

Animal Model Versus Polynomial Legendre Test-Day In Dairy Cattle

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ABSTRACT

The aim of the study was to compare the classical animal model (based on total milk for 305 days) with the Test-Day model (using monthly records of milk yield from Official Records of Performances). The data set derived from a total 175 animals (cows with records, parents of these animals and the descendants) from two Romanian breeds (Romanian Black Spotted and Montbeliarde), the phenotypic and the pedigree information arisen from National Research Development Institute for Animal Biology and Nutrition (IBNA-Balotesti). The selection criteria to be included in the analysis for each cow was to have at least 3 test-days and the days in milk between 200 and 330 for the Test-Day model and the total amount of the 305-day lactation yield for classical Animal Model respectively. Both models use B.L.U.P methodology and for that reason all the estimates were adjusted for fixed effects and all the breeding values and the solution for fixed effects were estimated simultaneous. For the animal model the fixed effects used was the breed and the year of performing and for the Test-Day model was an extra one, the test day effect. The correlation calculated between test days was very high (over 90%) for consecutive tests, and was getting lower when the days between tests was higher (under 40%). Also, in terms of heritability the values were in normal limits throughout lactation, except at the beginning and end of lactation period where these values were a little bit higher. The comparison of the ranking of breeding values with Spearman rank correlation shows that in 80% of the cases the ranking was similar for both models. As the ranking correlations shows, it is certain that the two models are very similar when they are used for genetic evaluation. But, in conclusion, we can say that for a better lactation curve estimation it is recommending to use test-day model for dairy cattle.

Keywords: animal model, Legendre Polynomial, test day models

INTRODUCTION

In Romania, the genetic evaluation of dairy cattle consists in using animal models including production traits based on normally standardized total milk yield at 305 days. Today, several countries use milk yield test-day model for genetic evaluation of dairy cows (Jensen 2001; Cobuci J.A. and Costa C.N. 2012). The main advantages of test-day models are: improved correction for environmental effects (Ptak and Schaeffer, 1993; Grosu and Rotar, 2015) and the ability to modeling the lactation curve for each cow (Dzomba E.F., 2010), leading to comparison with overall lactation curve and with the evaluation of lactation persistency (Jamrozik et al. 1997). One of the major problem of classical animal model is that by using the total amount of milk yield for 305 day, it makes the hypothesis that all the environmental factor action the same in every moment of lactation period, but it is very well known that the lactation curve have a different evolution in time. At the beginning of lactation the milk yield is increasing (approximately until day 60) after that it is the period when the quantity of milk it is the same from one day to another and then start to decrease until the drying period. Another important aspect in evolution of milk yield during lactation period is the gestation of the cow, when the calf it getting bigger and bigger the feed intake of the cow is decreasing and for that reason the milk quantity can be smaller. Also when we make the assumption that all the factor action the same throughout the lactation we are wrong because the fixed factor have different influence at different stages of lactation. Regarding test day models, it allows to solve the problems of fixed effects during lactation because the record are monthly and we can see the evolution from one month to another (Gharahveysi S. et al. 2012). It can model the shape of lactation curve more accurately and in the end we can obtain breeding values with higher accuracy. Another great advantage of test day models is that it can predict the lactation persistency (Kim B-W et al. 2009), and it can be see if there are different between bull's daughters and if they show superiority, information that can help producers to choose which bull to use in their herds. The objective of this study was to compare the traditional genetic evaluation system and test-day model, by using two dairy cattle breeds from Romania.

MATERIALS AND METHODS

Animals and production traits. A total of 175 animals (consisting in cows, their parents and their progenies) were evaluated based on performances of dairy cows from National Research Development Institute for Animal Biology and Nutrition (IBNA) experimental farm. Dairy cows belong to Montbeliarde (31 cows) and Romanian Black Spotted (38 cows) breeds. Milk yield was recorded at first lactation in 16 test-days. Data were filtered and animals with less than 3 test-days were eliminated. Also, cows under 200 or over 400 days

in milk were not taken into account. Table 1 summarizes number of animals, records and fixed effects from study.

Table 1. Number of test-days records, fixed effects, animals and mean daily milk yield in first lactation from studied animals

SPECIFICATION		NO./MEAN
TOTAL TEST DAY RECORDS		523
FIXED EFFECTS	Breed	2
	Performing year	2
	Test-days	16
ANIMALS	Total	175
	With records	69
MEAN TEST-DAY RECORD PER COW		7.58
MEAN DAILY MILK YIELD (KG)		19.37
DAILY MILK YIELD STANDARD DEVIATION (KG)		5.99

Ethical aspects. The cows from IBNA experimental facilities benefit of handle and care in accordance with the Romanian Law 206/2004 for handling and protection of animals used for experimental purposes. The study protocol was approved by the Ethical Committee of the IBNA.

