Breeding Values for Daughter Fertility in Norwegian Dairy Cattle; Data Quality and Model Validation

I. M. A.-Ranberg*[1,2], G. Klemetsdal[1], B. Heringstad[1], M. Svendsen[2] and T. Steine[2].

[1]*Department of Animal Science, Agricultural University of Norway, Box 5025, N-1432 Ås, Norway.*
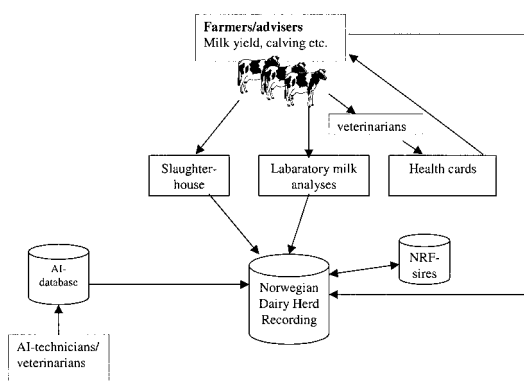[2]*GENO Breeding and A.I. Association, Box 5025, N-1432 Ås, Norway.*
(* Corresponding author, e-mail: ina.ranberg@ihf.nlh.no)

1. Introduction

In Norwegian Dairy Cattle (NRF) female fertility has been included in the total merit index for sires since 1972. The relative weight of the trait has increased from 8 to 15% over the period. The fertility trait selected for in NRF has been non-return rate in virgin heifers. Until 2000, evaluation was based solely on daughter information for the last batch of progeny tested sires, but since then the data from the entire period was used. The model has been an univariate linear sire model.

A natural extension is to include non-return rate in first lactation. The main aim was to validate two bivariate models, with and without a fixed effect of year (contemporary group effect fixed or random).

Figure 1. Data flow in Norwegian Dairy Herd Recording.

2. Material and Methods

2.1 Data

In Norway information on inseminations, done either by AI-technicians or veterinarians, are reported into the AI-database run by GENO

(Figur 1). The AI-technicians and veterinarians get paid based on inseminations reported and this contribute to high quality of the information in the AI-database. In 2001 there were only 31 farmers (GENO, 2002) nationwide that were inseminating in their own herd. From the AI-database recorded inseminations are transferred to the Norwegian Dairy Herd Recording. This databank was established in 1978 and contains information from many sources (Figure 1). In 2001, 95.4 % (266.235 cows) of all Norwegian cows and 91.9 % (18.125 herds) of all Norwegian herds took part in the Norwegian Dairy Herd Recording, (TINE, 2002). During the last decade, each year on average of 37.6% of the cows have been bred by NRF test bulls. The number of actual daughters per test bull ranges from 250 to 300 for the fertility trait.

In the analyses, information on heifers and first lactation cows with first inseminations from September 1., 1978, to Mars 15., 2001 were extracted from Norwegian Data Herd Recording. Only daughters of bulls that tested after 1979 were used. Heifers and cows with recorded reproductive veterinary treatments, that were culled within 56 days after first insemination, recorded natural service at first mating or irregular age at first insemination were discarded. In 2001, 2.5% of heifers and 4.7% of first lactation cows were treated for reproductive disorders. The traits analysed were 56 days non-return rate of heifers (NR56D0) and first lactation cows (NR56D1). Double insemination was defined if a new insemination occurred within 0-5 days after first insemination. Summary statistics of data used in the analyses are shown in Table 1.

In case of a non-reported natural mating, the cow is falsely assumed pregnant. Lack of reporting natural mating will increase the proportion of heifers or cows with prolonged interval, from insemination to calving (ICI). To

check whether reporting of natural mating has changed over time, data extract were restricted to heifers or cows having a reported calving after only one insemination. Figure 1 shows frequency of heifers and cows with ICI longer than 295 days and indicating no change in reporting of natural matings over time.

2.2 Model

Two bivariate mixed linear sire models were used to estimate variance components and genetic change. Model 1 was selected (A.-Ranberg *et al.,* 2002) to estimate breeding values for non-return rate in heifers and this model was used for both traits:

$$Y_{ijklmn} = A_i + MY_j + DI_k + hy_l + s_m + e_{ijklmnn}$$

where;

Y_{ijklmn} is the observation of 56 days non-return of daughter, A_i is fixed effect of age i at first insemination in weeks, MY_j is fixed effect of month x year at first insemination class j, DI_k is fixed effect of double insemination k, hy_l is random effect of herd x year at first insemination class l, s_m is random effect of sire m and e_{ijklmn} is the random residual term.

