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Comparative Research On Breeding Value Prediction For Milk Yield In Cattle

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Abstract

The paper compares four methods for breeding value prediction for milk production in cattle. The research was performed in experimental farm of the National Research Development Institute for Animal Biology and Nutrition (IBNA), Balotesti, Ilfov, Romania. The biological material consisted of 190 animals, 86 with performances, animals belonging to Montbeliarde, Black Spotted Romanian and Brown breeds. The studied trait was the test day milk yield. To enter the statistical analysis animals must fulfil the following requirements: minimum three test-days, minimum 100 days of lactation and a maximum of 330 days of lactation. The animal's breeding value was estimated separately based on the following biometric models: Wood, Ali and Schaeffer, Legendre Polynomial and P-Spline. The degree of agreement between the rankings of the same individuals using the four models was quantified with Spearman's rank correlation. Results showed a high degree of similarity between the 4 biometric models, leading to the conclusion that any of them could be used to predict animal breeding value. Although the results are similar, we recommend, for the practical genetic evaluation of cattle, for the specific trait (milk yield), the use of P-Spline function because its description of the lactation curve evolution was closest to the biological dynamics.

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1. Introduction

According to FAO statistics, it is estimated that the world population will reach 10 billion by 2050, compared with 7.5 billion today. Besides this demographic growth of the population, the rate of urbanization also increases, the current forecasts showing that about 30% of the world population will join the middle class. Under these conditions, in order to achieve food security for the population of the 2050s, the food demand will likely increase 60-70% compared to this moment, especially for protein (milk, meat and eggs). In cattle, milk production can be increased through the combined action of genetic an environmental factors. From the perspective of genetics factors, the identification of the animals with high genetic potential is a challenge for all specialists in animal breeding and genetics, both nationally and worldwide (Dragotoiu et al., 2015). Currently, the countries with animal husbandry developed in accordance with the methodologies recommended by ICAR and INTERBULL already use test-day models with fix and random regression. These regression coefficients, fix and random, can be estimated based on several classes of biometric models, parametric or nonparametric (Ali and Schaeffer, 1987; Ptak and Schaeffer, 1993; Schaeffer and Dekkers, 1994; Swalve, 2000).

2. Materials and Methods

A total of 190 animals were analyzed, of which, 86 cows with records, from the experimental farm of the National Research Development Institute for Animal Biology and Nutrition (IBNA), Balotesti. The animals were analyzed based on 3 lactations, from 2012 to 2015. Tobe eligible for the statistical analysis, the animals must meet the following requirements: minimum 3 test-days, minimum 100 days of lactation and a maximum of 330 days of lactation. The 86 animals with records belong to 3 breeds: Montbeliarde (35), Romanian Black Spotted (43) and Brown (8).

Table 1. Number of records, animals and herd-test-day

Category		Number	$\overline{X} \pm S_{\overline{X}}$ (kg)	S	CV (%)
Records	Lactation1	789	19.318 ± 0.186	5.24	27.1
	Lactation 2	357	20.83 ± 0.343	6.48	31.1
	Lactation 3	79	23.6 ± 0.833	7.41	31.4
Total records		1225	20.04 ± 0.168	5.89	29.4

Four models were used to estimate breeding value, as follows: Wood model; Ali & Schaeffer model; Legendre Polynomial model; P-Spline model.

Wood model:

In 1967 Wood proposed a variant of calculation, known as the gamma function (Wood, 1967):

$$y_t = a \cdot t \cdot exp^{-ct} \tag{1}$$

Which will became as follows:

$$y_{ijk} = HTD_i + \sum_{m=0}^{2}(b_m \cdot t_m) + \sum_{m=0}^{2}(\alpha_{jm} \cdot t_{jm}) + \sum_{m=0}^{2}(\gamma_{jm} \cdot t_{jm}) + e_{ijk} \tag{2}$$

Where: HTD_i - herd test day effect; b_m – fixed regression coefficients of the model; α_{jm} – random regression coefficients, for genetic effect; γ_{jm} – random regression coefficients, for permanent environmental effect; t - test day record; e_{ijm} - error of model.

Ali and Schaeffer model:
Ali and Schaeffer in 1987 used a logarithmic polynomial function (Ali and Schaeffer, 1987):

$$y_t = b_0 + b_1 \cdot \left(\frac{t}{305}\right) + b_2 \cdot \left(\frac{t}{305}\right)^2 + b_3 \cdot \log\left(\frac{305}{t}\right) + b_4 \cdot \left[\log\left(\frac{305}{t}\right)\right]^2 \tag{3}$$