Biometrical models. The first evaluation method is the **test-day model** with subsequent components (Grosu et al, 2015):

$$y_{ijkt} = TD_i + \sum_{m=0}^q (\beta_m \cdot \phi_{tjm}) + \sum_{m=0}^q (\alpha_{jm} \cdot \phi_{tjm}) + \sum_{m=0}^q (\gamma_{jm} \cdot \phi_{tjm}) + e_{tijk}$$

where:

y_{ijkt} = k milk yield of j cow, recorded at t time, in i test-day date;

TD_i = fix effect of i test-day date;

β_m = Legendre polynomial regression fixed coefficients;

α_{jm} = Legendre polynomial regression random coefficients for animals genetic values;

γ_{jm} = Legendre polynomial regression random coefficients for permanent environmental effects;

Φ_{tjm} = m milk yield Legendre polynomial vector of j cow at t time;

e_{tijk} = model residual.

In matrix notation the model became:

$$y = X_1 b + X_2 \beta + Z_1 \alpha + Z_2 \gamma + e$$

Breeding value will be estimated in any moment from 5-305 days range with further expression:

$$EBV_t = \alpha_{j_0} \cdot \phi_0(a_t) + \alpha_{j_1} \cdot \phi_1(a_t) + \alpha_{j_2} \cdot \phi_2(a_t)$$

Breeding value for a total of 305 days of lactation will be estimated with next formula:

$$EBV_{305} = \sum_{t=5}^{305} (EBV_t)$$

Second biometric model: **animal model** (introduced explicitly by Quaas and Pollak, 1980):

$$y_{ij} = \mu + h_i + a_j + e_{ij}$$

where:

y_{ij} = milk yield of j cow (normally standardized at 305 days);

μ = overall mean;

h_i = fixed effects of the model;

a_j = randomized effect of the model (genetic effects);

e_{ij} = model residual.

Breeding values for each animal can be obtained with general formula (V. Ducrocq, 1990):

$$\hat{a}_{ij} = \frac{(y_{ij} - \tilde{h}_i) + k \cdot d_j \cdot \left(\frac{\hat{a}_s + \hat{a}_d}{2} \right) + \sum_{j=1}^m \frac{1}{4} \cdot k \cdot d_p \cdot 2 \cdot \left(\hat{a}_{prog\ of\ \hat{a}_{ij}} - \frac{\hat{a}_{mate\ of\ \hat{a}_{if}}}{2} \right)}{n_j + k \cdot d_j + \sum_{j=1}^m \frac{1}{4} \cdot k \cdot d_p}$$

where:

a_{ij} = breeding value;

y_{ij} = phenotypic information;

n_j = number of records;

k = it is the ratio between the error variance divided by additive variance;

d = it is a constant and can have the next values:

- 2 if animal has two known parents;
- 1.33 if animal has only one known parent;
- 1 if animals has unknown parents;

Comparison between models were performed using Spearman correlation method applied to breeding values ranks.

RESULTS AND DISCUSSION

Breeding values were estimated for all the animals from data set, all estimates being adjusted for all other effects from the models. All effects are simultaneous estimated and predicted from each other. In Table 2 we have an example of EBV ranking for first 10 cows from data set.

Table 2. Estimated breeding values for the best 10 animals used in study

COW	EBV TEST- DAY	RANK TEST DAY	EBV ANIMAL MODEL	RANK ANIMAL MODEL
1	2173.79	1	499.45	3
2	2014.79	2	644.77	1
3	1893.43	3	67.81	28
4	1699.21	4	374.69	5
5	1589.73	5	509.92	2
6	1449.42	6	331.41	7
7	1447.64	7	472.59	4
8	1355.17	8	216.97	13
9	1230.65	9	223.63	11
10	1142.74	10	174.78	16

Data from Table 2 shows a wide similarity between ranks. Comparing the models, it can be noticed that 6 of 10 animals are among those ranked in both cases. Spearman rank correlation shown an 80% analogy between ranks. Also, using test day model, we can explain from the total variance more genetic influence and as table 2 shows an increase breeding value when we make the analysis by test day model, an increase in accuracy of estimation was obtained by Schaeffer, 2000.

One of the advantages of test-day model is a more accurate correction of the environmental effects. Those effects can be observed using a graphical analysis of heritability and genetic correlations between test days throughout lactation (Figure 1.).