In Model 2, the fixed effect of month x year was replaced with fixed effect of month at first insemination for first lactation cows.

An additive relationship matrix containing the relationships between sires was included in the analyses. (Co)variance components for random effects were estimated with REML using the program VCE4 (Neumaier and Groeneveld, 1998). PEST (Groeneveld & Kovac, 1990) was used to calculate breeding values for sires.

2.3 Model Validation

A method described by Boichard *et al.* (1995) was used for validation of the two models. This method has the underlying assumption that successive evaluations of the same bull have the same expectation, equal to their true breeding value, and should display only random variation associated with new information. Ten sub-sets of data were created from the dataset used for estimation of variance components (Table 1), and successive sire evaluations were carried out with increasing amounts of information. The data sets were restricted by year of first insemination of heifers and first insemination of first lactation cows from 1978 up until 1981, 1985, 1989, 1993 and 1997, respectively. To test bias of genetic change, the following weighted regression model was used (Boichard *et al.,* 1995):

$$v = Xg + ub + t\delta + e$$

where;

u and v are vectors of sire evaluations, u based on data of the first n daughters and v both on the data used for u and on subsequent data, g is an effect of birth year of sire, t is a known vector based on the number of additional daughters each year, δ is an estimate of the bias of genetic change and e is the random error term. Weights and t were calculated as described by Boichard *et al.* (1995).

3. Results and Discussion

Over the last 20 years, the phenotypic increase of non-return rate in heifers and first lactation cows were 3.7 and 2.8 % units, respectively.

REML estimates of variance components and heritabilities for the two models are given in Table 2. The variance components were all small and both models gave similar estimates. Model 2 gave slightly larger heritabilities than model 1. The heritabilities were 1.17% and 1.46% for heifers and first lactation cows, respectively. In both models, the genetic correlation between non-return in heifers and first lactation cows were 0.63. Genetic change for NR56D0 and NR56D1 estimated with the two models are presented in Figure 3. Model 2 without a fixed contemporary group showed the strongest positive trend. Results from model validation are shown in Table 3. None of the models in any of the four periods showed significant bias ($p < 0.01$).

4. Conclusion

The strength of the Norwegian fertility data is the recording of all AI-data and that fertility data can be combined with a set of other information e.g. health traits for a long period of time. This gives the opportunity to estimate genetic change, which were different between models when contemporary group effects were modelled as fixed or random. To avoid confounding between environmental and genetic effect on fertility, Model 1 is preferred to estimate genetic change. The method used for validation of
trend was not able to detect bias in the model pointing at the need for alternative approach when validating models with our data.

5. References

A.- Ranberg, I. M., Klemetsdal, G., Heringstad, B. & Svendsen, M. 2002. Heifer fertility in Norwegian Dairy Cattle; genetic parameters and genetic change. *In manuscript.*

Boichard, D., Bonaiti, B., Barbat, A. & Mattalia, S. 1995. Three methods to validate the estimation of genetic trend for dairy cattle. *J. Dairy Sci. 7,* 431-437.

GENO, 2002. Annual report 2001. Hamar, 48 pp.

Tine, 2002. Annual report 2001. Ås, 98 pp.
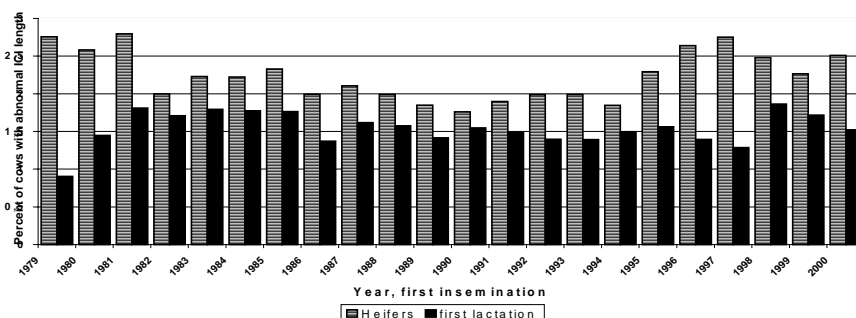
Figure 1. Percentage heifers and first lactation cows with only one insemination and more than 295 days from first insemination to calving.

