Genetic parameters for test day measurements in Spanish Holstein-Friesian

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Introduction

Advantages of using individual test day as an alternative to 305d lactation yield have been discussed previously (see, for example, Pander et al. 1992, Ptak and Schaeffer, 1993). Extensive work has been devoted to study different aspects of test day modelling. Several studies have considered definition of environmental factors such as contemporary groups (Herd-year-season, HYS, vs. Herd-test date, HTD. Meyer et al., 1989, Ptak and Schaeffer, 1993, Swalve, 1995) and lactation curve shape (Ali and Schaeffer, 1987), as well as (co)variance structure for random genetic and environmental factors (Ptak and Schaeffer, 1993, Barillet and Boichard, 1994). Many studies have obtained genetic parameter estimates for test day measurements (Kneown and Van Vleck, 1970, Danell, 1982, Meyer et al., 1989, Pander et al., 1992, Swalve, 1995) finding smaller heritability at the beginning and end of lactation and correlations ranging from figures over 0.9 for adjacent tests to correlations near 0.7 for distant measurements.

In this study, preliminary work was carried out to provide some insight about **lactation curve shape, contemporary group** definition and **genetic parameters** between test day milk yields within and between lactations.

Data and Methods

Test day records from one region in the northern part of Spain, including data from year 1982 to 1994, were used in this study. The original data set was edited so that complete lactation (at least 10 test day measurements per lactation), first test between day 4 and 34 after parturition, time interval between successive tests less than 40 days and total yield in 305d over 2000 kg were required. 140892 test day yields out of 12036 cows were used in the lactation curve shape analyses. 37500 data from 3750 first lactations were used in the case of estimation of genetic parameters between successive tests under HYS or HTD models. Records from first, second and third lactation of 4223 cows (required to have first, fifth and eighth tests) were used for the analysis of genetic parameters among lactations. Averages and coefficients of variation for test day milk yields in first lactation are shown in Table 1.

Alternative lactation curves

Two alternative lactation curves were compared in terms of quality of extended lactations,

a) Wood's (1967) gamma function,

$$y_t = a t^b e^{-ct}$$

where y_t is the daily yield on day t and a,b, and c, are parameters associated with peak yield and increasing and decreasing part of the lactation curve, respectively.

b) Linear multiple regression model (as in Ali and Schaeffer, 1987),

$$y_t = b_0 + b_1\frac{t}{c} + b_2\left(\frac{t}{c}\right)^2 + b_3\ln\left(\frac{c}{t}\right) + b_4\left(\ln\left(\frac{c}{t}\right)\right)^2 + \epsilon$$

where y_t is defined as previously, $b_0 \ldots b_4$ are regression coefficients and c is now a constant (c=305).

From these two lactation models extended 305d yields were obtained following Ouweltjes and

Wilmink (1992). In order to compare these two models, the product moment correlation between actual (y) and predicted ($\hat{y}$) 305d yields, the standard deviation of the prediction error (σ_{PE}), and the percentage squared bias (**PSB**) were obtained. PSB was computed as,

$$PSB = \frac{(y-\hat{y})'(y-\hat{y})}{y'y} x100$$

Genetic parameters for first lactation tests

Variance components were estimated under multiple trait models using the package MTDFREML (Boldman et al., 1993). Each test day was considered as a separate trait and all 10 traits were jointly analyzed with 305d milk yield. The following models were used,

1) Test day records,

$$Y_{ijk} = CG_i + \sum_{m=0}^{4} b_{m(j)} X_m + u_k + e_{ijk}$$

where,

- $\mathbf{y_{ijk}}$ is test day milk yield,
- $\mathbf{CG_i}$ Contemporary Group: herd-year-season (**HYS model**) or herd-test date (**HTD model**),
- $\mathbf{b_{m(j)}}$ regression coefficients on X variables nested to production level (j)
- $\mathbf{u_k}$ animal additive genetic effect,
- $\mathbf{e_{ijk}}$ residual term

($X_0= 1$; $X_1 = t/c$; $X_2 =(X_1)^2$; $X_3 =\ln(c/t)$; $X_4 =(X_3)^2$; t = days in milk; c = 305)

2) 305d milk yield,

$$y_{ijkl} = HYS_i + A_j + M_k + u_l + e_{ijkl}$$

where, **HYS** is herd-year-season of calving, **A** is age effect, **M** is month of calving and **u** and **e** are as previously defined.

