

Multiple-Lactation Random Regression Test-Day Model for Polish Black and White Cattle

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Introduction

A single-trait multi-lactation model based on 305-day yields is the current model used for genetic evaluation of dairy cattle in Poland. Random regression test-day model (**RRM**) is the method of choice to improve quality of evaluation and it has been already implemented in many countries. Based on the preliminary results, a multi-lactation test-day model with random regressions is proposed for genetic evaluation of production traits for Polish Black and White population.

The selection of the best model requires decisions concerning effects that are to be included in the model. Although the average size of herds in Poland has increased recently, they are still small, leading to almost 40% of Herd-Year-Season classes with single lactation records. Thus the model with random Herd-Test-Day (HTD) effect was considered and it was shown to be superior over the model with fixed HTD classes (Strabel *et al.*, 2003). Recent study on the shapes of lactation curves have shown that Polish Black and White cows reach the peak yield very early (Strabel, 2004). Hence, higher order of Legendre polynomials were chosen for better modeling average lactation curves at peripheries of lactation. Analysis of residuals illustrated that using 6 instead of 5 covariates clearly improved goodness of fit of the model

(unpublished results). Using the techniques designed to better account for environmental variation (heterogeneous error variance or higher order of polynomials for permanent environmental effects) implied that ignoring heterogeneity of residual variance across lactation has limited practical consequences.

The aim of this study was to estimate (co)variance components for milk, fat and protein yields of Polish Black and White cattle using the single trait multiple lactation random regression model and Gibbs sampling.

Material and Methods

Data were 16,410,429 test-day records on cows calving between 1995 and 2001. A total of 318,929 first, second and third lactation milk, fat and protein test-day records from 127 randomly selected herds were used for analysis. Only records collected between 5 and 305 DIM were included. The length of lactation had to be 150 DIM or more with a minimum of 5 tests per lactation. Herds were required to have at least 50 lactations. Records of 20,498 cows were assigned to one of 10, 8 and 6 subclasses of age-season of calving within first, second and third lactation, respectively. Details of the data used are given in Table 1.

Table 1. Description of the data set used in the study.

	Lactation		
	1	2	3
Mean daily yield (standard deviation)			
Milk (kg)	16.0 (6.25)	18.1 (7.40)	19.3 (7.77)
Fat (kg)	0.65 (0.28)	0.75 (0.34)	0.81 (0.36)
Protein (kg)	0.51 (0.19)	0.59 (0.23)	0.62 (0.23)
Number of lactations	20,498	12,424	6524
Number of records	170,382	98,768	49,779
Number of daughters per bull	7.7	5.9	4.4
Number of HTD classes	8848	6920	5260
Number of records per HTD	19.25	14.27	9.46

The following model was used:

$$Y_{ijklmo} = \text{HTD}_{io} + \sum b_{jlo} z_{mnlo} + \sum c_{klo} z_{mnlo} + \sum a_{mlo} z_{mnlo} + \sum p_{mlo} z_{mnlo} + e_{ijklmo}, \text{ where}$$

Y_{ijklm} is milk, fat or protein yield l of cow m from lactation o within herd-test day effect i , belonging to herd-year of calving k and j -th class of age-season of calving, HTD_i is a random herd-test day effect, b_{jlo} are fixed regression coefficients specific to age-season subclass j , c_{klo} are fixed regression coefficients specific to herd-year k , a_{mlo} are genetic random regression coefficients specific to animal (AG) m , p_{mlo} are random regression coefficients for permanent environmental (PE) effect, e_{ijklmo} is residual effect for each observation, z_{mnlo} are covariates. Fixed lactation curves for age-season were modeled using Legendre polynomials of order 5 (6 covariates). The same function with 4 parameters was used for all remaining regressions.

Homogeneous error variance was assumed for records from different DIM. Residuals were assumed to be uncorrelated between and within cows and lactations. Additive genetic and permanent environmental covariance matrices included covariances between lactations, hence they were of order 12 by 12.

Gibbs Sampling was used to generate 120,000 samples (Jamrozik *et al.*, 1998). Posterior means of (co)variance components were calculated using 100 000 samples after

discarding the first 20 000 iterations as a burn-in period.

