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ESTIMATION OF THE GENETIC PARAMETERS ON SPOTTED ROMANIAN CATTLE-SIMMENTAL TYPE, FOR PRODUCTION AND EXTERIOR TRAITS - REVIEW

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Abstract

Romanian Spotted cattle, a Simmental-type breed, play a significant role in Romania's livestock industry due to their dual-purpose nature, combining milk and beef production. Estimating genetic parameters such as heritability, genetic correlations and breeding values is critical for designing effective breeding programs. This review synthesizes findings from various studies on production traits (milk yield, fat, and protein content) and exterior traits (conformation, body measurements). The focus is on methods like Best Linear Unbiased Prediction (BLUP), Restricted Maximum Likelihood (REML) and genomic selection, highlighting their applications and comparative efficiency. The review identifies trends, challenges in genetic evaluations, and future directions for enhancing breed productivity and resilience, offering insights for sustainable breeding strategies that balance production and adaptability.

Key words: *genetic parameters, exterior traits, heritability, production traits, Romanian Spotted cattle.*

INTRODUCTION

Livestock genetic improvement remains a cornerstone of sustainable animal agriculture, directly influencing productivity, adaptability, and profitability across production systems. Among Romania's native and improved breeds, the Romanian Spotted cattle (Simmental-type) hold a prominent position due to their dual-purpose nature, providing both milk and meat in significant quantities (Okstate.edu, 2025; Neamț et al., 2024; Pelmuș et al. 2022; Nistor et al, 2014; Grosu et al., 2019). The breed originates from a successful cross between the Simmental breed and the local Grey Steppe cattle, resulting in animals that combine high production potential with adaptability to diverse environmental and management conditions. These attributes have made the Romanian Spotted cattle a vital component of the national livestock sector and a valuable genetic resource within Europe's Simmental population.

The economic importance of this breed has driven continuous interest in understanding the genetic basis of its production and exterior traits. Genetic parameters, such as heritability, genetic correlations, and breeding values, are essential indicators in evaluating the potential for improvement of quantitative traits (Dragotoiu et al., 2015; Carvalho et al., 2023; Pritchard et al., 2013; Batanov et al., 2020; Xue et al., 2022). Through their estimation, breeders and geneticists can identify traits under strong genetic control, predict selection responses, and design efficient breeding programs (Grigolleto et al., 2020; Gebreyesus et al. 2021; Oliveira et al., 2021; Frigo et al., 2012). Production traits - such as milk yield, fat percentage, and protein content - directly influence farm profitability and product quality, while exterior or conformation traits - such as udder depth, body size, and muscularity - impact longevity, functionality, and overall productivity.

Advances in quantitative genetics and molecular biology have transformed the accuracy and scope of genetic evaluations. Modern statistical methods like Best Linear Unbiased Prediction (BLUP) and Restricted Maximum Likelihood (REML) have provided robust frameworks for estimating breeding values and variance components, while genomic selection (GS) has introduced new opportunities to accelerate genetic gain by integrating genomic information with phenotypic data. These tools allow for the more precise identification of superior animals, even in the early stages of development, significantly reducing generation intervals and improving the efficiency of selection programs.

In Romania, ongoing research has aimed to refine the estimation of genetic parameters for the Romanian Spotted breed to support breeding objectives aligned with both production efficiency and sustainability. However, challenges such as limited data integration, variability in management systems, and the need for genomic infrastructure still constrain progress. Addressing these challenges is critical for enhancing the competitiveness of the breed in an increasingly demanding agricultural environment.

Therefore, this review compiles and synthesizes the most relevant studies focusing on the estimation of genetic parameters for production and exterior traits in Romanian Spotted (Simmental-type) cattle. By comparing findings from national and international research, the paper highlights the heritability values, methodological approaches, and applications of advanced genetic models, offering insights into the genetic improvement potential of the breed. The synthesis aims to inform future strategies for sustainable genetic selection, balancing productivity, adaptability, and animal welfare in Romania's evolving livestock sector.

MATERIALS AND METHODS

A review was conducted to synthesize and critically analyze the findings from genetic evaluations of Romanian Spotted cattle, Simmental type, with respect to both production and exterior traits. The review encompassed studies by Grosu et al. (2019), Pelmuș et al. (2021), Trivunović et al. (2011), Panić & Vidović (2006), Barba et al. (2016), Dragotoiu (2015) among others, aiming to compile and compare data on key production indicators such as milk yield, fat and protein content, as well as various body conformation traits. By integrating information from multiple sources, this review highlights the heritability estimates, genetic correlations, and potential for selection across traits, providing a comprehensive understanding of the genetic architecture of this important dual-purpose breed. Moreover, it underscores knowledge gaps and future research directions necessary to optimize breeding programs, enhance productivity, and improve overall breed sustainability in Romanian livestock systems.

