a herd-year level was not significantly different from 1 (i.e. only successful inseminations were recorded), fertility data from this herd-year were excluded. This data check was done separately for virgin heifers and cows. Table 1 summarises information about the data and pedigree used in the August 2007 test run.

Table 1. Descriptive statistics of the fertility data of German dairy breeds used in August 2007 test run.

	Insemination records	Females with data	Cows with data	Animals in pedigree	Herd-year classes	Total No. of equations
No. of levels	24,839,116	11,188,753	8,594,768	16,228,378	558,542	134,449,657

2.2. Statistical models for genetic evaluation

The fertility traits are analysed with a multiple trait animal model, where all fixed effects are denoted in upper case and random effects in lower case:

$$\mathrm{y}_{ijklmno} = \mathrm{HY}_i + \mathrm{PAM}_j + \mathrm{BOU}_o + \mathrm{F}_m + \mathrm{t}_{mn} + a_k + \mathrm{p}_k + e_{ijklmno} \qquad [1]$$

where

$\mathrm{y}_{ijklmno}$ denotes a fertility trait of *l*-th lactation of female animal *k*,

HY_i is fixed effect of the *i*-th herd-year,

PAM_j is the *j*-th parity group x age class x month of insemination,

BOU_o is the *o*-th effect of type of bull as service sire (proven sire and otherwise) x owner AI stud of service sire x user AI stud of female animal,

F_m represents fixed effect of service sire *m*,

t_{mn} represents random effect of insemination year class *n* within the service sire *m*,

a_k is additive genetic effect of *k*-th female animal,

p_k is random permanent environmental effect of cow *k*, and

$e_{ijklmno}$ is residual effect for this record.

Not all of the fertility traits are modelled with all the effects in model 1. For the interval trait of virgin heifer FLh, only HY_i, PAM_j and a_k are considered. The sub-model for NRh of virgin heifer contains BOU_o, F_m, t_{mn} in addition to the effects for FLh. In comparison to NRh, non-return rate of cow, NRc, is evaluated with an additional random permanent environmental effect p_k. The two interval traits of cow fertility: CF and FLc are analysed with a sub-model including HY_i, PAM_j, a_k and p_k.

It is assumed that residual correlation between any pair of the five traits is null, except between the two heifer traits FLh and NRh. Permanent environmental effects are correlated among the three cow traits, so are the additive genetic effects among all five traits.

In contrast to the single trait model currently used in Germany, paternal genetic effect is no longer included in the new genetic evaluation model. However, male fertility is still made available as $\mathrm{F}_m + t_{mn}$, though it is expressed only at phenotypic level. Permanent effects of service sires in different year classes are assumed to follow the distribution of first-order autoregressive process, AR(1) (Wade and Quaas, 1993). For progeny test or natural service bulls, only one year class is specified.

But there are four year classes defined for proven bulls. In routine genetic evaluation, the last insemination year of a proven sire is defined as the origin of this AR(1) process, and the last year class combines the fourth insemination and all previous years. It is assumed that there is no correlation between the progeny testing period and the time of second crop. For every proven sire, a matrix containing variance and auto-correlation of within-bull year effects is set up and inverted using the algorithm by Wade and Quaas (1993), which allows unequal spacing or missing years. The maximum number of year classes is set to four, but more than four years may be included in analysis as a result of possible missing years.

2.3. Genetic parameters estimated with residual maximum likelihood method

The genetic parameters were estimated with residual maximum likelihood method. As a linear function of CF and FLc, (co)variances of DO were derived using the (co)variances of these two component traits. Variance of year classes within service sire was 0.35% of phenotypic variance, and the auto-correlation was found to be 0.8 between two consecutive year classes.

2.4. Solving the mixed model equations

The mixed model equation system of the multiple trait model 1 was solved with preconditioned conjugate gradients method (PCG, Lidauer *et al.*, 1999; Ducrocq and Druet 2003) together with the iteration on data technique. All four PCG vectors plus right-hand-sides of the equation system were stored in double precision. As preconditioners, block diagonals were chosen for all the random effects, and scalar diagonals for all the fixed effects. Solutions of all effects from a previous evaluation were used as priors for current genetic evaluations. Phantom parents were grouped and merged automatically based on the country of origin, four selection paths and birth year of animal and pre-defined minimum number of animal per group. Trait values were scaled to a similar variance in order to make genetic evaluations numerically more stable. For monitoring convergence of the iteration process, three types of convergence criteria (CC) were calculated: normal CC which was defined as logarithm of squared solution differences between two consecutive rounds of iteration over squared solutions of the current round, relative PCG right-hand-side CC (Tsuruta *et al.*, 2001), and maximum changes in solutions between two rounds.

