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RESEARCHES REGARDING THE OPRIMIZATION OF THE MILK RECORDING IN ROMANIAN SPOTTED CATTLE BREED

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Abstract

This study aimed to determine the optimal number of records required to estimate the breeding value for milk production in Romanian Spotted cattle during the first and second lactations. Data from 9,235 test-day records (1,270 cows) for the first lactation and 9,984 records (1,409 cows) for the second were analyzed using the Best Linear Unbiased Prediction (BLUP) method in a Test-Day Random Regression model. Heritability estimates for milk yield, fat, and protein content ranged from 0.194 to 0.381 in the first lactation and 0.184 to 0.372 in the second. Although 10 test-day records were initially considered, results indicated that focusing on the first five intervals was sufficient, as they showed higher heritability. Reducing the number of test-day records to those with the highest genetic determination improves selection accuracy while lowering the costs of official milk performance recording. This streamlined approach enhances breeding efficiency, supporting genetic progress in Romanian Spotted Simmental cattle.

Key words*: BLUP, heritability, milk recording, regression model, Test-Day.*

INTRODUCTION

The genetic evaluation and selection of dairy cattle heavily rely on milk recording, which provides crucial information for calculating breeding values and enhancing overall production efficiency. For the Romanian Spotted breed, it is essential to optimize the number of milk recording tests to improve selection accuracy while minimizing performance recording expenses. An excessive number of test-day records may lead to increased costs without significantly improving genetic evaluations, whereas too few records could reduce the accuracy of selection (Pelmuș et al., 2021; Davidescu et al., 2023). Studies have shown that selecting the most informative test-day (Jensen, 2001) intervals can enhance the efficiency of genetic evaluations while maintaining reliable heritability estimates (Cecchinato et al., 2015). Furthermore, optimizing milk recording frequency can contribute to more sustainable breeding programs by reducing labor and testing costs while preserving genetic progress (Interbull, 2014).

The Romanian Spotted cattle, also referred to as Romanian Spotted Simmental, is a versatile breed raised for both dairy and beef production. This breed has adapted well to Transylvania's climate, where it is mainly found, as well as in Banat and North-Eastern Moldova. Its ability to thrive in these regions makes it a valuable asset to Romanian agriculture. Beyond its adaptability, the breed is known for its good milk yield, balanced fat and protein content, and favorable feed efficiency (Gantner et al., 2009). Moreover, the dual-purpose nature of Romanian Spotted cattle ensures its economic sustainability, as it contributes significantly to both milk and meat production sectors (Nistor et al., 2011). Ongoing genetic improvement programs aim to enhance production traits while maintaining the breed's resilience to environmental conditions and disease resistance.

Due to its strong genetic heritage, the breed exhibits high resilience to local environmental factors, including temperature variations and diverse feeding conditions. Romanian Spotted cattle are known for their adaptability to extensive and semi-intensive farming systems, making them a valuable asset to local farmers who seek sustainable and efficient livestock management. Their ability to maintain stable production levels under different management conditions highlights their economic importance (Rotar et al., 2020). Additionally, the breed demonstrates strong resistance to common diseases affecting dairy and beef cattle, reducing the need for veterinary interventions and contributing to lower production costs (Strabel & Misztal, 1999). These traits make Romanian Spotted cattle an ideal choice for small- and medium-scale farms, ensuring long-term productivity while aligning with sustainable agricultural practices.

The enhancement of dairy cows through genetic selection for characteristics such as milk yield, milk fat content, and breeding efficiency is influenced by various factors within the herd under evaluation. The genetic improvement process is influenced by several key elements. These include the range of observable and genetic diversity, the degree to which these characteristics are inherited, and the relationships between them. Moreover, the total productive capability of the evaluated cattle group is a significant factor in this genetic enhancement endeavor. In addition to genetic parameters, environmental factors such as nutrition, herd management, and climate conditions also play a crucial role in shaping production traits (García-Ruiz et al., 2016). Advances in genomic selection and marker-assisted breeding have further improved the accuracy of selecting animals with superior traits, accelerating genetic progress (Jamrozik et al., 1998). Furthermore, maintaining a balance between production efficiency and animal welfare is essential to ensure sustainable genetic improvement programs that benefit both farmers and livestock (Kaygisiz, 2013).