Genetic parameters for multiple lactations

(Co)variances among first, second and third lactation tests were analyzed in a multiple trait model, setting for first, fifth and eighth tests separately. MTDFREML (Boldman et al., 1993) was used again. The model fitted in these analyses was,

$$y_{ijk} = HYS_i + bX + u_j + e_k$$

where **X** is days in milk and **HYS**, **u** and **e** are defined as previously. A different model from the first lactation analysis had to be used now because of convergence problems due to small size of the HTD lactation analysis had to be used now because of convergence problems due to small size of the HTD classes. The number of days in milk was used instead of the lactation curve given the similar lactation stage in which data were collected in each analysis.

Results

Alternative lactation curves

Table 2 shows correlation between actual and predicted (with different parts of lactation supposed to be known) 305d milk yield, PSB and standard deviation of prediction error, for the gamma function and multiple regression model. The Gamma function yielded slightly larger correlations, smaller relative deviations of predicted vs. actual data and less variable predictions than the Multiple Regression method. On the contrary, Ali and Schaeffer (1987) found the regression model to be slightly superior to the gamma function when comparing actual and predicted test day milk yields.

Genetic parameters for first lactation tests

Table 3 shows heritability estimates for test day yields under the HYS and HTD models. Heritability estimates for HTD tended to be slightly larger. This was mostly due to the reduction of the residual variance estimate. Similar results were found by Meyer et al. (1989). Swalve (1995) found an increase of additive and permanent environmental variances and a decrease of the residual variance for HTD models. As in those studies, a reduction in number of observations per class in the HTD model was observed, questioning accuracy of the CG adjustment.

Estimates of heritabilities were lower at the beginning of lactation, as obtained in other studies (Keown and Van Vleck, 1970; Danell, 1982; Meyer et al., 1989; Pander et al., 1992; Swalve, 1995).

Table 4 shows the genetic and phenotypic correlations among yields in different tests and between each test and 305d yield. Genetic correlations were near or slightly over 0.9 for adjacent tests and decreased up to around 0.7 for tests from 180 to 210 days apart. Phenotypic correlations tended to be smaller than genetic correlations but followed the same trend. Correlation between test yields and 305d yield was largest for the first test and tended to decrease in the second half of lactation. Other studies (Keown and Van Vleck, 1970; Danell, 1982; Pander et al., 1992) found smaller correlations with 305d yield for the first test. This might be indicating that a larger weight to first test is being given in the calculation of 305d yield and should be further investigated by looking at more extensive data.

Genetic parameters for multiple lactations

Table 5 shows estimates of variance components for tests 1, 5 and 8 for the first three lactations. Residual variance estimates tended to increase with lactation number for the three tests. Genetic variances tended to increase from first to second lactation and then remain more stable. Table 6 shows heritabilities and genetic and phenotypic correlations between lactations for each test yield. Heritabilities for the same test in different lactations did not significantly differ. Genetic correlations between adjacent lactations were around 0.8 except for first test between first and second lactation. Correlations between first and second lactation tended to be smaller than those between second and third for all tests. Genetic correlations between first and third lactation were close to 0.6.

Discussion and conclusions

Wood's (1967) gamma function provided a more accurate prediction of 305 days yield than the multiple linear regression approach. However, developing estimation procedures to include non linear regression in current linear models is highly demanding from an analytical and computational point of view. In addition, available software for BV prediction or variance component estimation do not handle that kind of models.

