Short Communication: Validation of Two Animal Models for Estimation of Genetic Trends for Female Fertility in Norwegian Dairy Cattle

I. M. Andersen-Ranberg,*† G. Klemetsdal,* and B. Heringstad*

*Department of Animal Science, Agricultural University of Norway, N-1432 Ås, Norway and

†GENO Breeding and A.I. Association, N-1432 Ås, Norway

ABSTRACT

Two animal models were compared with respect to potential bias in genetic trend estimates for female fertility and for their predictive ability. In addition to either a fixed effect for month of first insemination or for month-year of first insemination, the models had fixed effects of age and double insemination and random effects of herd-year and animal. The model with a fixed effect of month of first insemination had a larger positive genetic trend for 56-d nonreturn rate in virgin heifers (0.16% yr), smaller downward bias, and somewhat higher predictive ability. These results demonstrate the importance of verifying models to be used in the calculation of breeding values.

(**Key words:** female fertility, genetic trend, model validation)

Abbreviation key: NRF = Norwegian dairy cattle, NR56D0 = 56-d nonreturn rate in virgin heifers.

In a previous analysis of female fertility in Norwegian dairy cattle (NRF) (Andersen-Ranberg et al., 2003), 6 linear sire models were compared. All models resulted in favorable, although different, estimates of genetic change of 56-d nonreturn rate in virgin heifers (NR56D0). However, the method used to validate estimates of genetic change, method 3 of Boichard et al. (1995), was not able to detect a biased trend in any of the 6 models. Prediction of randomly excluded observations showed that models treating herd-year effect as random were preferred as they had a smaller prediction error than models treating herd-year as fixed, in accordance with the recommendation by Ugarte (1992). However, the predictions did not distinguish between 2 models with 1) a fixed effect of month of first insemination

(model 1, corresponding with model 4 of Andersen-Ranberg et al., 2003) or 2) a fixed effect of month-year of first insemination (model 2, corresponding with model 6 of Andersen-Ranberg et al., 2003). Model 2 allows for separating the environmental trend common to all herds from genetic trend. The 2 sire models showed rather different results; the estimated genetic change was nearly 4 times larger for the model corresponding to model 1. Analyzing the data with an animal model would allow us to validate the 2 competing models with the second method of Boichard et al. (1995), which was the objective of this study.

With the second method of Boichard et al. (1995), daughter deviations of bulls (observations corrected for dam's breeding value, and all the effects included in the model, except daughter's breeding value) were analyzed for fixed effects of sire and year of use of sire. The year of use effect has an expectation of zero and should not be significantly different from zero when the estimate of genetic trend is unbiased.

The trait analyzed was NR56D0 (0 = nonreturn within 56 d, and 1 = return within 56 d after first insemination), with data from September 1, 1978, to December 1, 1998. These are the same data as analyzed by Andersen-Ranberg et al. (2003), except that in the present paper, the data were restricted to cows with a first insemination before December 1, 1998, as organized pedigrees of both females and males were only available until February 1999. A total of 1,463,005 NR56D0 records were analyzed, and the pedigree file included a total of 1,988,536 animals. In addition to either a fixed effect of month of first insemination for model 1, or a fixed effect of month-year for model 2, the 2 competing models had fixed effects for age and double insemination, and random effects of herd-year and animal. Breeding values were calculated using iteration on data routines in the DMU package (Jensen and Madsen, 1994). Variance components derived from results of Andersen-Ranberg et al. (2003) were 2.58×10^{-3} and 2.19×10^{-3} for the animal effect, and 4.05×10^{-3} and $4.04 \times$

Received June 3, 2003.

Accepted August 13, 2003.

Corresponding author: I. M. Andersen-Ranberg; e-mail: ina.ranberg@ihf.nlh.no.

Figure 1. Genetic trend of 56-d nonreturn (NR56D0) in virgin heifers, shown as mean EBV per year of first insemination. Model 1 with fixed effects of age at first insemination, month of first insemination and double insemination, and random effects of herd-year, animal, and residual. Model 2 was equal to Model 1 except that fixed effect of month-year of first insemination replaced month of first insemination.

10^{-3} for the herd-year effect, for models 1 and 2, respectively. The residual variance was 1.82×10^{-1} for both models.

