Analysis of First Lactation Test Day Milk Yields by Random Regression Model

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Summary

Test day data were used to estimate genetic parameters for daily milk production of first parity Finnish Ayrshire cows. Two random regression (RR) test day models were used: OPM_{PE1}, where normalized orthogonal polynomial RR sub-model was defined for animal effect and OPM_{PE3}, where RR function was used for permanent environmental effects also. Estimates of heritabilities for test days and genetic correlations between individual days obtained by RR models were compared to those from a multitrait (MT) model. For RR models, variance components were estimated using EM-REML and animal model. Estimates of heritabilities for production at day 25 (and 125) were .38, .25, and .26 (and .35, .16, and .34) for OPM_{PE1}, OPM_{PE3}, and MT models, respectively. Estimates of genetic correlations between test days were similar with OPM_{PE3} and MT models, but OPM_{PE1} model substantially underestimated the relationships among extreme ends of the lactation.

Introduction

Breeding value estimation of dairy cattle can use original test day (TD) yields instead of the traditional 305 day lactation records to achieve a more detailed statistical model. This approach enables to account for both genetic and environmental variation specific to each TD yield. In addition, effects due to pregnancy and stage of lactation can be more accurately described. One of the main improvements for Finnish dairy cattle evaluation is, however, that the definition of contemporary comparison group can be done in such way that seasonal variation within herds becomes accounted for.

The shape of the lactation curve can be described with various mathematical models. Ali and Schaeffer (1987) introduced a logarithmic polynomial where 4 covariates are functions of days in milk (DIM). These regression coefficients can be used to identify the average shape of lactation curve or the curve within different fixed effect classes. Moreover, individual deviations from the general shape of the lactation curve can be modelled by random regression (RR) coefficients (Schaeffer and Dekkers 1994).

Estimates of heritabilities for daily milk yields using RR model have been reported to be high, especially at the beginning and end of lactation (Jamrozik and Schaeffer 1997, Kettunen et al. 1997). Based on biological considerations estimates of h^2 and genetic correlations between daily yields are subject to criticism. Pattern of estimates of h^2 and genetic correlations out of RR work have not followed those estimated with multitrait models (Meyer et al. 1989, Pander et al. 1992) and an antagonistic relationship between early and late lactation was found.

The objective of this study was to estimate genetic parameters for first lactation TD milk yields using two RR approaches with different permanent environmental (co)variance structure and to compare these with estimates computed with a multitrait (MT) model.

Material and methods

The data comprised 63,331 TD milk records of 6,310 primiparous Finnish Ayrshire cows calving between April 1988 and March 1996. To optimize he size of the contemporary comparison group,

only fairly large herds were included in the analysis. As a result, cows were from 78 herds having at least 7 and maximum of 14 heifers calving during each year. (Co)variance components were estimated using EM-REML for RR and AI-REML for MT models. Test day milk was assumed to be described by the following model:

$$y_{hijkmnop} = a_h + dcc_i + h_j + \sum_{q=1}^{5} b_{q(k)} X_q + HTM_m$$
$$+ PE_{n(o)} + RR_o + e_{hijkmnop}$$

where

$y_{hijkmnop}$ is TD milk yield

a_h defines calving age class

dcc_i days carried calf class

h_j herd

$b_{q(k)}$ regression coefficients of milk on days in milk (DIM) functions describing the shape of lactation curves within calving month classes k ($X_1=1$, $X_2=DIM/c$, $X_3=(DIM/c)^2$, $X_4=\ln(c/DIM)$, $X_5=(\ln(c/DIM))^2$, c=305)

HTM_m random test month of production within the herd

$Pe_{n(o)}$ permanent environmental effect of cow o

RR_o random regression sub-model describing the shape of lactation curve of an individual cow o and

$e_{hijkmnop}$ is the residual

A normalized third order orthogonal polynomial (Snedecor and Cochran, 1980) was fitted as a RR sub-model. The $PE_{n(o)}$ was defined either to be the common permanent environment associated with all TD yields of a cow o (OPM_{PE1}) or described by a normalized second order orthogonal polynomial (OPM_{PE3}). With latter model, within cow residual variation is divided into a PE function and a residual term. To allow variance component estimation, OPM_{PE3} was fitted using constant residual variance 2.851, the value estimated with OPM_{PE1}. Thus, the number of

(co)variance components estimated was 13 for OPM_{PE1} and 17 for OPM_{PE3} models.

Traits for MT analysis were formed by dividing the lactation into 16 intervals according to DIM (4-350 d) at test. To better describe critical changes of daily yields in the beginning and end of lactation, 10 and 20 d intervals were used, whereas 30 d intervals were used for mid-lactation. 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)variance estimates from 37 trivariate REML runs were converted into a continuous covariance function with four polynomials (see, Kirkpatrick et al., 1994). Pedigree information was traced for two generations. Cows with records were daughters of 1,380 sires; total number of male and female animals in the data was 1,900 and 8,351, respectively.

Results and discussion

Heritabilities estimated using OPM_{PE1} were clearly higher than those with MT model (Table 1). The pattern of values was indentical to that found using logarithmic polynomials by Jamrozik and Schaeffer (1997). Highest estimates of h^2 were observed at the beginning and end of lactation. The form of the h^2 curves for OPM_{PE1} and OPM_{PE3} estimates were similar, but the values were lower with OPM_{PE3} (Figure 1).