RESULTS AND DISCUSSIONS

Genetic Parameters of Production Traits

Milk Yield

Milk yield is a primary trait in dual-purpose cattle. Studies report moderate-to-high heritability values (Table 1).

Pelmuș et al. (2021) found heritability for milk yield in Romanian Spotted cattle ranging from 0.377 to 0.417, indicating strong genetic control.

Table 1. Heritability estimated for milk yield

Heritability	Study
0.37-0.41	Pelmuş et al. (2021)
0.35	Trivunović et al. (2011)
0.22	Panić & Vidović (2006)
0.30	Barba et al. (2016) Pantelimon farm
0.28	Barba et al. (2016) Afumați farm
0.46 first lactation	Dragotoiu et al. (2015)
0.23 second lactation	
0.31 the third lactation	

Trivunović et al. (2011) reported similar values (0.350) for Simmental cattle. These values confirm milk yield as a highly heritable trait, emphasizing the potential for genetic improvement through selection.

Panić & Vidović (2006) found heritability for milk yield in Simmental cattle to be 0.22, indicating a low-to-moderate genetic influence. This suggests that while genetic improvement is possible, environmental factors play a substantial role in milk yield variation. Effective breeding programs should therefore combine genetic selection with optimized environmental management practices to achieve noticeable gains in milk production.

Fat and protein content

Fat and protein content are critical for determining milk quality and processing suitability. These traits often exhibit higher heritability compared to milk yield (Table 2).

Pelmuş et al. (2021) found heritability for fat content in Romanian Spotted cattle ranging from 0.11 to 0.23, indicating low genetic influence and a substantial role of environmental factors. Protein content heritability ranged from 0.30 to 0.37, reflecting moderate genetic control and potential for improvement through selection.

Table 2. Fat and protein content heritability

Fat content heritability	Protein content heritability	Study
0.11-0.23	0.30-0.37	Pelmuş et al. (2021)
0.35	-	Barba et al. (2016) Pantelimon farm
0.31	-	Barba et al. (2016) Afumați farm
0.26 (I lactation) 0.30 (II lactation)	0.17 (I lactation) 0.31 (II lactation)	Coşa et al. (2022)

Coşa et al. (2023) reported heritability for fat content as 0.26 in the first lactation and 0.30 in the second lactation, indicating moderate genetic influence across lactations. Protein content heritability was 0.17 in the first lactation, suggesting low genetic control, and 0.31 in the second lactation, highlighting stronger genetic influence in later lactations.

Lactation persistency

Lactation persistency, reflecting the ability to maintain milk production throughout the lactation cycle, is another economically significant trait.

Both studies consistently indicate a low genetic influence for this trait, with heritability estimates of 0.017 for Panić & Vidović (2006) and 0.014 for Trivunović et al. (2011). These near-identical values highlight the limited genetic variability for this characteristic, emphasizing the importance of environmental and management factors. A summary of these results is presented in Table 3

Table 3. Heritability for lactation persistency

Heritability for duration of lactation	Study
0.017	Panić & Vidović (2006)
0.014	Trivunović et al. (2011)

This consistency suggests that duration of lactation is not a genetically robust trait across Simmental-type cattle populations.

Genetic Parameters of exterior Traits

Conformation Traits

Conformation traits, such as udder depth, teat placement, rump length, and muscularity, play a vital role in cattle productivity and longevity. These traits impact milking efficiency, structural soundness, and overall adaptability, making them key targets in breeding programs. Heritability estimates for these traits vary, reflecting the balance between genetic influence and environmental factors, guiding effective strategies for improvement (Table 4).

Table 4. Heritability for conformation traits

Trait	Heritability	Study
Udder depth	0.23	Grosu et al., 2019
	0.35	Kirschten, 2001
Teat placement	0.25	Grosu et al., 2019
Body depth	0.30	Grosu et al., 2019
Rump length	0.54	Grosu et al., 2019
Hip width	0.33	Grosu et al., 2019
Pasterns	0.19	Grosu et al., 2019
	0.13	Kirschten, 2001
Muscularity	0.39	Grosu et al., 2019
	0.42	Kirschten, 2001

Grosu et al. (2019) found that the udder depth (0.23) and teat placement (0.25) exhibit low-to-moderate heritability, indicating that while genetic improvement is possible, environmental factors such as nutrition and management practices also play a significant role in trait expression.

