

# Analysis of Persistency of Lactation Calculated from a Random Regression Test Day Model

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## Introduction

Persistency of lactation is the ability of a cow to continue producing milk at a high level after the peak of her lactation. Differences in persistency, if not properly accounted for, reduce accuracy of genetic evaluation when incomplete records are used. Persistency has also direct economic value. Reduction of feed, health and reproductive costs are the major factors which favour more persistent cows (Dekkers et al., 1996; Sölkner and Fuchs, 1987).

Persistency can be measured in many different ways (Gengler, 1996). The major concepts are based on ratios of partial and total yields, variation of yields during the lactation or shape of the lactation curve. Random regression models for test day (TD) yields (Jamrozik et al., 1997a) allow curves to be estimated for each lactation of every cow. Therefore, a measure of persistency based on the shape of the lactation curve after peak seems to be a natural way of describing potential to maintain the level of production.

Milk, fat and protein TD yields have slightly different lactation curves. Curves for different lactations also differ in shape. Therefore, persistency for milk, fat and protein yields in consecutive lactations might be considered as different traits. The objective of this study was to estimate genetic and phenotypic parameters for milk, fat and protein persistencies, defined as the slope of the lactation curve after the peak, in the first three lactations of Canadian Holsteins. Possible expressions of estimated breeding values for first lactation milk persistency are also discussed.

## Materials and Methods

### Model

The multiple trait random regression model for simultaneous analysis of TD milk, fat and protein yields and somatic cell score (SCS) in the first three lactations (Jamrozik et al., 1997b) was used in this study. The model equation was assumed to be the same for all four traits. For trait *h* in lactation *n* it was

$$y_{hntijkl} = \text{HTD}_{hni} + \sum_k b_{hnkm} Z_{tm} + \sum_j a_{hnjm} Z_{tm} + \sum_j p_{hnjm} Z_{tm} + e_{hntijkl}$$

where

- $y_{hntijkl}$  is record *l* on cow *j* made on day *t* in herd-test day *i*, for a cow belonging to subclass *k* for region, parity, age and season of calving
- $\text{HTD}_{hni}$  is fixed herd-test day effect
- $b_{hnkm}$  are fixed regression coefficients for subclass *k* of region, age and season of calving
- $p_{hnjm}$  are random regression coefficients for permanent environmental (PE) effect on cow *j*
- $a_{hnjm}$  are random regression genetic coefficients specific to cow *j*
- $e_{hntijkl}$  is residual effect for each observation
- $Z_{tm}$  are covariates assumed to be the same for fixed and random regressions

Wilmink's function (Wilmink, 1987) was chosen to describe the shape of lactation curves. The function is

$$W(t) = w_0 z_{t0} + w_1 z_{t1} + w_2 z_{t2}$$

where

$$z_{t0} = 1 ; \quad z_{t1} = t ; \quad z_{t2} = \exp(-0.05t).$$

Residuals were assumed to be uncorrelated both within and between cows. Different residual (co)variances were allowed for different lactations (n) and time period within lactation (t). PE effects were modelled by random regressions so they could vary within lactation. The detailed description of the model was presented in Jamrozik et al. (1997b).

Let  $p_i$  be the animal's yield on DIM  $i$  for a given trait. Persistency (P) of lactation for this trait was defined as

$$P = p_{280} - p_{60}$$

which measure an average slope of the animal's lactation curve between DIM 60 and 280. Note that phenotypic values of persistencies were not available in this study. All results were based on genetic expressions of P, which resulted from an application of the random regression TD model.

### Genetic parameters

Genetic, PE and residual (co)variances were estimated on a subset of the Canadian Holstein TD data. Two disjoint sets of data were created by random selection of herds from Ontario and Quebec with at least 300 TD records. In total, 54,770 and 60,811 TD records with all traits (milk, fat, protein, SCS) recorded were used in data sets 1 and 2, respectively. Edits included DIM between 5 and 305 days, age at calving between 18 and 68 months, calving date after January 1, 1988. Gibbs technique was applied to generate samples from posterior distributions of variances and covariances for milk, fat and protein persistencies in the first three lactations. Genetic (PE) variances and covariances for persistency were calculated as functions of (co)variances of random regression

genetic (PE) coefficients. After burn in, 20,000 samples from each data set (40,000 samples in total) were used to estimate posterior means and standard deviations of distributions. See Jamrozik et al. (1998) for more detailed description of the data and the methods used.