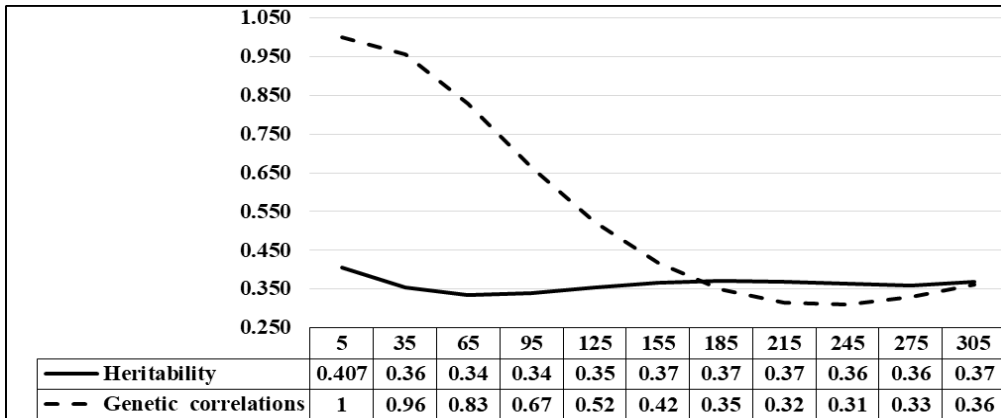


Figure 1. Evolution of heritability and genetic correlations throughout lactation (obtained by Test-Day method).

The heritability and genetic correlations at different days in milk (5 – 305 days) were calculated. As can be observed in Figure 1, genetic correlations between the test days is very high (0.96) on two consecutive tests, but decrease throughout lactation at the ends (0.36).

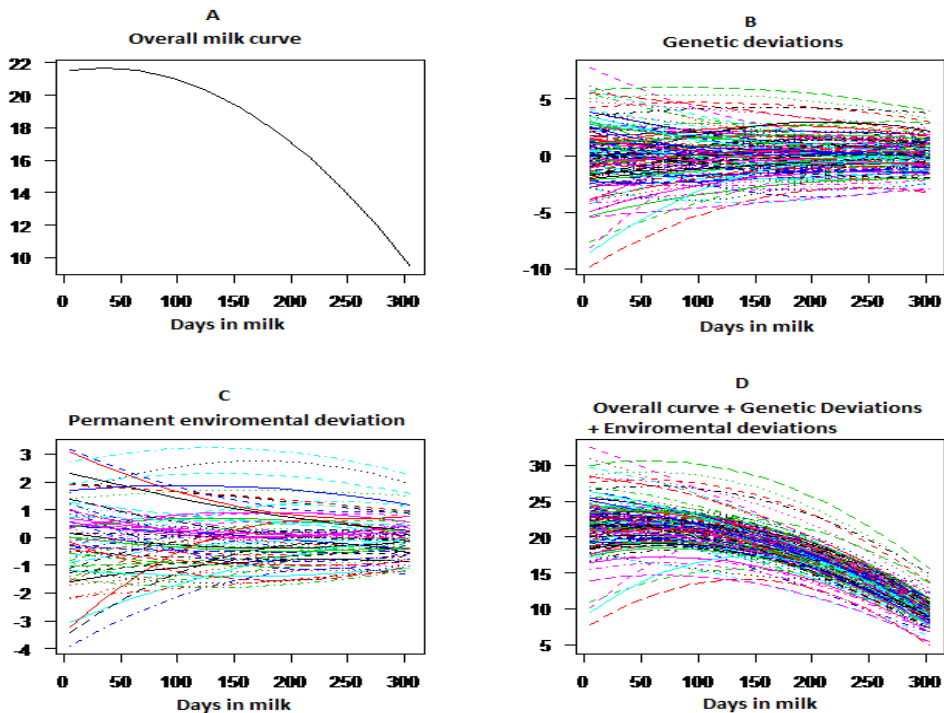


Figure 2. -Evolution of overall curves (A), genetic deviations (B), permanent environmental deviations (C) and graphical representation of estimated breeding value (D) throughout lactation.

Heritability is increased at the lactation extremities due to artefacts generated by Legendre polynomial procedure. Between 35 and 275 days in milk, heritability is trending normally. Hammami et. al. (2008) and Cobuci et al. (2010) show lower heritability in Holstein cattle.

Another advantage of test-day model is an increased ability of persistent lactation curve identification. In Figure 2 (A) can be observed overall milk curve trending. The sum of genetic deviations presented in Figure 2 (B) and of permanent environmental deviations (Figure 2(C)) generated estimated breeding value (Figure 2 (D)). The difference between overall and individual lactation curve will help to identify the most proper milking curve configuration, fitted with the farm management. Also, curve extrapolation can help to comparison between milk productions of different cows in the same moment of lactation.

CONCLUSION

The test-day model offer possibility to estimate more precise breeding values, with a better correction of environmental effects along lactation. Genetic evaluation of cows can be done also with just 3 controls over lactation, making much cheaper milk control program. High correlation ranks show a pronounced similitude between models, recommending test-day model in dairy cattle genetic evaluation.

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