Grosu et al. (2019) observed that the rump length (0.54) and muscularity (0.39) show high heritability, suggesting strong genetic control. These traits can be rapidly improved through selective breeding, offering opportunities to enhance structural and production characteristics.

Kirschten (2001) presented that the udder depth (0.35) and muscularity (0.42) have moderate-to-high heritability, highlighting their genetic potential for improvement. Consistent selection efforts can yield substantial progress in these traits.

Grosu et al. (2019) and Kirschten (2001) observed that the pasterns (0.19 and 0.13, respectively) demonstrate low heritability, emphasizing the dominant role of environmental factors like housing and flooring in determining these traits. Improvements in pastern traits will rely more on management interventions than on genetic selection.

Body measurements

Traits, such as thoracic perimeter and height at croup are critical body measurements in livestock that reflect overall growth, structural soundness, and productivity potential. Thoracic perimeter is associated with lung and heart capacity, influencing an animal's stamina and feed efficiency, while height at croup is a key indicator of skeletal development and adaptability. Both traits are essential for evaluating performance and selecting animals with superior genetic potential in breeding programs.

According to Barba et al. (2016), the thoracic perimeter exhibited moderate heritability values - 0.37 at Pantelimon and 0.35 at the Afumați farm (Table 5) - suggesting a balanced contribution of both genetic and environmental factors to this trait.

Table 5. Heritability for body measurements

Trait	Heritability estimate	Study
Thoracic perimeter	0.37 (Pantelimon) 0.35 (Afumati)	Barba et al. (2016)
Height at croup	0.47 (Pantelimon) 0.49 (Afumati)	Barba et al. (2016)

The consistency of heritability estimates across farms suggests that this trait remains relatively stable and can be reliably targeted for genetic improvement. These results emphasize the thoracic perimeter as a valuable selection criterion, with the potential to enhance body structure and feed intake capacity in Romanian Spotted cattle. The moderate level of genetic control further indicates that steady progress can be achieved through well-structured breeding programs.

In the same study, Barba et al. (2016) reported high heritability values for height at the croup - 0.47 at Pantelimon and 0.49 at the Afumați farm (Table 5) - indicating strong genetic determination. The consistency of these estimates across farms suggests that this trait is less affected by environmental variation compared to others. Consequently, height at the croup emerges as an ideal candidate for genetic improvement, enabling faster selection response and contributing to improved structural soundness and overall productivity in Romanian Spotted cattle

Methodological approaches in estimation

Estimating genetic parameters in Romanian Spotted cattle requires robust analytical techniques. Several statistical methodologies are applied to derive heritability, genetic correlations, and breeding values effectively. The following approaches are commonly used:

- *Best Linear Unbiased Prediction* (BLUP) is a cornerstone method in genetic evaluation, particularly for predicting breeding values in livestock. It effectively partitions phenotypic variance into genetic and environmental components by accounting for both fixed effects (e.g., management practices) and random genetic effects within a linear mixed model framework (Van der Werf, 2009).

The accuracy of BLUP in estimating breeding values is influenced by the depth and quality of pedigree data, as well as the validity of model assumptions. Incorporating genomic information has led to the development of Genomic BLUP (GBLUP), which utilizes genomic relationship matrices to enhance prediction accuracy. Studies have demonstrated that GBLUP can achieve equal or superior accuracy in breeding value predictions compared to traditional pedigree-based BLUP methods (Fernando & Garrick, 2013).

Furthermore, advancements such as single-step GBLUP (ssGBLUP) have been introduced to integrate genomic and phenotypic data seamlessly, improving the modeling of genetic effects in populations with varying pedigree depths. Research indicates that ssGBLUP effectively models small cattle populations, providing unbiased and more accurate genomic estimated breeding values (GEBVs) (Curzon et al., 2024).

Overall, BLUP and its genomic extensions remain integral to modern breeding programs, offering robust tools for the accurate prediction of genetic merit across diverse traits and populations.

- *Restricted Maximum Likelihood* (REML) is a robust statistical method widely used for estimating variance components, which are essential for calculating heritability in genetic studies. Unlike traditional methods such as Analysis of Variance (ANOVA), REML provides unbiased estimates by accounting for fixed effects and focusing on the likelihood of residuals. This approach leads to more accurate estimations of genetic parameters, especially in complex hierarchical data structures. For instance, a study by Lourenço et al. (2017)

introduced a robust derivative-free REML framework for variance component estimation in genetic studies. Their method demonstrated improved estimation of variance components and heritability by reducing bias and increasing precision, particularly in the presence of data contamination or deviations from model assumptions. Additionally, research by Dao et al. (2021) developed practical methods for estimating asymptotic variances and constructing confidence intervals for genetic parameters using REML in genome-wide association studies (GWAS). Their approach provided computationally convenient solutions for variance estimation, enhancing the reliability of heritability estimates in high-dimensional genetic data.