HTD models seem to provide a better description of the environmental factors determining test day yields. However, the use of HTD models should be judged in terms of the available information per HTD class according to the overall model (including several lactations as repeated measurements would increase HTD classes size).

Test day measurements within first lactation showed high genetic correlations and could be considered as repeated records of the same trait (Table 3). Heterogeneity of variances among first, middle and final part of lactation has been detected (Table 5).

Yields from the same test day in different lactations showed high genetic correlations between adjacent lactations but correlations between first and third lactation were only around 0.6.

Alternative models to approach test day genetic analyses when using several lactations can be developed from different assumptions,

1) Test day yields are repeated measurements of the same trait within and across lactations, variance of the permanent environmental effect is a constant, and no covariances exist among permanent environmental effects. This would be the simplest model, similar to the one used for 305d yields,

$$y_{ij} = (fixed\ effects)_i + u_j + p_j + e_{ij}$$

where y_{ij} is yield in test day i, obtained from animal j, u is additive genetic effect, p is permanent environmental effect and e is the residual term.

$var(u) = A_{qxq}\ \sigma_a^2$; q = number of additive genetic effects

$var(p) = I_{cxc}\ \sigma_p^2$; c = number of cows

$var(e) = I_{NxN}\ \sigma_e^2$; N = number of records

2) Test day yields are repeated measurements of the same trait within and across lactations, but variance of the permanent environmental effect is not constant, and covariances between permanent environmental effects are allowed among successive lactations (model proposed by Ptak and Schaeffer, 1993),

$$y_{ijl} = (fixed\ effects)_i + u_j + p_{jl} + e_{ijl}$$

where p_{jl} is now the permanent effect associated with the lactation l of the animal j.

$$var(p) = \begin{bmatrix} P_1 & 0 & . & . & 0 \\ & . & . & . & . \\ & & P_j & . & 0 \\ & sym & & . & . \\ & & & & P_c \end{bmatrix}$$

where P_j is a matrix that reflects the (co)variance structure of permanent environmental effects p_{jl} associated to each cow in each lactation,

$$P_j = \begin{bmatrix} \sigma^2_{p_{11}} & . & . & . & \sigma_{p_{1L}} \\ & \sigma^2_{p_{22}} & . & . & . \\ & & . & . & . \\ & sym & & . & . \\ & & & & \sigma^2_{p_{LL}} \end{bmatrix} \quad (L = total\ number\ of\ lactations\ per\ animal).$$

3) Test day yields are repeated records of the same trait within lactation but different traits across lactations, allowing (co)variances between permanent environmental effects as before. The model for each lactation (trait) would be like in the first case, but the (co)variance structure is, now,

$$var\begin{pmatrix} u_1 \\ \cdot \\ \cdot \\ u_L \end{pmatrix} = \begin{bmatrix} g_{11} & \cdot & \cdot & g_{1L} \\ & \cdot & \cdot & \cdot \\ sym & & \cdot & \cdot \\ & & & g_{LL} \end{bmatrix} \otimes A = G \otimes A$$

where g_{mn} is the (co)variance of additive effects (between)in different lactations. For the other random effects,

$$var\begin{pmatrix} p_1 \\ \cdot \\ \cdot \\ p_L \end{pmatrix} = P_{LxL} \otimes I_{cxc} \qquad var\begin{pmatrix} e_1 \\ \cdot \\ \cdot \\ e_L \end{pmatrix} = E_{LxL} \otimes I_{cxc}$$

Other models including heterogeneity of genetic variances within different parts of lactation could be implemented, as the one used by Barillet and Boichard (1995) when analyzing test day records of sheep within first lactation. Implementation of the more complex models to national evaluations would be limited by estimation of genetic parameters. Obtaining the required heritabilities and correlations is theoretically feasible although not free of heavy analytical development and large computation requirements. Accuracy of estimates and improvement over more simple models should be evaluated before they are implemented in evaluation routines.