2.5. Approximating reliability values of proofs and calculating daughter yield deviations

The multi-trait effective daughter contribution method (MTEDC, Liu *et al.*, 2004) was applied to approximate reliability values of proofs of all the fertility traits, including the derived, combined trait DO. Reliability values for fertility index was also calculated.

Using the method (Liu *et al.*, 2004) developed for test day model, yield deviations of female animals and daughter yield deviations of bulls were computed and also their associated effective daughter contribution based on the MTEDC procedure. Two sets of EDC were made available for either single trait or multiple trait MACE (Jorjani 2006).

3. Results

3.1. Selection of fertility traits for routine genetic evaluation

In the current genetic evaluation system paternal genetic effect is fitted as a correlated trait to maternal genetic effect for the non-return rate to 90 days. Because a very low heritability estimate was obtained in a parameter estimation for the paternal genetic effect, 0.002, it was decided to remove this effect from the new fertility model for the non-return rate traits. The decision of dropping this correlated genetic effect is also in agreement with the international harmonisation of fertility traits.

In the initial phase of this project DO and calving interval (CI) were chosen as evaluated traits within the multi-trait model. It was found that the proofs of DO or CI had much higher variation than a test run with a single trait model. The higher proof variances were caused by the fact that the information of the interval from calving to first insemination and/or the interval from first to last inseminations were double counted in the evaluation model, because CF and FLc are parts of DO and CI. Based on this finding, it was decided to include the component fertility traits CF and FLc in genetic evaluation and to derive proofs for DO as sum of the proofs of CF and FLc.

3.2. Genetic parameter estimates

Estimates of genetic parameters are presented in Table 2. On a low level, the heritability of the interval trait CF was found to be almost three times as high as for the cow's conception traits NRc and FLc. Heritability estimates of conception traits were similar for virgin heifers and cows.

The NR56 traits and CF were found to have very low genetic correlations. Because NRc was significantly lower correlated with DO than the interval traits CF and FLc, cow non-return rate NRc accounted for a much smaller proportion of variation in the whole conception complex than the interval traits.

Table 2. Heritabilities on the diagonal, genetic correlations above diagonal, and residual correlation of virgin heifer traits and permanent environmental correlations of cow traits below diagonal (units: % for NR and days for the interval fertility traits).

Trait	FLh	NRh	CF	NRc	FLc	DO	Ratio of residual variance	Ratio of cow p.e. variance	Genetic standard deviation	Phenotypic variance
FLh	**.014**	-.53	.17	-.25	.48	.37	.986		7.44	3949
NRh	-.49	**.012**	-.02	.63	-.15	-.09	.988		4.77	1895
CF			**.039**	.05	.37	.86	.851	.110	6.92	1228
NRc			.13	**.015**	-.39	-.18	.949	.036	5.95	2359
FLc			.30	-.37	**.010**	.78	.961	.029	4.88	2383
DO						**.026**			9.83	3695

3.3. Genetic trends of fertility traits

Figures 1 and 2 show genetic trends of the virgin heifer and cow fertility traits in Holstein A.I. bulls, approximately 1000 bulls per year, having at least 50 daughters in heifer trait NRh or cow trait CF. Unfavourable trends were obtained for all of the fertility traits. Between 1990 and 2001 there was an increase of about 7.4 days in DO, which amounted to 75% of its genetic standard deviation. In the same period proofs of cows' non-rate rate dropped 2.77% (47% of genetic standard deviation) and proofs of FLc increased 4.53 days (90% of genetic standard deviation). It is important to keep in mind that a much higher progress in production was achieved.

Unfavourable proof correlations were found between milk yield and the fertility proofs: CF .30, NRc -.09, FLc .36, and DO .37. The fertility traits were favourably correlated with combined longevity: CF -.39, NRc .06, FLc -.38, and DO -.46.

3.4. Verification studies and genetic trend validations

Genetic trends of the new fertility model were validated using Interbull trend validation method 3, in which current proofs of bulls were compared to their proofs four years ago. For bulls with at least 100 daughters, NR56 proofs of the current model have a correlation of c.a. 0.9 with NR maternal proofs from the current single trait model. Averages and variances of proofs of the fertility traits were examined over several factors, e.g. birth years of female animals. Solutions of the other effects in the genetic evaluation model, like p_k, were investigated using associated information, e.g. number of insemination records of cows.

