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RESEARCH ON THE GENETIC VALUE OF A FLECKVIEH BREED HERD AND ITS INFLUENCE ON THE PRODUCTIVE LEVEL

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Abstract

The present study aims to highlight the influence of the genetic merit of a Fleckvieh cattle herd on milk and beef production. The primary data were collected from 82 cows with completed lactations and 51 of their offspring, managed under a semi-intensive system on a farm located in Iași County, Romania. Using SAVC (Statistics, Analysis of Variance, and Covariance) software, the data were statistically processed to calculate the mean, variance, standard deviation, standard error of the mean, and coefficient of variation. For milk production, parameters included milk yield (MY), fat content (% F), and protein content (% P), as well as somatic cell count (SCC). For beef production, data regarding birth weight (BW) and average daily gain at 200 days (ADG200) were analyzed. Within the herd, the highest mean for milk yield was 6,643.80 kg/lactation, while the highest means for fat and protein percentages were 4.04% and 2.93%, respectively. Regarding beef production traits, the progeny group [family] of sire 20215 recorded the highest means, with a BW of 32.67 kg and a ADG200 of 973.33 g/day. The performances recorded by these animals fall within the specific standards of the breed, demonstrating that the herd possesses significant genetic potential.

Key words*: Fleckvieh, milk, meat production.*

INTRODUCTION

The Fleckvieh is a dual-purpose cattle breed exhibiting high performance in both milk and beef production, representing approximately 41 million head of cattle worldwide. Young cattle achieve an average average daily gain of 900 to 1,200 g up to 200 days of age. The average 305-day milk yield of cows ranges from 6,000 to 8,500 kg, with a content of 4.10 % fat and 3.40% protein. The average adult body weight ranges between 650 kg and 850 kg (Piccand et al., 2014).

In Romania, the breed's genetic improvement program aims to enhance milk production while simultaneously accounting for beef production and functional traits (Gociman et al., 2020). The breeding goals combine functional traits (with a weighting of 44%), milk production (38%), and beef performance (18%). The objective is to produce healthy, long-lived, productive, and efficient animals for both milk and beef outputs. The economic benefits of raising dual-purpose cattle are further reflected in the efficient utilization of increasingly limited resources, as high-quality forage is utilized in a balanced manner (Maciuc, 2006).

While the performance of the Fleckvieh breed is extensively documented in Central Europe, its phenotypic expression is influenced by genotype-by-environment interactions (Filipčík et al., 2020).

Fewer studies precisely demonstrate how Fleckvieh populations perform under the influence of management systems specific to Northeastern Romania.

The novelty of this study lies in its comprehensive analysis of growth performance in young bulls alongside the performance of dams from the same population, thereby providing an overview of dual-purpose production efficiency under the environmental conditions of the Moldavian Plateau.

The objective of the present study was to evaluate the influence of genetic factors on the zootechnical performance of a Fleckvieh cattle herd (Bucher et al., 2024). The main quantitative and qualitative indicators of milk production in adult cows were analyzed, as well as the determining parameters of beef production in young fattening bulls. Although microclimate factors and nutritional management modulate phenotypic expression, the genetic structure of the analyzed population remains the major

determinant of productive performance and carcass quality (Acatincăi, 2004).

MATERIALS AND METHODS

The research was conducted from January 2023 to December 2025 within a cattle cattle-breeding facility located in Iași County (Northeastern Region of Romania). The biological material for this study consisted of a herd of 82 adult cows belonging to the Fleckvieh breed (Figure 1) and 51 of their offspring. The animals were housed and managed under a semi-intensive system, benefiting from homogenous microclimate and herd management conditions. Nutritional management was provided through the administration of a Total Mixed Ration (TMR), computer-formulated to fully meet the energy, protein, and mineral requirements of the lactating cows.



