J. Dairy Sci. 88:2190–2198

Comparison Between Bivariate Models for 56-Day Nonreturn and Interval from Calving to First Insemination in Norwegian Red

I. M. Andersen-Ranberg,[1,2] B. Heringstad,[1,2] D. Gianola,[1,3] Y. M. Chang,[3] and G. Klemetsdal[1]
[1]Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, N-1432 Ås, Norway
[2]GENO Breeding and AI Association, N-1432 Ås, Norway
[3]Department of Dairy Science, University of Wisconsin, Madison 53706

ABSTRACT

A bivariate threshold-linear (TL) and a bivariate linear-linear (LL) model were assessed for the genetic analysis of 56-d nonreturn (NR56) and interval from calving to first insemination (CFI) in first-lactation Norwegian Red (former Norwegian Dairy Cattle) (NRF). Three different datasets were used to infer genetic parameters and to predict transmitting abilities for NRF sires. Mean progeny group sizes were 147.8, 102.7, and 56.5 daughters, and the corresponding number of sires were 746, 743, and 742 in the 3 datasets. Otherwise, the structures of the 3 datasets were similar. When the TL model was used, heritability of liability to NR56 was 2.8% in the 2 larger datasets and 3.8% in the smallest dataset. In the LL model, the heritability of NR56 in the largest dataset and in the 2 smaller datasets was 1.2 and 0.9%, respectively. For CFI, the heritability was similar in TL and LL models, ranging from 2.4 to 2.7%. The small heritability of the 2 reproductive traits implies that most of the variation is environmental and that large progeny groups are required to get accurate sire PTA. The point estimates of the genetic correlation between NR56 and CFI were near zero in both models. The 2 bivariate models were compared in terms of predictive ability using logistic regression and a χ^2 statistic based on differences between observed and predicted outcomes for NR56 in a separate dataset. Comparison was also with respect to ranking of sires and correlations between sire posterior means (TL model) and PTA (LL model). We found very small differences in ability to predict NR56 between the 2 bivariate models, regardless of the dataset used. Correlations between sire posterior means (TL) and sire PTA (LL) and rank correlations between sire evaluations were all >0.98 in the 3 datasets. At present, the LL model is preferred for sire evaluations of NR56 and CFI in NRF. This is because the LL model is less computationally demanding and more robust with respect to the structure of the data than TL.
(**Key words:** female fertility, genetic parameter, model comparison, bivariate threshold model)

Abbreviation key: CFI = interval from calving to first insemination, **LL** = linear-linear, **MCMC** = Markov chain Monte Carlo, **NR56** = 56-d nonreturn rate, **NRF** = Norwegian Red, **TL** = threshold-linear.

INTRODUCTION

After milk production and mastitis, fertility is the trait receiving the most emphasis in the breeding program for Norwegian Red (former Norwegian Dairy Cattle) (**NRF**). At present, the relative weight on fertility in the total merit index used for selection of sires is 15%. Fertility traits used for selection of NRF sires are 56-d nonreturn rates (**NR56**) in first-lactation cows and in virgin heifers. Both traits are scored as binary response variables, and genetic evaluation is currently based on a bivariate linear model. Average number of daughters per proven sire has been between 200 and 300.

Roxström et al. (2001) and Andersen-Ranberg et al. (2005) found relatively high correlations between fertility in heifers and in first-lactation cows, varying from 0.54 to 0.67. However, because the estimated correlations are not 1, the 2 traits are probably not genetically the same trait (Thaller, 1997). Andersen-Ranberg (2005) concluded that the interval from calving to first insemination (**CFI**) should be included in the fertility index for NRF and reported low correlation between NR56 in first-lactation cows CFI in first-lactation cows. However, in a simulation study, Gates et al. (1999) concluded that genetic correlations involving categorical traits might be underestimated in linear sire models. This leads us to further investigation on the traits NR56 and CFI.

Estimates of heritability for fertility traits are typically low, ranging from 1 to 5% when linear models have been used for statistical analysis (Distl, 1982; Weigel and Rekaya, 2000; Roxström et al., 2001; Wall et al., 2003). A standard linear model assumes that the

Received December 10, 2004.
Accepted February 11, 2005.
Corresponding author: I. M. Andersen-Ranberg; e-mail: ina.ranberg@umb.no.

observed binary response follows a normal distribution, and variance component estimates obtained with such models may be misleading (Hoeschele et al., 1987). For example, heritability is frequency dependent, as the variance of the distribution depends on the mean (Dempster and Lerner, 1950), which implies that observed genetic change may be inconsistent with what would be expected from heritability estimates based on a linear model. Statistically, it is inappropriate to use standard linear model methodology for analyzing categorical response data (Gianola, 1982; Agresti, 1996).