Table 1. Summary statistics of data used in the analyses.

	Heifers	First lactation
Records, no.	1.755.107	1.1485.16
Sires (with daughters), no.	2984	2832
Sires in pedigree file, no.	3312	3312
Daughters per sire, mean no.	588	406
Herd x year classes, no.	409.135	353.162
Records per herd x year class, mean no.	4,3	3,3
Double insemination, %	8,4	10,5
Non-return rate within 56 days, %	74,7	66,9
Insemination, year	1978 – 2001	1978 - 2001

Table 2. Variance components and heritability estimates of non-return rate within 56 days in heifers and first lactation cows and genetic correlation between the two traits [1].

	Model 1		Model 2	
	Heifer	First lactation	Heifer	First lactation
Sire variance	5.45×10^{-4}	7.25×10^{-4}	5.50×10^{-4}	8.07×10^{-4}
Herd X year variance	3.96×10^{-3}	6.56×10^{-3}	3.96×10^{-3}	6.55×10^{-3}
Residual variance	0.18	0.21	0.18	0.21
Total variance	0.18	0.22	0.19	0.22
Heritability ($4\sigma_s^2$/total variance)	1.16×10^{-2}	1.32×10^{-2}	1.17×10^{-2}	1.46×10^{-2}
Genetic correlation	0.63		0.63	

[1]Contemporary group effect modelled as: Model 1, herd x year random and month x year of first insemination fixed; Model 2, herd x year random and month of first insemination fixed.
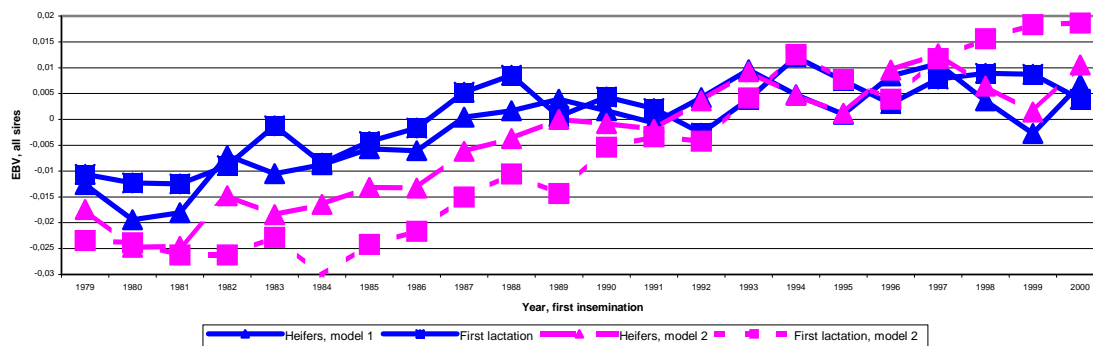
Figure 3. Genetic change of non-return rate within 56 days in heifers and first lactation cows, for the two models.

Table 3. Estimated bias of annual genetic change of 56 days non-return rate from regression analyses of sires estimated breeding values on the same sires breeding values estimated at an earlier stage, for the two models.

	Evaluation as			Bias	
Model	Dependent variable	Independent variable	Estimate	SE	P > |t|
Model 1	1985	1981	-0.0006	0.0038	0.8821
Heifers	1989	1985	-0.0001	0.0030	0.9580
	1993	1989	-0.0014	0.0034	0.6741
	1997	1993	0.0020	0.0028	0.4828
Model 1	1985	1981	0.0020	0.0057	0.7303
First lactation	1989	1985	0.0026	0.0049	0.6022
	1993	1989	-0.0004	0.0059	0.9475
	1997	1993	0.0014	0.0043	0.7463
Model 2	1985	1981	-0.0013	0.0038	0.7329
heifers	1989	1985	0.0006	0.0012	0.6156
	1993	1989	0.0001	0.0038	0.9720
	1997	1993	0.0026	0.0029	0.3670
Model 2	1985	1981	-0.0003	0.0052	0.9511
(first lactation)	1989	1985	0.0017	0.0047	0.7137
	1993	1989	0.0045	0.0065	0.4885
	1997	1993	0.0031	0.0040	0.4307

[1]For hypothesis, bias estimate = 0.