Figure 1. Fleckvieh cows on the farm (original source)

The weighted daily ration structure per head of animal comprised: 4.00 kg alfalfa hay, 28.00 kg corn silage, 5.30 kg ground corn grain, 3.10 kg sunflower meal, along with a mineral intake consisting of 0.034 kg dicalcium phosphate and 0.06 kg feed-grade limestone [forage chalk]. The primary data regarding the quantitative and qualitative performance of milk production were extracted from the official analysis reports issued following official milk recording (OMR). The phenotypic indicators monitored were: milk yield per standard 305-day lactation (MY, kg), fat content (F, %), protein content (P, %), and somatic cell count (SCC X 10^3/mL). To ensure the accuracy of the transgenerational genetic potential evaluation, the statistical processing focused on three consecutive completed standard lactations, namely the 2nd, 3rd, and 4th lactations (SL2, SL3, SL4). Data pertaining to the first lactation (SL1) were excluded from the experimental model, considering that primiparous cows do not fully express their maximum productive ceiling due to concurrent processes of somatic growth and development. Regarding beef production traits, the analysis was based on raw data recorded in the technical logs of the farm, targeting calf birth weight (BW, kg) and average average daily gain from birth to 200 days of age (ADG200, g/day). The primary processing of the data and the calculation of measures of central tendency and dispersion (arithmetic mean, standard error of the mean, standard deviation, and coefficient of variation) were performed using the specialized SAVC (Statistics, Analysis of Variance, and Covariance) software package. This software was used to determine the degree of homogeneity of the experimental groups for the traits under study. To test the statistical significance of differences between means and to analyze the correlations and complex interdependencies between milk and beef indicators, the SPSS v.20.00 software package for Windows was utilized. The statistical significance thresholds considered for interpreting the results according to zootechnical methodology were set at $p < 0.05$ (significant), $p < 0.01$ (distinctly significant), and $p < 0.001$ highly significant).

RESULTS AND DISCUSSIONS

Within the study, the progeny structure and productive performances of several sire families were analyzed to evaluate the genetic potential and the stability of traits transmission for milk and beef production to the offspring. Regarding milk production, data concerning the productive performance and the values of the main quality indicators were processed for the second, third, and fourth standard lactations (SL2, SL3, SL4) across the entire analyzed cow herd.

Table 1 presents the mean values of milk production for the sire families within the studied herd. Thus, it can be observed that the productive performance of the cows ranges between 4,955 and 6,977 kg of milk per lactation.

Table 1. Values of means ($\bar{X}$) and coefficient of variability (V%) for milk yieald (MY) per lactation

Bull	Number of descendances	MY (kg)/ SL2 ($\bar{X}$)	V %	MY (kg)/ SL3 ($\bar{X}$)	V %	MY (kg)/ SL4 ($\bar{X}$)	V %
53756	18	6628.00	5.00	6642.60	9.71	6660.20	12.00
53435	13	6122.25	17.13	5782.00	15.32	6134.25	20.10
54464	11	6358.00	10.13	5847.00	16.31	6019.25	20.48
13272	6	5438.33	7.30	5666.00	19.34	6351.67	12.51
53050	7	5685.00	14.89	4955.00	20.43	6246.33	16.69
53433	6	5745.00	9.13	6199.00	12.67	5850.00	6.54
37218	6	6862.50	31.56	6780.50	4.29	6278.00	12.28
70264	9	6157.50	11.84	5685.00	27.59	5904.50	13.93
52033	6	5791.00	2.83	6977.00	4.26	5103.50	10.00

For milk production traits, sire 53756 exhibits the largest progeny group, with 5 daughters and 13 granddaughters within the herd, followed by sire 53435 with 4 daughters and 9 granddaughters, and sire 54464 with 4 daughters and 7 granddaughters recorded. The progeny of sire 53050 comprises 3 daughters and 4 granddaughters, while sire 59672 has 3 daughters and 6 granddaughters. Sires 53433, 37218, and 52033 each have 2 daughters and 4 granddaughters, and sire 70264 presents a progeny group consisting of 2 daughters and 3 granddaughters. The analysis of lactation performance across the three consecutive completed lactations (SL2, SL3, and SL4) highlights pronounced inter-line variability, driven by the genetic potential of the sires. Within the second lactation (SL2), the daughters of sire 37218 recorded the highest mean yield of 6,862.50 kg of milk per lactation, a performance that deviates positively from the general breed average reported in Eastern European semi-intensive operations (Maciuc, 2006).

