

Using Spline Test-Day Model for Estimating the Genetic Parameters for Cow's Milk Yield

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Abstract

Genetic parameters of Montbeliarde cows were estimated for test-day milk yield with a random regression spline model. The spline model has been considered as a good alternative to Legendre polynomials to direct interpretation of parameters. With this model the lactation curve is divided into sections by knots. The milk yield between any two knots is assumed to be changing linearly. The random regression was fitted with linear splines with five knots: 7, 54, 111, 246, 302. The herd-test-day is the fixed effect of the model. The heritability estimates for test-day milk yield ranged from 0.346 at 65th day in milk, to 0.422 at 35th day in milk. Genetic correlations between individual test days were positive and tended to decrease with an increase in days between when the yields were measured. Random regression models using linear splines were proved to be useful for genetic evaluations of cows.

Keywords: cows, genetic evaluation, heritability, linear spline

1. Introduction

The aim of this study was to determine the genetic parameters using spline test-day model. Splines have been recently considered as a good alternative to Legendre polynomial due direct interpretation of parameters [1]. The advantage of models with splines can be explained by smaller overestimation of additive genetic variance compared to the Legendre polynomial [2]. In the literature many authors were used the splines models to estimate the genetic parameters for production traits [1-9]).

White et al. [3] and Silvestre et al. [7] used the natural cubic splines to model lactation curves. Random regression model with splines has good flexibility, are smooth and has limited sensitivity to the data [8]. Bohmanova et al. [2] used linear splines to estimate the genetic parameters. A

linear spline is a spline function where the segments are fitted by linear polynomials.

2. Materials and methods

The 254 test-day milk records from 28 Montbeliarde cows at the first calving (2011-2012) from experimental farm of National Research-Development Institute for Animal Biology and Nutrition were used in this study. In the linear splines model were used 5 knots: $T_1=7$, $T_2=54$, $T_3=111$, $T_4=246$, $T_5=302$.

t =a particular days in milk between 4 and 305

T_i =represent the five knots;

The covariates, x_i for the spline function are determined as follows: [11]

If $t < T_1$, then $x_1=t/T_1$ and other x_i for $i > 1$ are zero.

If $t > T_5$, then $x_5=t/T_5$ and other x_i for $i < 5$ are zero.

If $T_i < t < T_{i+1}$, then

$x_i = (t - T_i) / (T_{i+1} - T_i)$

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$x_{i+1} = T_{i+1} - t / (T_{i+1} - T_i)$ and the other covariates are zero.

Linear model is described as follows: [12]

$$y_{ijk} = HTD_i + \sum_{m=0}^q (b_m \cdot v_{mjk}) + \sum_{m=0}^q (a_{mj} \cdot v_{mjk}) + \sum_{m=0}^q (p_{mj} \cdot v_{mjk}) + e_{ijk}$$

y_{ijk} = test day (TD) milk yield record "k" of cow "j" in first lactation measured at time "t";
HTD_i=HTD effect "i";

b_m = fixed regression coefficient;

a_{jm} = random regression coefficients for the breeding value;

p_{jm} = random regression coefficients for the permanent environmental effect;

v_{mjk} = Spline coefficient at time "t";

e_{ijk} = residual error.

The model is:

$$y = Xb + Z_1u + Z_2p + e$$

where: y=vector of observations;

b = vector of fixed effect for test-day;

u, p, e=vectors of additive genetic, permanent environmental, and residual values;

X, Z₁, Z₂= incidence matrices;

The (co)variance structure was assumed for random effects of model:

$$V = \begin{bmatrix} A \otimes G & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Where:

Var (a)=A ⊗ G;

Var (a)=additive variance;

Where ⊗ is Kronecker product function;

Var (p)=I ⊗ P;

Var (p)=environmental variance;

G and P are the matrices of genetic and permanent environmental variances and covariances between random regression coefficients.

I=represents the identity matrix with the size equal with the number of cows with records;

σ_e^2 =residual variance for lactation assumed to be constant throughout the lactation;

The estimates of heritability for milk yield during days in milk t were obtained by:

$$h_{tt}^2 = \frac{g_{tt}}{(g_{tt} + p_{tt} + \sigma_e^2)}$$

where:

h_{tt}^2 =heritability for milk yield during days in milk t;

g_{tt} =genetic variance for milk yield during any days in milk t;

$$g_{tt} = z_t' * G * z_t$$

$$p_{tt} = z_t' * P * z_t$$

p_{tt} =permanent environmental variance for milk yield during any days in milk t;

z_t =co(variables) related to a specific test day l measured during days in milk t;

σ_e^2 =residual variance;

The estimates of genetic correlations between test-day t' and t milk yields were calculated by:

$$r_{g_{t't}} = \frac{g_{t't}}{\sqrt{g_{t't} * g_{tt}}}$$

where:

$r_{g_{t't}}$ =genetic correlations between test-day t' and t milk yields;