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Table 1.- Means and coefficients of variation (CV) of test day milk yields in first lactation

Test	Mean (Kg)	CV
1	22.90	17.55
2	23.10	18.10
3	22.09	19.92
4	21.16	20.27
5	20.49	21.20
6	19.94	21.50
7	19.23	21.75
8	18.74	22.46
9	17.68	23.08
10	15.94	26.33

Table 2.- Correlation between actual and predicted 305d milk yield, percentage of squared bias and standard deviation of prediction error for the Wood's gamma function (Γ) and multiple regression (MR) models

Days[1]	r[2]		PSB (%)[3]		σ_{pe}[4]	
	Γ	MR	Γ	MR	Γ	MR
65	0.912	0.891	0.8290	0.9470	559.9	635.2
95	0.938	0.914	0.5940	0.6270	463.0	508.5
125	0.950	0.932	0.4824	0.5312	417.0	449.6
155	0.972	0.961	0.2770	0.3210	313.8	352.7
185	0.985	0.973	0.1440	0.1910	223.4	291.1
215	0.993	0.985	0.0676	0.0950	149.9	183.9
245	0.998	0.992	0.0205	0.0470	78.2	102.1
275	0.999	0.998	0.0006	0.0008	11.6	15.5

(1) Known part of the lactation used to predict 305 days yield

(2) Correlation between predicted and actual 305 days yield

(3) $PSB = \frac{(y-\hat{y})'(y-\hat{y})}{y'y} x100$

(4) Standard deviation of the prediction error ($PE=(y-\hat{y})$)

Table 3.- Heritabilities of test day and 305 days yields under two different models (first lactation)

Test	HYS model	HTD model
1	.17	.18
2	.19	.19
3	.20	.22
4	.22	.21
5	.22	.23
6	.23	.25
7	.23	.25
8	.25	.27
9	.25	.28
10	.26	.27
305d	.29	.31

Table 4.-Genetic and phenotypic correlations among yields in different tests and between each test and 305d yield (HTD model; first lactation)[1]

Test	1	2	3	4	5	6	7	8	9	10	305d
1		.92	.88	.78	.75	.73	.71	.71	.72	.69	.89
2	.76		.91	.89	.82	.79	.76	.74	.73	.71	.76
3	.76	.79		.91	.88	.84	.82	.83	.83	.73	.72
4	.72	.78	.78		.90	.88	.81	.86	.85	.84	.74
5	.69	.71	.74	.74		.89	.82	.78	.79	.84	.78
6	.65	.67	.68	.75	.75		.90	.81	.85	.81	.74
7	.66	.68	.68	.72	.73	.74		.92	.88	.86	.70
8	.64	.66	.67	.68	.70	.72	.73		.90	.88	.72
9	.61	.61	.64	.66	.65	.66	.68	.74		.89	.68
10	.58	.59	.62	.61	.64	.64	.67	.70	.74		.72
305d	.65	.70	.69	.70	.71	.70	.72	.73	.72	.63	

[1] Genetic correlations above

Table 5.- Estimates of the variances of the first (T1), fifth (T5) and eighth (T8) tests in the three considered lactations

Lactation	Genetic variance			Residual variance		
	T1	T5	T8	T1	T5	T8
1	3.04	4.27	4.47	13.40	10.43	11.20
2	4.11	5.59	7.16	15.75	14.88	15.92
3	3.96	6.72	6.87	20.03	16.57	16.09

Table 6.- Heritabilities (diagonal), and genetic (above) and phenotypic (below) correlations among lactations at first (T1), fifth (T5) and eighth (T8) tests

Lactation	1	2	3
T1			
1	0.19	0.67	0.52
2	0.20	0.20	0.81
3	0.21	0.18	0.17
T5			
1	0.29	0.83	0.61
2	0.35	0.27	0.86
3	0.22	0.36	0.28
T8			
1	0.28	0.79	0.58
2	0.37	0.31	0.88
3	0.21	0.34	0.30