

Genetic Evaluation of Persistency in Random Regression Test Day Model

Tomasz Strabel, Witold Kopacki, Tomasz Szwaczkowski

Department of Genetics and Animal Breeding

August Cieszkowski Agricultural University

Ul. Wolynska 33, 60-637 Poznan

e-mail: strabel@jay.au.poznan.pl

Abstract

Random regression model was applied to estimate variance components and study persistency of test-day records of milk yield of Polish Black and White cattle. Data comprised 578,599 test day records. The model included fixed herd test-day effect, three covariates to describe lactation curve nested within age-season classes, and random regressions for additive genetic and permanent environmental effects. Legendre polynomials were used to describe all curves. Persistency was defined as the difference between estimated breeding values at 280 and 60 day in lactation. Estimated heritability of persistency was 0,17. Correlation between breeding values and persistency was 0,09 and 0,29 for bulls with less or more than 87,5% of Holstein Friesian genes, respectively which allows for quite an independent selection for these traits. Curves of average breeding values of two groups of studied bulls showed that crossing Polish dairy cattle with Holstein Friesian changes the shape of lactation. It is shown that persistency measure used in this study may not be very informative for farmers using different management strategies when estimated values of persistency are moderate.

Introduction

Lactation persistency, often defined as the ability to maintain constant yield throughout lactation, is an economically important trait. More persistent lactations are desired as they allow avoiding health problems and reduce feeding and reproductive costs. It also means better performance for longer lactations.

Many precise definitions of persistency were applied in various studies (see Swalve and Gengler 1999 for more details). Since random regression models were proposed for genetic evaluation of dairy cattle, and already introduced in some countries, definition based on individual genetic curves has become of interest. Jamrozik et al. (1998) defined genetic persistency as the slope of the animal's lactation curve between days-in-milk (DIM) 60 and 280.

The objective of this study was to estimate heritability of persistency and compare persistency of different groups of crossbred bulls. The relationship between genetic persistency and shape of genetic curves was also discussed.

Material and Methods

Data comprised 64,026 first lactations collected in herds of the Wielkopolska region (Poland) from 1992 to 1996. A total of 578,599 milk TD records were analyzed. Average lactation yield was 4349 kg (standard deviation – 98,04 kg).

The following linear model was used:

$$y_{ijkl} = HTD_i + \sum_{m=1}^3 b_{km} z_{tm} + \sum_{m=1}^3 a_{jm} z_{tm} + \sum_{m=1}^3 p_{jm} z_{tm} + e_{ijkl}$$

where y_{ijkl} = TD milk yield record l of cow j in first lactation belonging to subclass k of age-season of calving; HTD_i = herd TD effect; b = fixed regression coefficient, a and p = random regression coefficients, and z_{1-3} = Legendre polynomials modified by Gengler et al. (1999):

$$z_1=1; z_2=\sqrt{3} x; z_3=\sqrt{5/4} (3x^2-1)$$

where $x = -1 + 2 \cdot \text{DIM}$, and DIM are standardized between -1 and $+1$. Residuals were assumed to be uncorrelated within and between cows. The detailed model assumptions were as presented by Strabel and Misztal (1999).

Variance components were estimated on the subset of the data set and comprised 57,093 test day records of 6 347 lactations. The calculations were done using Ignacy Misztal's package (Misztal, 1999). Genetic persistency was defined as follows:

$$gp_i = EBV_{i,280} - EBV_{i,60}$$

where gp_i – genetic persistency of an animal i ; $EBV_{i,280}$, $EBV_{i,60}$ are estimated breeding values of an animal i at DIM 280 and 60.

As the population of Polish lowland dairy cattle is consistently crossed with Holstein Friesian cattle part of the analysis was carried out separately for bulls with a lower (<87,5%) and higher (>87,5%) amount of HF genes.

Results and Discussion

Heritability estimate of milk persistency was equal to 0.17 what is in the range of h^2 for milk yield at different DIM estimated for the same population.

To check whether persistency measure is related to EBV correlation between persistency and breeding value for bulls was calculated. Correlation was significant and equaled 0.09 for bulls with lower proportion of HF genes and 0.29 for bulls with more than 87,5% of HF genes.

Figure 1 presents average EBVs for studied groups of bulls. The genetic curve (EBVs for 5-305 DIM) for bulls with a higher proportion of HF genes was less persistent ($\overline{gp} = -0,22$) than for the rest of bulls ($\overline{gp} = 0,23$). Further comparison of these curves shows clearly higher genetic potential of HF cattle, especially at the middle part of lactation. It also explains why phenotypic curves of Polish dairy cattle have peaks at around 30 DIM while for high producing US Holsteins it varies between 40 and 80 DIM.