The use of test-day random regression models has been widely adopted in developed countries for genetic evaluation due to its ability to increase selection accuracy by utilizing multiple records and reduce production control costs while allowing for earlier selection (Jakobsen et al., 2002; Ptak & Schaeffer, 1993). Previous research has demonstrated that genetic parameters, such as heritability, fluctuate across different stages of lactation. Understanding these variations allows for the identification of the most informative test-day intervals, which can improve the precision of selection while minimizing unnecessary data collection. Moreover, random regression models provide a more detailed analysis of individual lactation curves, capturing genetic variability more effectively than traditional models (Strabel and Misztal, 1999). The application of the Best Linear Unbiased Prediction (BLUP) methodology in combination with Test-Day Random Regression Models has been widely used to analyze such phenotypic data, providing valuable insights into the genetic potential of dairy cattle (Grosu et al., 2019). These advancements contribute to more efficient breeding programs, ultimately enhancing the productivity and sustainability of dairy farming (Gantner et al., 2009).

This study aims to assess the optimal number of test-day records required for the estimation of breeding values in Romanian Spotted cattle during the first and second lactations. By analyzing a comprehensive dataset using advanced statistical models, we seek to determine the most effective recording strategy that maximizes genetic gain while reducing operational costs. Identifying the most informative test-day intervals is crucial for improving selection accuracy while minimizing redundant data collection. Additionally, optimizing milk recording frequency can enhance the cost-effectiveness of genetic evaluation programs and ensure a more sustainable approach to dairy cattle breeding (Pandey & Rajak, 2020). The findings of this research are expected to contribute to the refinement of milk recording protocols, ultimately benefiting dairy farmers and breeding programs through improved efficiency and selection accuracy. Moreover, integrating refined test-day models with genomic selection approaches could further accelerate genetic progress in dual-purpose breeds such as the Romanian Spotted cattle (Buaban et al., 2020).

MATERIALS AND METHODS

Two lactations were taken into account. From first lactation was analyzed a sample of 9,235 test recording belonging to 1,270 Romanian Spotted Simmental cows, in first lactation. From second lactation a sample of 9,984 test recording made of 1,409 of the same breed.

To determine the optimal number of controls for calculating the breeding value over a 5-305 day lactation period, we considered 10 controls.

The statistical analysis of the data was conducted using R software (version 4), employing the BLUP methodology within the Test Day Random Regression Model.

This study aimed to determine the optimal number of controls required for calculating the breeding value in the Romanian Spotted Cattle population.

The following biometrical model was used to describe the performances at the monthly control level:

$$y_{itklm} = HYS_l + AGE_m + DIM_t + \sum_{k=0}^{q} (\beta \cdot z_{itk}) + \sum_{k=0}^{q} (\alpha_{ik} \cdot z_{itk}) + \sum_{k=0}^{q} (\gamma_{ik} \cdot z_{itk}) + e_{itklm} \quad [1]$$

where:

y_{itklm} is the observation of cow i measured at time t within herd-year-season (HYS), subclass l and age (AGE) subclass m;

DIM_t is the fixed effect of DIM clases;

b is the fixed covariate effect on the ith cow;

α_{ik} and γ_{ik} are the kth random regression of additive genetic and permanent environmental effects for cow i, respectively;

z_{itk} is the kth order of LPs/P-Spline/NCS for cow i measured at DIM_t, DIM_t denote the order of LPs;

eitklm is the random residual.

The covariates are customized, case by case, depending on the biometric model used and the function used (Legendre polynomial, P-Spline or Natural cubic Spline functions).

In matrix notation, the model [1] can be rewritten as follows:

$$y = X_1b_1 + X_2b_2 + X_3b_3 + X_4\beta + Z_\alpha + Z_\gamma + e \quad [2]$$

where:

y = vector of TD milk yield record;

X_1= incidence matrix of fixed effect for HYS;

b_1 = vector of fixed effect for HYS;

X_2= incidence matrix of fixed effect for Age of calving;

b_2 = vector of fixed effect for Age of calving;

X_3= incidence matrix of fixed effect for Days in Milk;

b_3 = vector of fixed effect for Days in Milk (DIM);

X_4 = covariate matrix for Days in Milk (DIM);

β = fixed regression coefficients;

Z_1= covariates matrix for all animals;

α = random regression coefficients for the breeding value;

Z_2 = covariates matrix for cows with records;

γ = random regression coefficients for the permanent environmental effect;

e = vector of residual effects.