### Genetic evaluation for persistency

Data were 11,544,946 TD records from the first three lactations on Canadian Holsteins. First test in each lactation had to be recorded before 90 DIM. Only records collected between DIM 5 and 305 were included. Cows were assigned to one of 19 subclasses for age at calving within lactation and one of two seasons of calving. Combined with region this gave 152 region-age-season of calving subclasses. The total number of animals was 1,520,096. Groups for unknown parents and inbreeding coefficient in  $\mathbf{A}^{-1}$  were included in the model. Details on the data and the model used can be found in Jamrozik et al. (1997b).

Let  $g_i$  be the animal's estimated breeding value for DIM  $i$  calculated from its random genetic curve for a given yield trait, and  $PG = g_{280} - g_{60}$  be the genetic component of the phenotypic persistency, P. Bull indices for persistency, expressed as transmitting abilities, were defined as:

- A =  $55 * PG$  - the average additional yield of daughters between day 60 and 280 of lactation relative to an average cow with the same yield at day 60
- B =  $0.5 * PG$  - the average decline in yield of daughters from day 60 to day 280 relative to the average cow
- C =  $(y_{280} + 0.5 * PG) / y_{60} * 100$  - the expected yield of daughters on day 280 expressed as a percentage of the average actual base population yield on day 60
- D =  $280 - m - (440 * (2 * y_{60}^2 + 2 * (y_{280} + 0.5 * PG)^2)^{0.5} - 880 * (y_{280} + 0.5 * PG)) / (4 * (y_{60} - (y_{280} + 0.5 * PG)))$  - number of days in which daughters reach  $\frac{1}{2}$  of their production between days 60 and 280, relative to an average base population cow with the same yield at day 60

and m days to 1/2 of her production between days 60 and 280.

## Results and Discussion

### *Genetic parameters*

Heritabilities, genetic and PE correlations for milk, fat and protein persistencies in 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> lactation are shown in Table 1. Estimates of heritabilities were 25 - 35 %, higher than reported elsewhere (Gengler, 1996). Heritability increased from first to later lactations but without apparent differences between 2<sup>nd</sup> and 3<sup>rd</sup> lactation. Persistency of fat yield was less heritable in comparison with milk and protein. Genetic correlations between lactations for the same trait were low, especially between 1<sup>st</sup> and later lactations. This suggests that different lactations are characterised by genetically different persistencies. Milk and protein yields were more related for persistency than any other combination of analysed traits. Correlations between PE effects followed the trend shown by the genetic relationships between traits, with smaller values of correlations between different lactations.

A good persistency measure should be independent of the level of production (Gengler, 1996). Correlations between persistency and 305d yield for milk, fat and protein in the first three lactations are shown in Table 2. All traits showed very low level of relationship between their respective persistency and the total production on both genetic and PE level. Persistency of protein yield seemed to be more related to the 305d yield than milk or fat persistencies.

### *Persistency expressions*

Average phenotypic lactation curves (Wilmink function) were fitted to TD milk yield (285,414 records) of Holstein cows that calved in 1995. This group of cows form the current base for expressing indices from the national genetic evaluation in Canada and it was also chosen to be a base for expression of ETA<sub>1</sub> for persistency. Results are shown in Table 3.

Average curves for milk yield in 1<sup>st</sup> and later lactations were different in shape. It was also shown that genetic correlations between persistency in 1<sup>st</sup> and later lactations were not perfect. Hence, persistency in different lactations should be considered as separate traits and combined later into one overall persistency index. Since relative economic weights of persistency in different lactation are unknown yet, only ETA<sub>1</sub> for persistency of milk yield in first lactation were analysed further.

ETA<sub>1</sub> for persistency of milk yield in 1<sup>st</sup> lactation expressed as A, B, C or D were compared for a group of 3,429 Holstein bulls with at least 12 daughters in 10 herds. A summary of results is given in Table 4. Expressing proofs as ETA<sub>1</sub> reduced the range of indexes in comparison with estimated breeding values but on the other hand, it made the interpretation of proofs easier. A and B were expressed in kilograms of milk yield, whereas C and D were expressed in different units, namely percentages or days. It might be more appropriate to select a scale of persistency expression not related directly to the actual yields, thus leaving less room for possible confusion with EBV<sub>1</sub> for production. Correlations between ETA<sub>1</sub> for A, B and C were all equal 1 (A and C are linear functions of B). Correlations between ETA<sub>1</sub> for D and A, B, C were also close to 1 (>0.99). Thus, all of these options can be seen as different expressions of the same trait. The general relationship between B and D is nonlinear, but it seems to be close to linear in the interval from 60 to 280 DIM. It can be approximated by a linear function  $D = 0.9 + 1.0/0.78 * B$ . All expressions of persistency were equally related to the EBV<sub>1</sub> for 305d yield. Note that this correlation, although not equal to zero, is much smaller than respective correlations for other measures of persistency based on ratios of yields (Jamrozik et al., 1997a). It was relatively easy to estimate genetic parameters for persistency defined as A, B or C (linear functions of P). It is difficult to estimate  $h^2$  for D in a direct way using variance and covariance components from the random regression model. It can be speculated however, based on close relationship between ETA<sub>1</sub> for D and other expressions for persistency, that heritability of D is close to these for A, B and C.