However, this group was characterized by heterogeneity, with the coefficient of variation reaching a value of V % = 31.56%, indicating non-uniformity in individual performance and increased genotype instability in response to farm management factors. In contrast, during the same lactation stage (SL2), the daughters of sire 53756 achieved an average yield of 6,628.00 kg of milk per lactation, demonstrating homogeneity for this trait. This phenotypic uniformity denotes high stability in trait transmission from the paternal ancestor. At the opposite spectrum, the progeny group of sire 13272 recorded the lowest productive level (5,438.33 kg of milk per lactation), a value falling below current breeding standards for the breed, suggesting an inferior breeding value of this sire for milk production. In the third lactation (SL3), the group belonging to sire 37218 consolidated its top position in quantitative terms, recording 6,780.50 kg of milk per lactation. Unlike the previous stage, the trait showed evident genetic stabilization, materialized by an extremely low coefficient of variation (V % = 4.29%), which confirms that the expression of productive potential becomes more predictable as the herd reaches biological maturity.

Performance consistency is also firmly supported by the line of sire 53756, whose daughters achieved 6,642.60 kg of milk per lactation. The poorest results in SL3 were attributed to the progeny of sire 53050 (4,955.00 kg of milk per lactation), a performance with marked heterogeneity, translating into genetic instability and a non-uniform adaptive response to farm management conditions. In the advanced stage of exploitation, represented by the fourth lactation (SL4), the progeny group of sire 53756 ranked first, with a mean production value of 6,660.20 kg of milk per lactation.

Maintaining high phenotypic uniformity throughout the entire production dynamic (SL2-SL4) validates the genetic superiority of this sire relative to the rest of the analyzed nucleus. During the same period, the lines of sires 53435 and 54464 exhibited moderate mean yields and heterogeneous profiles, reflecting less conserved hereditary transmission mechanisms. The minimum yield in SL4 was reached by the progeny of sire 52033 (5,103.50 kg of milk per lactation), confirming the placement of this line within the category of genetic resources with a deficient dual-purpose potential for the lactation component.

The overall comparative evaluation of the three lactations indicates that while the line of sire 37218 excels punctually in the early stages, the line of sire 53756 offers the most robust productive consistency and metabolic resilience along the lactation curve.

The average production level obtained by the high-performing lines in this herd (6,600-6,800 kg) aligns with results obtained in similar Fleckvieh populations (Ducháček et al., 2020), demonstrating that a well-optimized semi-intensive management system can efficiently exploit the local genetic pool despite limitations induced by regional climate stress (Filipčík et al., 2020). From the perspective of future selection, sire 53756 is recommended as a proven bull for the milk yield per standard lactation trait within this nucleus.

The significance of productive differences among the studied paternal lines was established by statistical testing of the null hypothesis, with the interpretation of variability based on the following relevance thresholds:

- $p < 0.05$ (significant): validates the existence of real differences between the performance of daughters from different sires at the same lactation stage, such as the productive superiority of sire line 37218 compared to line 13272 within SL2;
- $p < 0.01$ (distinctly significant): confirms a pronounced genetic determination of the quantitative trait for lines that conserve their hierarchical position when transitioning from one lactation to another, despite microclimate changes during the experimental years;
- $p < 0.001$ (highly significant): demonstrates that extreme differences in production (the yield difference of 1,873.5 kg of milk in SL4 between the daughters of high-performing sire 53756 and those of sire 52033) are dictated by differing breeding values.