Genetic correlations of daily yields between consecutive TDs estimated with MT model were high but decreased down to 0.38 between the most distant TDs of lactation (Table 2). The OPM_{PE1} model greatly underestimated the genetic correlation when the days were further than 50 days apart. The correlations from the OPM_{PE3} were consistent with MT estimates except for those between the mid and the end lactation, and also close to those found in literature (Meyer et al., 1989).

The reason for fitting a separate RR function for permanent environmental effects of a cow was the unsatisfactory behavior of earlier RR models. The covariances among the TD measurements are composed of dependencies originating from genetic and permanent environmental effects. A model with a common PE effect estimates constant environmental covariance among TDs. This

underestimates the true covariance between TDs nearby and overvalues the covariance between individual TDs far apart. Ignoring the changes in magnitude of covariance seems to overrate h^2, and at the same time generates negative genetic correlations between TD yields at the early and late lactation. Cow-wise PE effect described by RR function allows covariances to vary, and the genetic component becomes more accurately estimated.

The heritabilities estimated with OPM_{PE3} were distinctly lower than those from OPM_{PE1} model with common PE effect. Thus the general level of h^2 was close to the level expected by MT results. Comparable decrease in h^2 estimates has been found in other studies when a PE function was added in the model (pers. communication: L.R. Schaeffer, 1997, AGDG). The pattern of the h^2 values during the lactation seems to depend on the function chosen to describe the breeding values. Simple polynomial function, as used in our model, could be responsible for high genetic variances in the early lactation, leading also to higher h^2 estimates at the extreme ends. We suspect that the pattern of h^2 could better correspond MT estimates if another RR breeding value function was adapted.

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Table 1. Estimates of variance components and heritabilities for daily yields using orthogonal polynomial random regression models (OPM_{PE1} and OPM_{PE3}) and a multitrait (MT) model.

	OPM_{PE1}		OPM_{PE3}			MT		
DIM	σ_g^2	h^2	σ_g^2	σ_P^2	h^2	σ_g^2	σ_P^2	h^2
5	8.32	0.49	5.35	17.15	0.33	2.67	12.08	0.23
25	5.30	0.38	3.40	14.58	0.25	3.04	12.28	0.26
45	3.81	0.31	2.36	13.38	0.19	3.33	12.39	0.29
85	3.49	0.29	1.80	13.28	0.15	3.68	12.44	0.32
125	4.63	0.35	2.14	14.27	0.16	3.81	12.37	0.34
165	5.78	0.40	2.77	15.15	0.20	3.76	12.32	0.34
205	6.40	0.43	3.44	15.49	0.24	3.63	12.42	0.33
265	7.07	0.45	4.19	15.43	0.29	3.39	13.17	0.28
285	7.86	0.48	4.37	15.63	0.30	3.34	13.65	0.26
305	9.44	0.53	4.58	16.27	0.30	3.31	14.28	0.25

Effect	σ^2	σ^2
HTM	1.16	1.12
pe	5.67	-
e	2.85	2.85
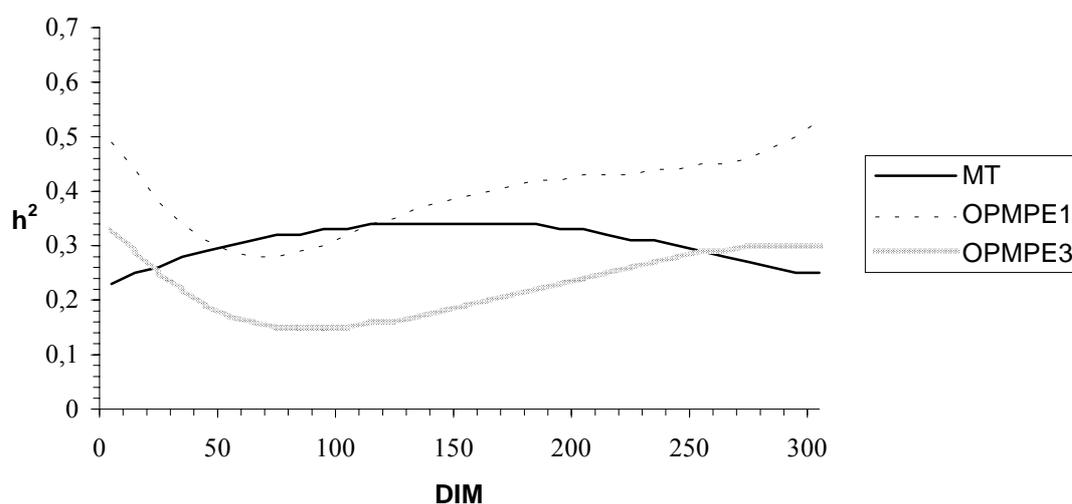
Figure 1. Estimates of heritabilities for daily yields during the lactation orthogonal polynomial using random regression models (OPM_{PE1} and OPM_{PE3}) and a multitrait (MT) model.

Table 2. Estimates of genetic correlations between daily milk on selected test days with MT (upper triangle), OPM_{PE1} and OPM_{PE3} (lower triangle, OPM_{PE} in italics) models.

DIM	5		25		85		165		285		305
5	-		0.91		0.74		0.59		0.41		0.38
25	0.98	*0.99*	-		0.83		0.69		0.53		0.50
85	0.48	*0.73*	0.65	*0.82*	-		0.87		0.74		0.72
165	0.01	*0.48*	0.19	*0.57*	0.82	*0.90*	-		0.88		0.85
285	-0.19	*0.42*	-0.21	*0.41*	0.03	*0.47*	0.49	*0.71*	-		0.97
305	-0.22	*0.35*	-0.28	*0.32*	-0.20	*0.31*	0.26	*0.57*	0.97	*0.98*	-