The system of equations corresponding to model [2] is as follows:

$$\begin{bmatrix} X^T \cdot X & X^T \cdot Z_1 & X^T \cdot Z_2 \\ {Z_1}^T \cdot X & {Z_1}^T \cdot Z_1 + \sigma_e^2 \cdot (A^{-1} \otimes G^{-1}) & {Z_1}^T \cdot Z_2 \\ {Z_2}^T \cdot X & {Z_2}^T \cdot Z_1 & {Z_2}^T \cdot Z_2 + \sigma_e^2 \cdot (I \otimes P^{-1}) \end{bmatrix} \cdot \begin{bmatrix} \tilde{b}_1 \\ \hat{\alpha} \\ \gamma \end{bmatrix} = \begin{bmatrix} X^T \cdot y \\ Z_1 \cdot y \\ {Z_2}^T \cdot X \end{bmatrix}$$

Where: $X = (X_1, X_2, X_3, X_4)$.

The (co)variance structure was assumed for random effects of model:

$$V = \begin{bmatrix} A \otimes G & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where:

Var (a) =A ⊗ G;

Var (a) = additive variance;

Where ⊗ is Kronecker product function;

Var (p) = I ⊗ P;

Var (p) = environmental variance;

G and P are the matrices of genetic and permanent environmental variances and covariances between random regression coefficients.

I = represents the identity matrix with the size equal with the number of cows with records;

σ_e^2= residual variance for lactation assumed to be constant throughout the lactation.

RESULTS AND DISCUSSIONS

A study on milk production in Romanian Spotted cattle during their first lactation showed an average daily milk yield of 18.76 kg, with fat and protein yields of 0.77 kg and 0.65 kg, respectively (Table 1).

Table 1. Average milk production performance of the Romanian Spotted Cattle breed for the first lactation

COP	n	Milk (kg) $\bar{X} \pm S_{\bar{X}}$	Fat (kg) $\bar{X} \pm S_{\bar{X}}$	Protein (kg) $\bar{X} \pm S_{\bar{X}}$
1	862	21.12±0.198	0.87±0.010	071±0.007
2	908	21.18±0.206	0.85±0.010	0.70±0.008
3	914	20.81±0.202	0.84±0.009	0.69±0.007
4	947	19.91±0.199	0.81±0.009	0.67±0.007
5	997	18.93±0.189	0.77±0.009	0.65±0.007
6	1,003	18.38±0.186	0.75±0.008	0.64±0.007
7	976	17.70±0.189	0.73±0.008	0.62±0.007
8	980	17.02±0.181	0.71±0.008	0.61±0.007
9	900	16.37±0.196	0.68±0.009	0.59±0.007
10	748	15.97±0.214	0.67±0.009	0.58±0.008
Average		18.76±0.195	0.77±0.009	0.65±0.007

The research utilized 9,235 test-day records, which demonstrated the breed's milk production capabilities. The results align with previous research conducted on comparable cattle groups. For instance, a study by Pelmuș et al. (2021) observed that the Romanian Spotted breed yielded an average milk production of 5,545 kg during a 305-day lactation cycle.

For the second lactation, the study evaluated 9,984 test-day records, where the mean daily milk yield increased to 19.76 kg, with fat and protein yields reaching 0.8 kg and 0.68 kg, respectively.

These values suggest a natural increase in milk production with lactation progression, a common trend observed in dairy cattle.

Table 2 has shown the average milk production performances of the breed, for the second lactation Romanian Spotted Cattle Breed.