$g_{t't}$ =genetic covariances between two test days during days in milk;

$$g_{t't} = z_{t'}' * G * z_t$$

$z_{t'}'$ =transpose of z;

The breeding value estimate (EBV) was calculated with the formula:

$$EBV_{305} = \sum_{m=0}^q (a_{mj} \cdot v_{mjk})$$

3. Results and discussion

In table 1 shows the average milk yield and standard deviation of milk yield due to different month of lactation. In table 2 gives the breeding value for the best 10 cows. In table 3 presents the additive genetic and environmental variance estimates throughout lactation and the heritability

Table 1. Mean, standard error mean and standard deviation of test day milk yield

Test day	Mean	Standard deviation	Number of cows
1	16.67±1.20	2.08	3
2	20.80±1.08	3.42	10
3	21.25±0.93	3.51	14
4	19.18±1.22	5.33	19
5	20.04±0.77	3.80	24
6	20.75±0.67	3.56	28
7	20.38±0.63	3.35	28
8	17.96±0.57	3.03	28
9	18.09±0.63	3.36	28
10	15.34±0.61	3.23	28
11	15.4±0.73	3.69	25
12	14.39±0.71	3.03	18
Mean daily yield	18.33±0.26	4.17	

for test-day milk yield. High additive genetic variances were observed at the beginning and at the end of lactation compared with the middle of lactation. The additive genetic variances were constant in the middle of the lactation. White et al. [3], Silvestre et al. [7], Bohmanova et al. [2] were found the high additive genetic variances at the beginning and the end of lactation. The environmental variances were also high at the beginning and the end of lactation. The heritability estimates for test-day milk yield ranged from 0.346 at 65th day in milk, to 0.422 at 35th day in milk. The high average daily heritability for milk (0.45) was observed by Bohmanova et al. [2], in first lactation of

Canadian Holstein cows. The lower values of the heritability for test-day milk yield, 0.19 at 18th day in milk and 0.23 at mid-lactation was found by Silvestre et al. [7] and White et al. [3] obtained the heritability 0.23 at 18th day in milk and 0.27 at 290th day in milk. DeGroot et al. [8] reported lower test-day milk yields heritability that ranged from 0.10 to 0.15 for Holstein cows. The genetic correlations between test-day milk yields during the selected lactation periods obtained by spline model were shown in table 4. All correlations were positive ranging from 0.24 to 1. High estimates of genetic correlations between test day yields throughout lactation have been reported by White et al. [3] and Silvestre et al. [7].

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Table 2. The breeding value of the Montbeliarde cows from our study

No.	Estimate breeding value
1	722.528
2	712.668
3	456.101
4	455.307
5	441.807
6	440.075
7	423.058
8	407.591
9	359.995
10	328.700

Table 3. Estimates of genetic and environmental variances for selected days in milk and the heritability for daily yields

Days in milk	Genetic variance	Environmental variance	Heritability
5	4.97	1.95	0.389
35	5.97	2.32	0.422
65	3.93	1.57	0.346
95	4.78	1.88	0.382
125	4.45	1.78	0.368
155	4.23	1.69	0.359
185	4.11	1.65	0.353
215	4.08	1.64	0.352
245	4.14	1.66	0.355
275	4.08	1.64	0.352
305	5.21	2.10	0.395

Table 4. Genetic correlation estimates between selected days in milk (DIM) of daily yields

DIM	5	35	65	95	125	155	185	215	245	275	305
5	1	0.93	0.45	0.44	0.40	0.41	0.42	0.42	0.42	0.35	0.24
35	0.93	1	0.66	0.74	0.62	0.62	0.61	0.60	0.59	0.53	0.35
65	0.45	0.66	1	0.88	0.94	0.97	0.98	0.99	0.98	0.92	0.74
95	0.44	0.74	0.88	1	0.87	0.86	0.84	0.82	0.78	0.77	0.54
125	0.4	0.62	0.94	0.87	1	1	0.98	0.95	0.91	0.92	0.67
155	0.41	0.62	0.97	0.86	1	1	1	0.98	0.95	0.93	0.71
185	0.42	0.61	0.98	0.84	0.98	1	1	0.99	0.98	0.94	0.74
215	0.42	0.60	0.99	0.82	0.95	0.98	0.99	1	1	0.93	0.76
245	0.42	0.59	0.98	0.78	0.91	0.95	0.98	1	1	0.92	0.78
275	0.35	0.53	0.92	0.77	0.92	0.93	0.94	0.93	0.92	1	0.91
305	0.24	0.35	0.74	0.54	0.67	0.71	0.74	0.76	0.78	0.91	1

4. Conclusions

The spline random regression model estimated more precise the genetic parameters. The heritability estimates for test-day milk yield were high, ranged from 0.346 at 65th day in milk, to 0.422 at 35th day in milk. Estimates of genetic correlations decreased with an increase in days between when the yields were measured.

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