58th Annual Meeting of the European Association for Animal Production in Dublin, Ireland
Session 10, Abstract 0699

Estimation of breeding values for test day somatic cell score and clinical mastitis using threshold model

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Introduction

Genetic evaluations of udder health traits for Finnish Ayrshire cattle are estimated within the joint Nordic genetic evaluation. The current model is based on multitrait linear sire model for lactation average (LA) records of somatic sell score (SCS) and clinical mastitis (CM). LA models do not use effectively the information available for SCS. Moreover, linear model discards the fact that CM is a categorical trait. The analysis of CM with correlated trait using threshold model is theoretically more appropriate. This leads to a model with two different data structures, where the other trait is longitudinal and the other is lactation wise.

The objective of this study was to compare a bivariate test-day (TD) threshold model with bivariate linear TD and LA models for the genetic evaluation of SCS and CM traits.

Material and methods

The data used were 323336 first lactation records and 1.5 million TD records of Finnish Ayrshire cows with first calving from 1995 to 2006. The pedigree had 6790 sires.

The three models compared were:
Model 1) Bivariate linear model based on LA SCS and CM records

$$\begin{bmatrix}\mathbf{SCS}_{\mathrm{LA}}\\ \mathbf{CM}_{\mathrm{LA}}\end{bmatrix} = \underbrace{\mathbf{hy5}+\mathbf{ym}+\mathbf{age}}_{\text{fixed effects}} + \underbrace{\mathbf{hy1}+\mathbf{s}+\mathbf{e}}_{\text{random effects}}$$

Model 2) Bivariate linear model based on TD SCS and LA CM

$$\begin{bmatrix}\mathbf{SCS}_{\mathbf{TD}}\\ \mathbf{CM}_{\mathbf{LA}}\end{bmatrix} = \underbrace{\mathbf{hy5}+\mathbf{ym}+\mathbf{age}+\begin{bmatrix}\sum_{r=0}^{1}\phi(d)_r\,\mathbf{ys}_r\\ \mathbf{0}\end{bmatrix}}_{\textbf{fixed effects}}$$

$$\underbrace{+\begin{bmatrix}\mathbf{0}\\ \mathbf{hy1}\end{bmatrix}+\begin{bmatrix}\mathbf{htd}\\ \mathbf{0}\end{bmatrix}+\begin{bmatrix}\sum_{r=0}^{1}\phi(d)_r\,\mathbf{pe}_r\\ \sum_{r=0}^{0}\phi(d)_r\,\mathbf{pe}_r\end{bmatrix}+\begin{bmatrix}\sum_{r=0}^{1}\phi(d)_r\,\mathbf{s}_r\\ \sum_{r=0}^{0}\phi(d)_r\,\mathbf{s}_r\end{bmatrix}+\mathbf{e}}_{\textbf{random effects}}$$

Model 3) Bivariate threshold model based on TD SCS and LA CM on the underlying liability scale

$$\begin{bmatrix} \mathbf{SCS_{TD}} \\ \lambda_{\mathbf{CM_{LA}}} \end{bmatrix} = \mathbf{Model\ 2}$$

Covariances for models 1 and 2 were calculated from a sample of first lactation data (Negussie et. al. 2007). The covariances for threshold model were transformed as proposed in Dempster and Lerner (1950). Models were solved by the MiX99 breeding value estimation software (Vuori et. al. 2006). Program uses preconditioned conjugate gradient algorithm and iteration on data. Estimation of threshold model was based on empirical Bayes method (Janss and Foulley 1993), which was implemented in MiX99.

Comparisons between models were made for CM in terms of predictive ability (correlations of evaluations from two data sets, created by splitting original data into half within daughter groups) and number of common sires in the rank of the top 50 sires. Both statistics were calculated for group of young sires born 1996-1998 with at least 20 daughters (N=487).

Results

Predictive ability increased along with the increase in model complexity. Correlations of evaluations from two split data sets were 0.55, 0.60 and 0.62 for the models 1, 2 and 3, respectively.

In the rank of top 50 bulls, there were 32 common sires between models 1 and 2, and 31 common sires between models 1 and 3. Furthermore, 37 common sires were found in the lists of top 50 bulls for models 2 and 3.

Solving times with MiX99 were <1min, 5min and 30min for models 1, 2 and 3, respectively.

Conclusions

New methods are developed in order to get more accurate genetic evaluations. We tested the effect of bivariate threshold model for TD SCS and binary CM in Finnish Ayrshire data. Based on our results, TD models were better than LA model, and the threshold model showed little advantage over linear model. However, estimation by linear models was computationally less demanding than by nonlinear threshold model.

References

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