Table 2. Average milk production performance of the Romanian Spotted Cattle breed for the second lactation

COP	n	Milk (kg) $\bar{X} \pm S_{\bar{X}}$	Fat (kg) $\bar{X} \pm S_{\bar{X}}$	Protein (kg) $\bar{X} \pm S_{\bar{X}}$
1	910	24.14±0.237	0.97±0.011	0.82±0.009
2	1,014	23.25±0.224	0.92±0.010	0.77±0.008
3	1,036	22.27±0.228	0.89±0.010	0.75±0.008
4	1,061	21.18±0.22	0.84±0.010	0.72±0.008
5	1,070	20.00±0.205	0.80±0.009	0.69±0.007
6	1,035	19.29±0.212	0.78±0.009	0.67±0.008
7	1,055	18.02±0.195	0.73±0.008	0.64±0.007
8	1,053	17.17±0.189	0.71±0.008	0.61±0.007
9	958	16.25±0.192	0.68±0.008	0.59±0.007
10	792	15.38±0.204	0.64±0.009	0.56±0.008
Average		19.76±0.210	0.8±0.009	0.68±0.008

When comparing these values with results reported for other Simmental breeds, Croatian Simmental cows (Gantner et al., 2009) exhibited similar performance, while Italian Simmental cattle (Cecchinato et al., 2015; Ablondi et al., 2023) had higher daily milk yields, ranging between 22.56 kg and 25.4 kg. This discrepancy may be attributed to differences in genetic selection, feeding management, and environmental conditions across different countries.

Comparable findings were reported by Gantner et al. (2009), who observed fat (0.75 kg) and protein (0.63 kg) yields akin to those in the current research. The genetic relationships among milk yield, fat yield, and protein yield were evaluated based on earlier investigations. In Holstein cattle, Hammami et al. (2008) discovered strong genetic correlations (0.98-0.99) between milk and protein yields, with slightly lower correlations (0.79-0.96) between fat and protein yields.

These results indicate that selection for one trait is likely to affect the others. Likewise, Buaban et al. (2020) noted moderate genetic correlations in Thai dairy cattle, with values ranging from 0.56 to 0.69 for milk-fat and milk-protein relationships. The calculation of genetic, environmental, and phenotypic variance components offered important insights into the heritability of milk production characteristics. The values of the causal components of phenotypic variance and heritability are presented in Table 3 for first lactation.

Table 3. The causal components of phenotypic variance and heritability for first lactation

Milk record nr.	Genotypic variance	Permanent environmental variance	Error variance	Phenotypic variance	Heritability
1	10.32	4.13	18.41	32.86	0.314
2	7.4	2.96	16.9	27.27	0.272
3	7.23	2.89	20.53	30.66	0.236
4	7.8	3.12	19.81	30.73	0.254
5	5.5	2.2	20.69	28.39	0.194
6	7.74	3.1	19.97	30.8	0.251
7	6.92	2.77	19.16	28.85	0.24
8	7.09	2.84	19.92	29.84	0.238
9	9.98	3.99	18.83	32.8	0.304
10	16.2	6.48	19.82	42.5	0.381

Genotypic variance ranged from 5.5 to 16.2, reflecting substantial genetic differences among individuals.

Permanent environmental variance was between 2.2 and 6.48, indicating the influence of environmental factors across multiple lactations.

Error variance was estimated between 16.9 and 20.69, representing unexplained variability.

Phenotypic variance varied from 27.27 to 42.5, capturing the combined effects of genetic and environmental contributions.

Heritability estimates ranged from 0.194 to 0.381, classifying these traits as moderately heritable.

The findings indicate that milk yield is genetically influenced but also significantly affected by environmental conditions. Higher heritability in the first five test-day intervals suggests that fewer but strategically chosen controls may be sufficient for accurate selection decisions.

A comparable trend was observed during the second lactation, where:

Genotypic variance ranged from 8.71 to 25.68, exhibiting a slight decrease compared to the first lactation.

Permanent environmental variance fluctuated between 3.48 and 10.27, demonstrating relative stability.

Error variance remained within the range of 30.01 to 35.69.

Phenotypic variance was recorded between 46.44 and 69.04, aligning with values observed in the first lactation.

Heritability estimates were slightly lower, ranging from 0.184 to 0.372, while still indicating a moderate genetic influence.

The values of the causal components of genetic, phenotypic, environmental variance and heritability are presented in Table 4 for the second lactation.