These studies underscore the effectiveness of REML in providing reliable estimates of heritability and genetic correlations, making it a preferred method in quantitative genetics for evaluating complex traits.

- *Genomic Selection* (GS) enhances genetic evaluation by integrating molecular marker data with phenotypic observations, improving accuracy over traditional pedigree-based methods. By utilizing genome-wide single nucleotide poly-morphism (SNP) markers, GS captures comprehensive genetic variance, expediting genetic gains and reducing generation intervals. In dairy cattle breeding, GS enables the identification of genetically superior animals at a much earlier age, allowing for accurate genomic estimated breeding values (GEBVs) before animals reach sexual maturity (Hayes et al., 2013).

The implementation of GS in Romanian cattle breeds has been explored, with studies indicating its potential to revolutionize genetic improvement programs. Research suggests that genomic selection can transform genetic improvement for economically important traits in Romanian cattle breeds, despite challenges such as data collection and economic feasibility (Hayes et al., 2013).

However, the adoption of GS is contingent upon the availability of comprehensive genomic databases and the development of cost-effective genotyping methods. These resources are essential to fully realize the benefits of GS in Romanian Spotted cattle and other breeds.

In summary, genomic selection offers a promising avenue for accelerating genetic progress in livestock populations, including Romanian Spotted cattle, by leveraging extensive genomic data to inform breeding decisions.

- *Bayesian methods*

Bayesian inference techniques offer alternative solutions for parameter estimation by incorporating prior distributions of genetic effects (Fernando et al., 2014). These methods are particularly valuable for non-normally distributed traits or when dealing with limited data. Bayesian approaches allow flexibility in modeling complex genetic architectures but are computationally demanding. Their application in Romanian Spotted cattle is less documented but presents future opportunities for refining parameter estimates.

Software Tools

Modern genetic evaluation relies on specialized software packages:

- ASReml and DMU are popular for REML-based analyses;
- Pest and MiX99 facilitate BLUP evaluations;
- GEMMA and BLUPF90 are used in genomic prediction frameworks.

The choice of methodology depends on the trait of interest, data structure, and breeding objectives. Proper model specification and validation remain critical to obtaining reliable and interpretable genetic parameters.

Implications for breeding programs

Milk production improvement

Moderate heritability values for milk yield and higher values for fat and protein content indicate that production traits can be effectively improved through selective breeding. Genomic selection and marker-assisted selection offer additional precision.

Exterior traits and longevity

High heritability values for conformation traits underscore their potential for improvement. Selecting for traits like udder depth and teat placement can enhance milking efficiency and reduce health issues, contributing to longevity and productivity.

Balancing milk and beef objectives

As a dual-purpose breed, Romanian Spotted cattle require a balanced approach to genetic improvement. Breeding programs must consider the trade-offs between milk and beef traits to optimize overall profitability.

Challenges and future directions

While significant progress has been made, several challenges remain:

- *Data quality and availability*: inconsistent recording practices across farms can limit the accuracy of genetic evaluations. Standardized data collection protocols are therefore essential to ensure reliable and comparable information.
- *Integration of genomics*: although genomic tools show great promise, their adoption in Romania has been slow due to cost and infrastructure constraints. Increased investment in genomic resources and training is crucial to fully leverage these technologies.
- *Future research priorities*: efforts should focus on expanding datasets to include more diverse traits, such as disease resistance and feed efficiency, as well as incorporating advanced genomic tools to refine heritability estimates. Additionally, developing sustainable breeding programs that balance production performance with environmental resilience is essential for the long-term success of animal breeding initiatives.

CONCLUSIONS

The estimation of genetic parameters in Romanian Spotted cattle offers valuable insights for targeted genetic improvement. Moderate to high heritability values for both production and exterior traits indicate substantial potential for genetic progress. By integrating advanced statistical models and genomic tools, breeding programs can enhance both the productivity and adaptability of this important breed.

A holistic approach that considers genetic, environmental, and management factors is essential for sustainable development. Opportunities exist in improving genetic evaluations through genomic technologies and in better accounting for genotype-environment interactions. Collaborative efforts among research institutions, farmers, and policymakers are key to driving progress.

Furthermore, strengthening infrastructure for data collection, combined with educational initiatives, will support more effective breeding strategies. Maintaining a balanced focus on milk and beef objectives will ensure that Romanian Spotted cattle remain competitive, resilient, and sustainable within evolving agricultural systems.

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