4. Discussion

A multiple trait model was developed for evaluating five fertility traits of dairy cattle in Germany. The paternal genetic effect for non-return rates was removed from the model as a result of very low heritability and international harmonization of fertility trait definition. Instead of including combined fertility trait DO in the model, the component traits CF and FLc were evaluated in the genetic evaluation besides the NR traits. Proofs of the combined trait DO were derived subsequently. The model with component traits was preferred to those with the combined traits, because it avoided double counting of information of CF or FLc. Low heritability values were obtained for all traits, ranging from 1% to 4%. The heritability estimates were lower than those in Canada where a similar multi-trait model was developed. Genetic and environmental correlations among the traits ranged from low to moderate. Notably unfavourable genetic trends were found in all the fertility traits.

5. Further development

An index for female fertility including the five traits NRh, FLh, CF, NRc and FLc are to be developed. This index should have a high correlation to the combined fertility traits DO and CI. In addition, a ‘fertilisation ability’ for service sires will be derived from the new model. An index for general male fertility could be calculated as $\mu + \hat{\mathrm{F}}_m$, where μ is population average of NR56. This index ranks fertilising ability of service sires over all years. Besides the general male fertility index, a ranking of male fertility for current year class could be defined as $\mu + \hat{\mathrm{F}}_m + \hat{t}_{mn}$, where $\hat{t}_{mn}$ denotes solution of service sire *m* in the current year class *n*.

6. References

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Figure 1. Genetic trends of virgin heifer fertility traits in Holstein bulls.

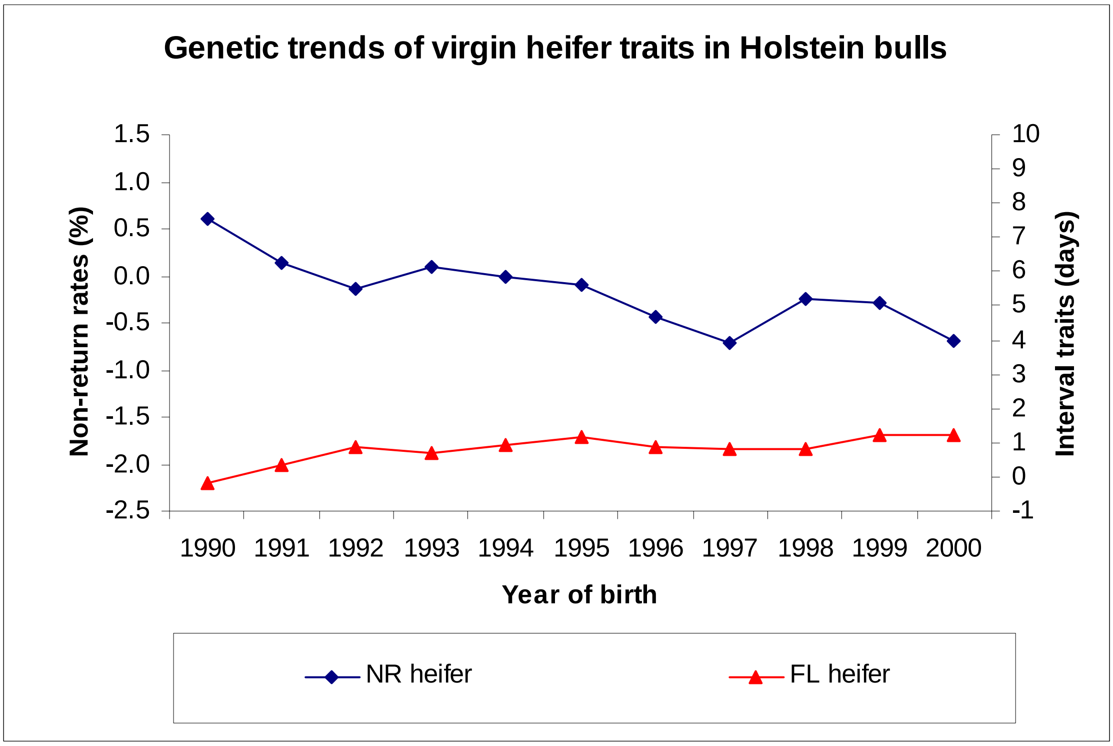

Figure 2. Genetic trends of cow fertility traits in Holstein bulls.