Table 2. Values of mean ($\bar{X}$) and coefficient of variability (V %) for fat (F %), protein (P %) and number of somatic cells (x 10^3 NSC/mL)

Bull	Number of descendances (n)	Lactation rank	Fat content (F %)		Protein content (P %)		NSC (10^3/mL)	
			($\bar{X}$)	V%	($\bar{X}$)	V%	($\bar{X}$)	V%
53756	18	LN2	4.29	17.99	3.03	5.67	117.08	25.47
		LN3	3.86	15.92	2.88	11.61	537.32	41.38
		LN4	3.49	8.14	2.72	12.09	421	56.41
53435	13	LN2	4.11	11.25	3	11.30	115.10	12.35
		LN3	3.88	10.32	2.77	14.26	129	14.48
		LN4	4.13	14.32	2.71	11.88	210	51.28
54464	11	LN2	3.93	14.11	2.57	9.07	58	12.00
		LN3	3.71	11.26	2.76	10.38	396	18.93
		LN4	3.87	11.63	2.57	12.21	222	25.59
13272	6	LN2	3.81	4.62	3.19	10.52	231	33.14
		LN3	4.50	11.91	2.80	16.50	93	31.00
		LN4	3.82	14.92	2.71	17.07	145	18.21
53050	7	LN2	3.57	13.25	2.93	25.59	91.90	18.50
		LN3	3.62	8.35	2.57	11.66	99	14.21
		LN4	3.83	10.54	2.84	8.86	60	12.61
53433	6	LN2	3.83	2.77	3.00	8.00	121	22.01
		LN3	3.97	1.25	2.00	4.18	470.50	20.21
		LN4	4.00	11.21	3.00	4.23	223	27.92
37218	6	LN2	3.66	8.11	2.55	19.41	186	19.90
		LN3	4.20	23.57	3.35	6.33	235.85	32.22
		LN4	4.07	20.65	2.39	3.25	376	17.00
70264	9	LN2	3.58	5.14	3.95	10.88	300	34.85
		LN3	3.15	2.24	2.63	13.93	336.30	24.90
		LN4	3.31	15.71	2.23	6.98	465	15.31
52033	6	LN2	3.55	9.96	2.84	5.72	210	32.01
		LN3	4.04	5.07	2.77	22.17	110	28.76
		LN4	3.67	4.43	2.92	0.97	532	19.89

The analysis of milk quality indicators (Table 2) highlights pronounced inter-line variability, reflecting the manner in which paternal selection influences the synthesis of useful milk components. Within the second lactation (SL2), the progeny group of sire 53756 stood out due to superior performances, recording a mean value of 4.29% fat and 3.03% protein.

The uniformity of this group (characterized by high-to-moderate homogeneity) indicates a high capacity for hereditary transmission of traits to the offspring. This was maintained during subsequent lactations (SL3 and SL4), where the daughters of sire 53756 exhibited stable profiles (3.86-4.20% fat; 2.72-2.88% protein).

The productive behavior of this line confirms findings in the literature, where certain Fleckvieh lines manifest a remarkable stability of the quality curve throughout their productive life (Filipčík et al., 2020). In contrast, the progeny of sire 37218 exhibited oscillating dynamics and a high degree of heterogeneity in SL2 (with V % for fat and protein exceeding stability thresholds), although individual punctual means were relatively high (4.20% fat in SL3). This association between high means and marked heterogeneity suggests an increased sensitivity of the genotype to environmental factors and a reduced capacity for genetic fixation of the trait during the early stages of exploitation.

A biological phenomenon of interest was observed in the progeny of sire 70264 in SL2, which recorded a maximum protein content (3.95%) but a sharp minimum for fat content in SL3 (3.15%). This phenotypic dissociation reflects the partial independence of genetic determinism for the two major milk components and confirms the complexity of breeding the Fleckvieh breed for quality traits.

The inferior lines, represented by sires 52033 and 53343 (which reached minimums of 3.55% fat and 2.00% protein, respectively), indicate the presence within the herd of genotypes with a deficient breeding value for milk quality, requiring selective culling.

From a quantitative genetics perspective, these inter-line differences are justified by the moderate-to-high heritability ($h^2 = 0.25$-0.40) of fat and protein percentages reported for the Fleckvieh breed (Maciuc, 2006). The results indicate that, under unified nutritional management (a single TMR ration), selection based on high-performing paternal lines (such as the line of sire 53756) represents an efficient strategy for consolidating milk quality while limiting the uncontrolled dispersion of performance in animal exploitation.

