

ESTIMATION OF GENETIC PARAMETERS FOR FIRST LACTATION TEST DAY MILK PRODUCTION USING RANDOM REGRESSION MODELS

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SUMMARY

Test day data on 6,310 primiparous Finnish Ayrshire cows were used in the estimation of genetic parameters for daily milk production. Two different random regression (RR) sub-models were fitted to describe individual lactation curves, a five parameter logarithmic (ASM) and a normalized fourth order orthogonal (OPM) polynomial. Estimates of heritabilities for test day yields and genetic correlations between individual days obtained by RR models were compared to those from a multitrait (MT) model. (Co)variance components for RR models were estimated using EM-REML and animal model. Significantly higher heritabilities were found with both ASM (0.41-0.58) and OPM (0.29-0.52) compared to those from MT analysis (0.23-0.34). Heritabilities estimated with both ASM and OPM seemed to follow a similar pattern being highest at the beginning and end of lactation. As expected, genetic correlations between consecutive test days were high (0.81-0.98), decreasing when test day intervals increased and turned negative when tests were 200 or more days apart. With the MT model genetic correlation reached its lowest (0.35) between test days 1 and 305.

Keywords: test day model, random regressions, milk production, animal model

INTRODUCTION

The main improvement in using original test day measurements instead of 305 day lactation records to estimate dairy cattle breeding values is that both genetic and environmental effects specific to each test day yield can be considered. Use of this approach gives a more precise definition of the contemporary comparison group, and allows a more accurate description of the changing effects due to pregnancy and stage of lactation. Furthermore, individual deviations from the general shape of the lactation curve can be modelled by random regression (RR) coefficients (Schaeffer and Dekkers 1994). Jamrozik and Schaeffer (1997) reported estimates of heritabilities for daily yields of milk, fat and protein as well as genetic correlations between individual days using the RR model. Based on biological considerations, correlations between yields are subject to criticism, since an antagonistic relationship between early and late lactation existed.

The objective of this study was to estimate genetic parameters for first lactation test day milk yield using two RR approaches and to compare these with estimates computed with a multitrait model (MT). Further improvements of the statistical model are discussed in brief.

MATERIAL AND METHODS

Data consisted of 63,331 test day milk records of 6,310 primiparous Finnish Ayrshire cows from 78 herds, calving between April 1988 and March 1996. (Co)variance components were estimated using EM-REML and AI-REML for RR and MT models, respectively. Test day milk was assumed to be described by the following model:

$$y_{ijklmnop} = \text{age}_i + \text{dcc}_j + \text{herd}_k + \sum_{q=1}^5 b_{q(l)} X_q + \text{HTM}_m + \text{pe}_{n(o)} + \text{RR}_o + e_{ijklmnop}$$

where $y_{ijklmnop}$ is test day milk yield; age_i , fixed effect of calving age class; dcc_j , fixed effect of days carried calf class; herd_k , fixed effect of herd; $b_{q(l)}$, regression coefficients of milk on days in milk (DIM) functions describing the shape of lactation curves within calving month classes l ($X_1=1$, $X_2=\text{DIM}/c$, $X_3=(\text{DIM}/c)^2$, $X_4=\ln(c/\text{DIM})$, $X_5=(\ln(c/\text{DIM}))^2$, $c=305$); HTM_m , random effect of test month of production within the herd; $\text{pe}_{n(o)}$, permanent environmental effect of cow o ; RR_o is the random regression sub-model describing the shape of a lactation curve of an individual cow o and $e_{ijklmnop}$ is the residual pertaining to $y_{ijklmnop}$. The first RR sub-model fitted the same five parameter logarithmic polynomial which describes the lactation curve (Ali and Schaeffer 1987) as a random effect (ASM). Alternatively, a normalized fourth order orthogonal polynomial (Snedecor and Cochran 1980) was fitted (OPM). In the MT approach, lactation was divided into 16 intervals according to DIM at test, and each interval was considered as a different trait. The statistical model included the same fixed effects as above, with the exception that only linear effects of DIM were considered. Random effects were herd-calving year (HY) and animal. (Co)variances for DIM intervals were estimated using 37 trivariate REML runs, and were converted into a continuous covariance function with four polynomials (see, Kirkpatrick *et al.* 1994). For computational reasons, pedigree information was traced for only two generations, resulting in a data set containing 3,037 animals without records.

RESULTS AND DISCUSSION

Both RR models gave unexpectedly high estimates of heritability compared to MT (Table 1). Values from ASM were higher but followed an identical pattern to those reported by Jamrozik and Schaeffer (1997). Highest estimates of heritabilities were observed at the beginning and end of lactation. Estimates with OPM, however, were lower than MT estimates between days 55 and 95 (Figure 1). Jamrozik *et al.* (1996) reported a similar shaped curve for genetic variances, but also observed high estimates of error variances during early and late lactation.

Genetic correlations of daily milk yield between consecutive test days estimated by RR models were high but decreased as the interval between test days increased and became negative when test days were further apart than 200 days (Table 2). A similar pattern of genetic correlations for daily fat and protein yields has been reported (Jamrozik and Schaeffer 1997). With the MT model genetic correlations were uniformly higher (Table 2), reaching its lowest (0.35) between days 1 and 305.