Table 4. The causal components of phenotypic variance and heritability for second lactation

Milk record no.	Genotypic variance	Permanent environmental variance	Error variance	Phenotypic variance	Heritability
1	16.36	6.54	32.14	55.04	0.297
2	11.74	4.69	30.01	46.44	0.253
3	11.47	4.59	35.69	51.74	0.222
4	12.36	4.95	34.94	52.25	0.237
5	8.71	3.48	35.09	47.28	0.184
6	12.27	4.91	33.74	50.91	0.241
7	10.97	4.39	33.3	48.67	0.225
8	11.24	4.5	33.57	49.3	0.228
9	15.81	6.32	32.92	55.05	0.287
10	25.68	10.27	33.09	69.04	0.372

Similar to the findings from the first lactation, the results suggest that prioritizing early test-day intervals represents an effective approach for optimizing recording strategies, reducing costs, and preserving selection accuracy.

Optimization of Test-Day Controls

The graphical analysis of genetic variance across test-day intervals revealed a distinct trend, indicating that heritability was highest during the first five test-day intervals. This finding suggests that genetic progress is directly influenced by the heritability of the analyzed trait. Specifically, the observed heritability values ranged from 0.194 to 0.381, implying that among the 10-11 recorded test-day intervals, focusing on the first 1-5 intervals would be sufficient due to their higher heritability (Figure 1). A similar pattern was observed in the second lactation, where heritability values ranged from 0.184 to 0.372, reinforcing the conclusion that the early test-day intervals provide the most genetically informative data (Figure 2). This trend is further illustrated in the graphical representation below, supporting the notion that optimizing the number of test-day records can enhance selection efficiency while minimizing recording efforts (Figures 1 and 2).

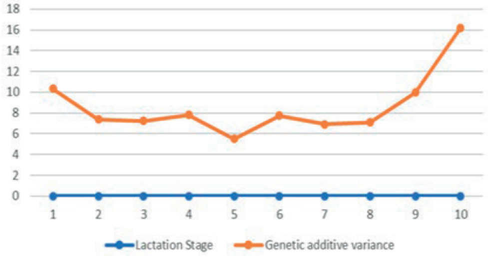

Figure 1. The evolution of additive genetic variance between 5-305 days in milk (DIM)

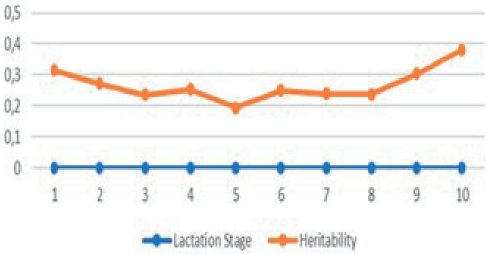

Figure 2. The evolution of heritability between 5-305 days in milk (DIM)

Recording milk yield during the first five test-day intervals provides the most genetically informative data for selection. Limiting test-day recordings beyond this threshold can lead to a substantial reduction in costs while maintaining selection accuracy.

CONCLUSIONS

This study aimed to determine the optimal number of test-day milk recordings required for accurate breeding value estimation in Romanian Spotted cattle during the first two lactations. The findings indicate that heritability estimates ranged from 0.194 to 0.381 in the first lactation and from 0.184 to 0.372 in the second, confirming a moderate genetic influence on milk yield, fat, and protein content. Notably, the analysis demonstrated that the first five test-day records provide sufficient genetic information for selection, as these intervals exhibit the highest heritability values. This strategic approach ensures accurate genetic evaluations while significantly reducing the costs associated with official performance recording.

Furthermore, the consistent pattern of higher heritability in early lactation suggests that genetic progress in milk production traits can be effectively achieved by focusing on the most informative test-day intervals. By refining traditional milk recording methods and integrating statistical models such as Best Linear Unbiased Prediction (BLUP), this research offers valuable insights for improving selection efficiency in the Romanian Spotted breed. These findings may also serve as a reference for optimizing milk recording systems in other dairy cattle breeds. Future research should further explore the impact of reduced testing frequencies on long-term genetic gains and the economic sustainability of dairy farming.

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