To test bias of genetic trend, the following model described by Boichard et al. (1995) was used:

$$d_{ijk} = s_i + t_m + e_{ijk},$$

where d_{ijk} is the deviation of daughter k of sire i obtained in year j , s_i is the fixed effect of sire i , t_m is the fixed effect of the year m of use of sire i , and e_{ijk} is the error random term. The year of use was defined as: $m = j - j_0 + 1$, where j is as previously defined, and j_0 is the year of first insemination of the first daughter of sire i .

The 2 models were also compared with respect to their ability to predict randomly excluded observations.

From herd-year groups containing more than 2 heifers, 10,000 records were deleted at random. The predicted ($\hat{y}$) values for the 10,000 records were obtained from solutions for the different effects in the 2 models. The observed NR56D0 (y) had the value 1 or 0. The correlation ($r_{\hat{y},y}$) between y and $\hat{y}$ was used to evaluate the models.

The genetic trends for models 1 and 2 are shown in Figure 1. Both models showed favorable genetic trends for fertility, amounting to an annual genetic improvement for NR56D0 of 0.16% ($P < 0.01$) and 0.07% ($P < 0.01$) for models 1 and 2, respectively. The corresponding estimates from sire models were 0.15 and 0.04%, respectively (Andersen-Ranberg et al., 2003).

The use of sires is illustrated in Figure 2, with m values of 1 to 3 for first-crop daughters and with larger

Figure 2. Number of daughters by year of use of sire, ($m = j - j_0 + 1$, where j is year of first insemination of a daughter and j_0 is year of first insemination of the first daughter of sire).

Figure 3. Least squares mean (LSM) of daughter deviation for 56-d nonreturn in virgin heifers by sires' year of use. Model 1 with fixed effects of age at first insemination, month at first insemination and double insemination, and random effects of herd-year, animal, and residual. Model 2 was equal to Model 1 except that fixed effect of month-year of first insemination replaced month of first insemination.

values for second-crop daughters. The ANOVA of daughter deviations showed significant bias for both models, although it was much larger for model 2 ($P < 0.0004$) than for model 1 ($P < 0.046$). Figure 3 shows that daughter deviations decreased between first- and second-crop daughters for both models, demonstrating a downward bias. Consequently, the true genetic trends should be larger than those found in this study.

For both models, the genetic trend calculated with the animal model was close to the estimates of genetic change from the sire model, but somewhat larger. This was not expected as the sire model does not account for genetic change in dams, causing genetic change estimates from sire models to be generally larger than trend estimates from animal models. Hence, another effect must induce the enhancing trend. A closer look shows that the difference in trends between sire and animal model was largest for the most biased model, model 2. The correlation between predicted and observed values was higher in the animal models than in the sire models, being 0.37 and 0.35 for models 1 and 2, respectively, and 0.108 and 0.107 for corresponding sire models (Andersen-Ranberg et al., 2003). This allows improved separation of model effects in the animal model, and this affects the genetic trend.

Contrary to the third method of Boichard et al. (1995) their second method was able to reveal bias in genetic

trend of NR56D0 in our data. The analysis pointed out that the true genetic trend is larger than the calculated one for both models. However, as the bias was smaller in model 1 than model 2, and the predictive ability was higher for Model 1, this model is to be preferred in genetic analysis of NR56D0 in NRF.

ACKNOWLEDGMENTS

Access to the data was granted in agreement No. 005.2000 by the Norwegian Dairy Herd Recording System on February 24, 2000. GENO Breeding and A. I. Association is acknowledged for providing pedigree information on sires.

REFERENCES

- Andersen-Ranberg, I. M., B. Heringstad, G. Klemetsdal, M. Svendsen, and T. Steine. 2003. Heifer fertility in Norwegian dairy cattle: Variance components and genetic change. *J. Dairy Sci.* 86:2706–2714.
- Boichard, D., B. Bonaiti, A. Barbat, and S. Mattalia. 1995. Three methods to validate the estimation of genetic trend for dairy cattle. *J. Dairy Sci.* 78:431–437.
- Jensen, J., and P. Madsen. 1994. DMU: A package for the analysis of multivariate mixed models. Pages 45–46 in *Proc. 5th World Congr. Genet. Appl. Livest. Prod. Guelph, Canada. Comput. Stat. Software* 22.
- Ugarte, E., R. Alenda, and M. J. Carabaño. 1992. Fixed or random contemporary groups in genetic evaluations. *J. Dairy Sci.* 75: 269–278.