Table 1. Estimates of variance components and heritabilities for daily yields using logarithmic (ASM) and orthogonal (OPM) polynomial random regression and multitrait (MT) models

| DIM | ASM | | OPM | | MT | | | |
|--------|--------------|-------|--------------|-------|-------|--------|--------------|-------|
| | σ_g^2 | h^2 | σ_g^2 | h^2 | HY | e | σ_g^2 | h^2 |
| 5 | 10.374 | 0.58 | 8.823 | 0.51 | 0.635 | 8.775 | 2.675 | 0.23 |
| 25 | 5.781 | 0.44 | 5.357 | 0.39 | 0.737 | 8.500 | 3.043 | 0.26 |
| 45 | 5.111 | 0.41 | 3.804 | 0.31 | 0.838 | 8.226 | 3.328 | 0.29 |
| 85 | 6.071 | 0.45 | 3.687 | 0.31 | 1.030 | 7.730 | 3.682 | 0.32 |
| 125 | 6.990 | 0.48 | 5.061 | 0.38 | 1.184 | 7.381 | 3.805 | 0.34 |
| 165 | 7.111 | 0.49 | 6.042 | 0.42 | 1.278 | 7.275 | 3.765 | 0.34 |
| 205 | 6.715 | 0.47 | 6.239 | 0.43 | 1.289 | 7.505 | 3.628 | 0.33 |
| 265 | 6.838 | 0.48 | 6.969 | 0.46 | 1.094 | 8.688 | 3.392 | 0.28 |
| 285 | 7.600 | 0.50 | 7.697 | 0.48 | 0.962 | 9.353 | 3.339 | 0.26 |
| 305 | 8.987 | 0.55 | 8.963 | 0.52 | 0.790 | 10.173 | 3.313 | 0.25 |
| Effect | σ^2 | | σ^2 | | | | | |
| HTM | 1.179 | | 1.140 | | | | | |
| pe | 4.616 | | 5.570 | | | | | |
| e | 2.871 | | 2.742 | | | | | |

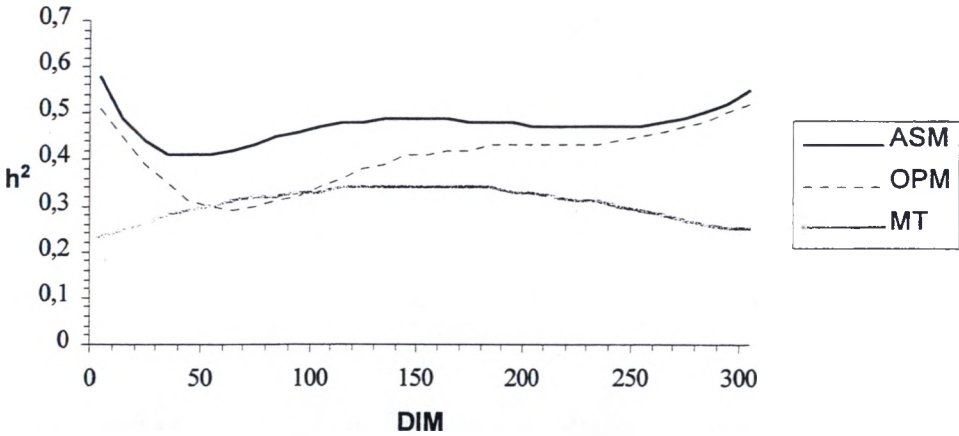


Figure 1. Estimates of heritabilities for daily yields during the lactation using logarithmic (ASM) and orthogonal (OPM) polynomial random regression and multitrait (MT) models.

The RR model estimates were used to construct genetic correlations between 305 day and individual test day yields. Correlations were highest during mid-lactation (0.86-0.97). Lower estimates of genetic correlations were obtained by OPM compared to ASM, particularly at the beginning and end of lactation.

Both RR models led to unexpectedly high estimates of heritabilities for daily milk yield as well as negative genetic correlations between the most distant tests. This may be due to the mathematical characteristics of RR sub-models which could result in an overprojection of genetic variances in the edges of a defined lactation curve trajectory. In RR models the change in genetic variation itself is not modelled. Instead, it is an outcome of multiplication of covariables and corresponding fitted breeding value coefficients. Thus, it becomes unclear whether traditional heritability applies to RR models. It is more likely, however, that part of the environmental variation enters genetic components as a consequence of a simple structure being assumed for within-cow covariances. Fitting random regressions within permanent environmental effects or considering residual covariances between test days, should improve model properties.

Table 2. Estimates of genetic correlations between daily milk on selected test days with MT (upper triangle), ASM and OPM (lower triangle, OPM in italics) models

| DIM | 5 | | 25 | | 85 | | 165 | | 285 | | 305 |
|-----|------|--------------|-------|--------------|-------|--------------|------|-------------|------|-------------|------|
| 5 | - | | 0.91 | | 0.74 | | 0.59 | | 0.41 | | 0.38 |
| 25 | 0.90 | <i>0.97</i> | - | | 0.83 | | 0.69 | | 0.53 | | 0.50 |
| 85 | 0.43 | <i>0.47</i> | 0.65 | <i>0.64</i> | - | | 0.87 | | 0.74 | | 0.72 |
| 165 | 0.17 | <i>0.03</i> | 0.28 | <i>0.19</i> | 0.88 | <i>0.83</i> | - | | 0.88 | | 0.85 |
| 285 | 0.07 | <i>-0.25</i> | -0.22 | <i>-0.25</i> | 0.15 | <i>-0.03</i> | 0.55 | <i>0.41</i> | - | | 0.97 |
| 305 | 0.06 | <i>-0.25</i> | -0.28 | <i>-0.31</i> | -0.02 | <i>-0.23</i> | 0.38 | <i>0.23</i> | 0.98 | <i>0.97</i> | - |

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