From a genetic point of view, the threshold-liability (**TL**) model (Wright, 1934; Dempster and Lerner, 1950; Falconer and Mackay, 1996) has the theoretical appeal of producing estimates of parameters that are interpretable on an underlying continuous (liability) scale where gene substitutions are supposed to take place. This model was discussed by several authors (Thompson, 1979; Gianola 1982), and the threshold model was developed in practice in the early 1980s (Gianola and Foulley, 1983; Harville and Mee, 1984; Gilmour et al., 1985).

Because of advances in Markov chain Monte Carlo (**MCMC**) methods, such as Gibbs sampling, it has become possible to carry out exact (within the limits of Monte Carlo error) Bayesian analysis of large linear and nonlinear hierarchical models (Gilks et al., 1996; Wang, 1998; Sorensen and Gianola, 2002). The MCMC methods avoid the need for numerical integration by taking repeated samples from the posterior distributions of interest. A Bayesian MCMC implementation of the threshold model in a quantitative genetic context can be found in Sorensen et al. (1995).

Despite the theoretical appeal of the threshold model, there is an issue of how much difference it can make in a given animal breeding setting. For example, the simulation study of Meijering and Gianola (1985) compared sire evaluations obtained with linear and threshold models and found an advantage of the latter in situations with moderate or high heritability in the liability scale and low incidence (<25%) of the trait.

Studies with field data have reported very high correlations between sire PTA obtained from linear and threshold models (Weller et al., 1988; Heringstad et al., 2003). Conversely, Varona et al. (1999) found that a bivariate TL model for birth weight and calving ease had better predictions than the corresponding bivariate linear-linear (**LL**) model. It seems sensible to examine whether or not a threshold model can enhance genetic improvement of fertility of dairy cattle, as most fertility-related traits are recorded on a categorical scale.

In this study, heritability was estimated for liability to NR56 and for CFI, as well as their genetic correlation, in first-lactation NRF cows. A bivariate model was fitted, in which NR56 was regarded as a threshold trait, and CFI was treated as Gaussian. A main objective of this paper was to compare the bivariate sire TL with a bivariate LL model in terms of estimates of genetic parameters and of sire evaluations for NR56 and CFI. We also wanted to examine how differences between models are affected by varying progeny group sizes.

MATERIALS AND METHODS

Data

Records for NR56 and CFI in first-lactation NRF cows calving from 1991 through 1997 were extracted from a dataset reported by Andersen-Ranberg et al. (2005). Only records from first-batch daughters of sires having their first progeny test from 1992 through 1997 were used in the analysis. The trait NR56 was defined as a binary trait (0 = return; 1 = nonreturn) based on whether or not the cow had a second insemination within 56 d after the first insemination; CFI values ranged from 20 to 210 d. All cows had information on each of the 2 traits. Only cows out of sires with at least 20 daughters were included, and each of the herd classes was required to contain at least 5 first-lactation cows. The set of all records meeting these edits is referred to as DATA.

Four thousand herds were randomly chosen from DATA, yielding a data subset (TEST) with 41,467 records, which was used for model comparison (predictive ability) but not for parameter estimation. Three different datasets were created with decreasing mean progeny sizes. This was done because we wanted to investigate the effect of decreasing mean progeny group using the TL vs. LL model. The subset of records in DATA, other than those in TEST, was termed DATA1. Herds were randomly deleted from DATA1, which had 110,245 records, to make 2 smaller datasets (DATA2 and DATA3) with intended average sire progeny group sizes of 100 and 50 daughters, respectively. Hence, DATA3 was a subset of DATA2, which, in turn, was contained in DATA1. The actual mean progeny group sizes were 147.8, 102.7, and 56.5 daughters per sire in DATA1, DATA2, and DATA3, respectively.

Table 1 shows summary statistics for the 4 datasets. A total of 746, 743, and 742 NRF sires were represented in DATA1, DATA2, and DATA3, respectively (Table 1), whereas 742 were in TEST. A between-sire additive relationship matrix caused by sires and maternal grandsires was built by tracing back the pedigree through sires for as many generations as possible. This resulted in pedigree files with a total of 1120, 1117, and 1116 males for DATA1, DATA2, and DATA3, respectively (Table 1). Number of sires, cows per herd, mean NR56, and mean CFI were similar in all 4 datasets.