Results and discussion

The first coefficient of orthogonal Legendre polynomials describes the total yield in lactation. Heritabilities of this parameter were relatively low (Table 2), and they were higher for milk yield than for other traits. All estimates of h^2 rose with parity number but did not exceed 0.2 in any lactation.

Table 2. Heritability of first Legendre coefficient and genetic correlations between lactations for milk, fat and protein yields.

Parameter	Milk	Fat	Protein
Heritabilities			
I lactation	0.14	0.07	0.11
II lactation	0.18	0.11	0.15
III lactation	0.19	0.14	0.17
Gen. Correlations			
I-II lactation	0.72	0.70	0.69
I-III lactation	0.62	0.60	0.53
II-III lactation	0.74	0.72	0.69

Genetic correlations between adjacent lactations were around 0.7 for all three traits whereas between I and III lactations were lower (0.53-0.63). As in case of heritabilities correlations were higher for milk yield than for fat and protein.

Heritabilities for daily yields are shown in Figures 1-3. They were higher than heritabilities of the total yield approaching the value of 0.3 at peripheries of lactation, particularly for third parity. The current estimates were slightly higher than those obtained by Strabel and Misztal (1999) for first and second lactation. Differences could be caused by generally higher production of cows studied and larger data set used for this analysis, as well as by using more sophisticated model in the present study. The estimates of heritability were similar to those reported for lactation yields by Jagusiak and Żarnecki (2000). However, relatively low estimates for fat yield were noticed in this study and changes in estimates of h^2 for consecutive parities showed the opposite tendency than changes in other studies (h^2 was increasing with parity number) (Strabel and Misztal 1999).

Figure 1. Heritability of daily milk yields for first (◆), second (▲) and third lactation (■)

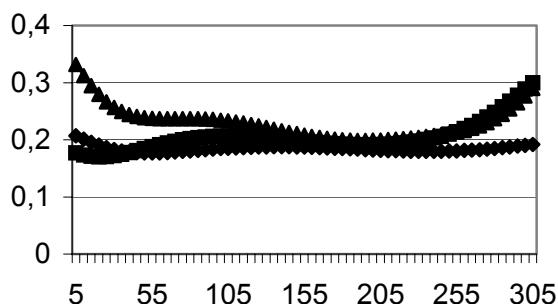
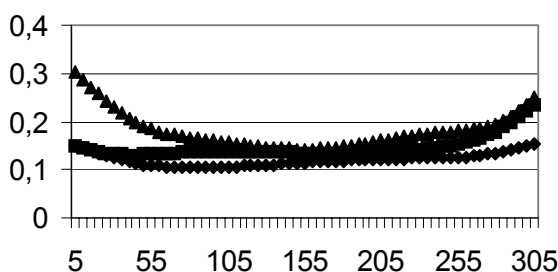
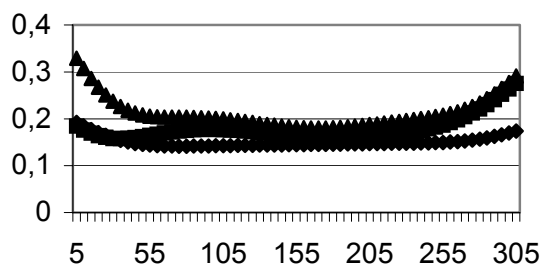


Figure 2. Heritability of daily fat yields for first (◆), second (▲) and third lactation (■)



Much higher estimates of heritability can be found in literature for Holsteins in Canada (Muir *et al.*, 2004) and in the Netherlands (Roost *et al.*, 2001). This could be probably caused by different data structure and slightly different environmental conditions between Poland and other countries.

Figure 3. Heritability of daily protein yields for first (◆), second (▲) and third lactation (■)



There are approximately 0.5 million of cows in milk recording system in Poland and test-day records have been available since 1995. Solving mixed model equations for the presented three-lactation model and TD yields for approximately 0.8 million of cows (calved in 1995-2001) took three days. Preconditioned conjugate gradient algorithm (Misztal *et al.*, 2002) was used on PC computer under Linux operating system. Thus the model seems to be feasible for routine genetic evaluation of Polish Black and White population.

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