The evolution of somatic cell count (SCC) across the three lactations represents a fundamental indirect indicator of mastitis resistance and the immune status of the mammary gland. Unlike the quality parameters, the SCC analysis reveals generalized structural heterogeneity across all analyzed lines, with no single family falling into the category of homogeneous groups. In SL2, mean values oscillated within wide limits, from an optimal minimum of 58 x 10^3 cells/mL (line 54464) up to values of 300 x 10^3 cells/mL. Even from this early stage, lines such as those of sires 53756 and 53435 demonstrated frequent exceedances of the ideal physiological threshold (100 - 150 x 10^3 cells/mL), suggesting a latent genetic susceptibility to subclinical udder inflammation.

As the animals advanced in age, in SL3 and SL4, an exacerbation of both mean values and dispersion indices was observed. This phenomenon is best illustrated by the line of sire 53756, whose daughters recorded means of 537.32 x 10^3 cells/mL in SL3 and 421 x 10^3 cells/mL in SL4.

Substantial parallel increases were also identified in lines 54464 and 52033, whose extremes migrated toward the range of 210- 532 x 10^3 cells/mL. From a biological standpoint, this upward dynamic of SCC correlated with lactation number reflects the cumulative effect of teat sphincter microtraumas induced by mechanical milking and the physiological wear of the secretory glandular tissue (Filipčík et al., 2020).

In addition, the low heritability of this trait (h^2~ 0.15) explains why phenotypic variation is dominated by physiological factors (milking management, housing hygiene, and individual mammary pathology) (Mihai et al., 2019). However, maintaining constant moderate homogeneity and relatively low SCC values throughout the study in the lines of sires 54464, 53050, and 13272 suggests the existence of exploitable genetic variability for infection resistance. In modern Fleckvieh breeding programs, where functional and health traits carry a major selection weight (44%),

identifying and promoting these lines with controlled SCC represents a necessity to ensure productive longevity and reduce veterinary treatment costs on Romanian farms.

The results of the main statistical estimators for birth weight and average daily gain are included in the data in Table 3.

Table 3. Principal estimates for calving weight (BW) and average daily gain (ADG200)

Bull	Number of descendances (n)	Traits	$\bar{X}$	s_x	V %	MIN.	MAX.
54463	10	BW (kg)	31.20	0.59	15.39	29	34
		ADG200 (g/day)	914	28.06	8.63	800	1050
20191	18	BW (kg)	31.11	0.91	7.71	27	35
		ADG200 (g/day)	891.11	21.40	7.98	810	1100
54547	15	BW (kg)	31.80	0.86	5.88	28	35
		ADG200 (g/day)	903.33	25.61	4.93	820	990
20192	2	BW (kg)	30.50	0.68	2.32	30	31
		ADG200 (g/day)	955	16.52	8.14	900	1010
54461	3	BW (kg)	31	1	3.23	30	32
		ADG200 (g/day)	916.67	80	25.73	890	940
20215	3	BW (kg)	32.67	0.45	7.70	30	35
		ADG200 (g/day)	973.33	11.91	5.84	910	1020

The genetic structure of the analyzed herd for beef production traits highlights a contrasting numerical distribution among male offspring (sires' sons). The primary families were dominated by the lines of sires 20191 (n = 18 sons) and 54547 (n = 15 sons), followed by the sons of sire 54463 (n = 10 sons).

Lines 54461, 20125 (20215), and 20192 exhibit a limited representation, pooling between 2 and 3 offspring per sire - a scenario frequently encountered in commercial operations where bloodline rotation is practiced. Regarding birth weight (BW), the calculated mean values ranged from 30.50 kg (line 20192) to 32.67 kg (line 20215). From a biological standpoint, this pronounced uniformity in birth weights (with groups classified as homogeneous) reveals a rigorous control of the maternal factor and

gestation management, but also an intrinsic characteristic of the Fleckvieh breed, which tends to maintain moderate birth weights to prevent dystocia (Bucher et al., 2024).