Analysis of plots of many genetic curves for bulls lead to the observation that lactations with moderate persistency might have completely various shapes. Figure 2 presents possible curves with the same, average persistency. In practice probably the curve with a peak would be preferred because it describes higher total lactation yield. However, this curve may not be preferable for herds where cows are usually milked for more than 305 days.

Figure 1. The average genetic curves representing breeding values and genetic persistency for bulls with more and less than 87,5% of Holstein Friesian genes.

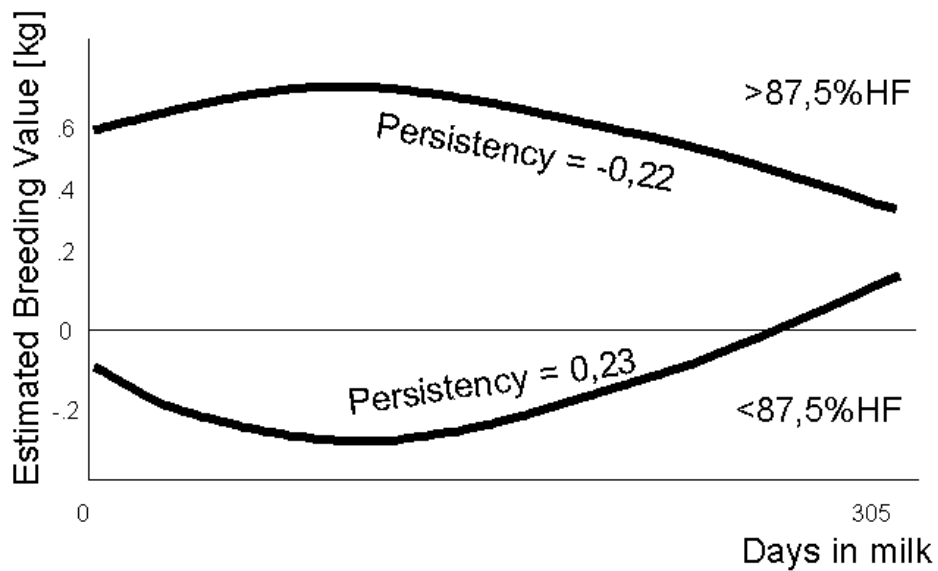
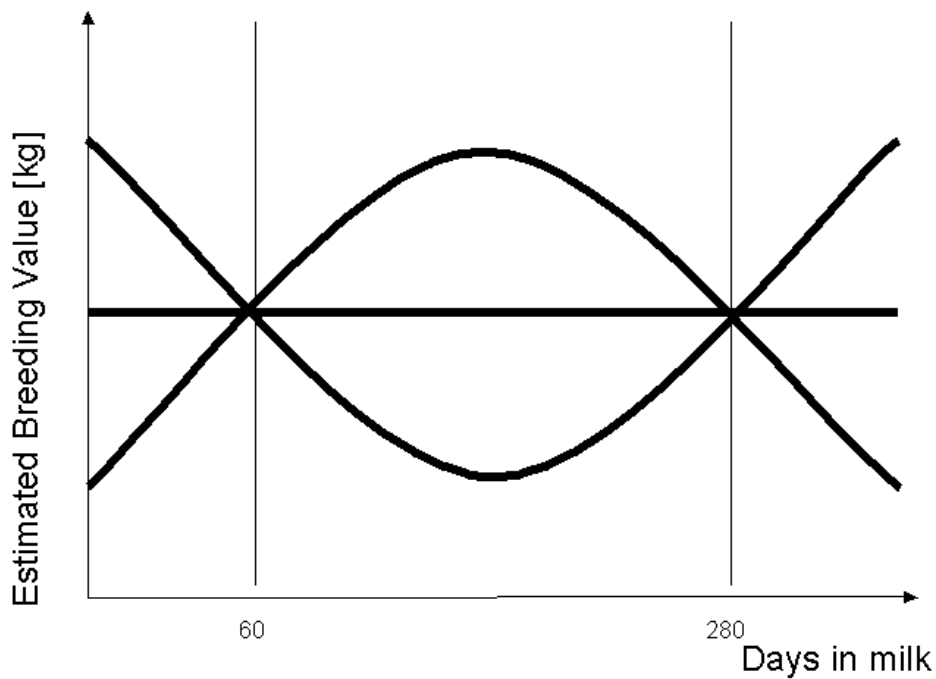


Figure 2. Possible genetic curves for the same measure of persistency defined as the difference between $EBV_{280} - EBV_{60}$.



Conclusions

- Heritability estimate of first lactation milk yield persistency is close to average heritability of milk yield for this population.
- Low correlations between persistency and milk yield means it is possible to select quite independently for both traits.
- Crossing Polish lowland cattle with pure Holstein-Friesians modifies the shape of lactation.
- The used persistency measure may not be very informative for farmers using different management strategies when estimated values are moderate.

References

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