Table 1. Means of posterior distributions<sup>1)</sup> for heritabilities (diagonal), genetic (above diagonal) and PE (below diagonal) correlations between persistencies of milk (M), fat (F) and protein (P) yield of Canadian Holsteins in first (I), second (II) and third (III) lactation.

	<b>M I</b>	<b>F I</b>	<b>P I</b>	<b>M II</b>	<b>F II</b>	<b>P II</b>	<b>M III</b>	<b>F III</b>	<b>P III</b>
<b>M I</b>	<b>0.30</b>	0.81	0.90	0.37	0.30	0.33	0.31	0.23	0.26
<b>F I</b>	0.81	<b>0.25</b>	0.82	0.27	0.35	0.29	0.22	0.27	0.22
<b>P I</b>	0.92	0.83	<b>0.28</b>	0.30	0.30	0.36	0.26	0.25	0.30
<b>M II</b>	0.29	0.23	0.23	<b>0.37</b>	0.86	0.92	0.60	0.49	0.54
<b>F II</b>	0.26	0.32	0.26	0.86	<b>0.30</b>	0.89	0.50	0.56	0.50
<b>P II</b>	0.27	0.26	0.29	0.93	0.89	<b>0.35</b>	0.54	0.52	0.58
<b>M III</b>	0.25	0.18	0.22	0.51	0.43	0.48	<b>0.39</b>	0.85	0.93
<b>F III</b>	0.20	0.25	0.23	0.43	0.51	0.47	0.85	<b>0.32</b>	0.88
<b>P III</b>	0.21	0.20	0.24	0.46	0.45	0.50	0.93	0.88	<b>0.38</b>

<sup>1)</sup>Standard deviations of distributions were 0.02 - 0.03 for heritabilities and 0.01 - 0.07 for correlations.

Table 2. Means of posterior distributions<sup>1)</sup> for genetic and PE correlations between persistency and 305d yield for milk (M), fat (F) and protein (P) yields of Canadian Holsteins in first (I), second (II) and third (III) lactation.

	<b>M I</b>	<b>F I</b>	<b>P I</b>	<b>M II</b>	<b>F II</b>	<b>P II</b>	<b>M III</b>	<b>F III</b>	<b>P III</b>
<b>Genetic</b>	-0.10	-0.06	0.13	0.01	0.15	0.27	-0.00	0.14	0.22
<b>PE</b>	-0.14	-0.14	-0.01	0.05	0.09	0.17	-0.04	0.08	0.14

<sup>1)</sup>Standard deviations of distributions were 0.06 - 0.08.

Table 3. Summary of phenotypic lactation curves (milk yield only) fitted to base population cows (n=85,414).

	Lactation I	Lactation II	Lactation III
TD records	2,172,736	1,503,491	679,785
$y_{60}$ = yield at day 60 (kg)	28.3	35.0	37.5
$y_{280}$ = yield at day 280 (kg)	20.1	18.8	19.2
305d yield (kg)	7452	8461	8934
cumulative yield between days 60 and 280 (kg)	5399	5991	6329
DIM at peak (day)	53	40	41
& days between 5 and 305 (day)	139	127	125
m = & days between 60 and 280 (day)	160	153	152

Table 4. Characteristics of ETA's for milk yield persistency in 1<sup>st</sup> lactation.

	ETA(A) (kg)	ETA(B) (kg)	ETA(C) (%)	ETA(D) (day)
Mean	-6.4	-0.06	70.8	0.8
SD	85.3	0.78	2.7	1.0
Min	-308	-2.8	61	-3.1
Max	272	2.5	80	3.8
Correlation with EBV for 305d yield	0.29	0.29	0.29	0.29

## Conclusions

Persistency of lactation defined as a slope of the genetic lactation curve after peak can be calculated as a by-product of the random regression TD model. Persistency of yield traits is moderately heritable and unrelated to the total 305d production, thus allowing

for efficient selection for the shape of lactation curve. Different lactations, however, are characterized by genetically different persistencies. Different expressions on a phenotypic scale for animal's estimated breeding value for persistency are possible.

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