The sole exception was represented by the line of sire 54463, which fell into the moderate homogeneity class, a fact correlated with a variation range of 5 kg (29.00-34.00 kg). The total absence of heterogeneous lines for the BW trait demonstrates remarkable stability in the hereditary transmission of this trait across the entire breeding nucleus.

The analysis of growth dynamics through average average daily gain from birth to weaning (ADG200) reveals an outstanding biological potential specific to this dual-purpose breed, with means ranging from 891.11 g/day (line 20191) to a maximum of 973.33 g/day (line 20215). A particularly strong performance was also achieved by the progeny of sire 20192 (955.00 g/day), with both lines highlighting sound genetic potential for early muscle accretion rates.

From a genetic perspective, a statistical paradox is observed in the line of sire 20191: although the group is classified as homogeneous (V % = 7.98%), it exhibits the largest absolute variation range (290 g/day, with values ranging between 810 and 1,100 g/day). Biologically, this phenomenon is explained by the large sample size (n = 18), which allowed the full spectrum of polygenic genetic recombinations to manifest under environmental influences without destabilizing the overall group mean.

At the opposite spectrum, the line of sire 54461 was defined as heterogeneous, recording a wide dispersion in individual growth rates among its offspring, despite a narrow absolute range (890-940 g/day). This pronounced heterogeneity within a limited sample suggests strong instability in the transmission of beef breeding value by the paternal genitor, with the offspring being highly reactive to fluctuations in the barn's structural microclimate.

When comparing these results with recent scientific literature focused on Fleckvieh performance under the pedoclimatic conditions of Romania, the values obtained for ADG200 (approaching or exceeding the 900-950 g/day threshold in 5 out of the 6 lines) confirm an excellent feed conversion efficiency of TMR rations into muscle tissue (Kosińska-Selbi et al., 2020). The results consolidate the status of the Fleckvieh breed as a viable economic alternative in the region, demonstrating that targeted selection utilizing the lines of sires 20215 or 20192 can maximize young beef production without inducing major risks associated with dystocic calvings on the farm.

CONCLUSIONS

The genetic structure of the analyzed herd denotes a pronounced inter-line variability for both quantitative and qualitative milk traits. The absence of a single paternal line that aggregates peak performances across all traits reflects the antagonistic genetic correlations between milk yield and the concentration of useful dry matter components (fat, protein). This scenario underscores the necessity of implementing weighted selection indexes rather than unidirectional selection.

For commercial farms focused on maximizing delivery volume, the line of sire 53756 represents an important genetic resource, recording a remarkable mean of 6,643.80 kg of milk per standard lactation. Conversely, for milk processing operations where coagulation yield is dictated by solids-not-fat (SNF), the use of lines 13272 and 53435 (with a maximum of 4.04% fat) or line 70264 (with a peak of 2.93% protein) is recommended to compensate for their lower quantitative potential.

Somatic cell count (SCC) proved to be the most unstable trait, being heavily influenced by genotype-by-environment interactions. In breeding programs aimed at increasing mastitis resistance and improving the functional longevity of cows, the line of sire 53050 presents major applicative interest, demonstrating the most stable and lowest SCC level (83.56 x 10^3 cells/mL), in contrast to line 53756.

Regarding young cattle, the line of sire 20215 positioned itself as the most valuable dual-purpose genetic resource within the herd, excelling in both optimal birth weight (32.67 kg, which reduces the risk of maternal dystocia) and the highest growth rate (ADG200 = 973.33 g/day). This line is strongly recommended for producing offspring intended for intensive fattening.

All identified mean values fall within the biological standards of the Fleckvieh breed; however, the dispersion of performances confirms the need for targeted corrective mating strategies.

It is proposed to utilize sire 53756 to improve quantitative milk traits and sire 20215 to consolidate the growth rate of young cattle, thereby ensuring the sustainable and balanced exploitation of this dual-purpose breed within the breeding area of Iași County.

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