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Research article

EVALUATION OF MILK COMPONENTS AND SOMATIC CELL COUNT IN MONTBÉLIARDE DAIRY COWS

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ABSTRACT

The Montbéliarde (MO) breed is part of the Jurassic branch, originating from Bos frontosus and giving rise to the Pie Rouge group of breeds. This study aimed to evaluate the milk components and somatic cell count (SCC) in a selected herd of Montbéliarde cattle. The data for the evaluation of milk components and SCC in the Montbéliarde herds considered were provided by the B.S. SR database. A total of 1,015 dairy cows from the years 2019 to 2022 were included in the evaluation, which assessed the daily milk yield (DMY, kg), fat content (%), protein content (%), lactose content (%), and SCC (cells/ml). Basic statistical and variability characteristics were analyzed using the SAS software. The following average values for the daily milk traits and SCC in Montbéliarde cows were recorded: 27.09 kg DMY, 3.99% fat, 3.63% protein, 4.83% lactose, and 380.28 somatic cells/ml (SCC). In 2019, a total of 791 samples were analyzed, yielding an average of 26.24 kg DMY, 3.95% fat content, 3.67% protein content, 4.75% lactose content, and 366.86 cells/ml SCC. For the years 2020, 2021, and 2022, higher average values for the daily milk yield, milk components, and SCC were observed. The correlation between the SCC and milk components was low, negative, and statistically highly significant. The following correlation coefficients between the SCC and daily milk yield, fat percentage, protein percentage, and lactose percentage were recorded: r = -0.1060, r = 0.0439, r = 0.0654, and r = -0.3662, respectively. In the linear model for SCC evaluation, the lactation order had the highest effect (R^2 = 0.0379), whereas the sire effect was found lower (R^2 = 0.0232).

Key words:
Montbéliarde, milk components, somatic cell count, correlation, coefficients of determination

Abbreviations:
DMY - daily milk yield; FC - fat content; LC - lactose content; PC - protein content; SCC - somatic cells count

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INTRODUCTION

The Montbéliarde (MO) breed is part of the Jurassic branch, originating from Bos frontosus and giving rise to the Pie Rouge group of breeds. Therefore, the breed is part of the Simmental and Fleckvieh families, and is a member of both the World Simmental Fleckvieh Federation (WSFF) and the European Simmental Federation, which it chaired

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from 1993 to 1997 (Montbéliarde Association). These cattle are renowned for their milk, which is traditionally processed into Emmental and Gruyère cheese (Allouche et al. 2018; Sadek et al., 2021).
The somatic cells count (SCC) in milk is widely used to monitor udder health and milk quality (Alhussien and Dang, 2018; Rienesl et al., 2022). The composition of cow's milk is critical not only for the dairy industry but also for its nutritional value and processability. The quality and quantity of milk depend on both genetic and non-genetic factors, as outlined below. Many genetic factors, such as the effects of sire, season, parity, breed, and age, influence milk components and SCC (Borkowska and Januś, 2010; Ivanov et al., 2017; Alhussien and Dang, 2018; Tančin et al., 2018; Marinov et al., 2019; Bujko et al., 2018b, 2019, 2020; Sahin, 2023). However, significant non-genetic factors, such as nutrition (Juráček et al., 2020) and breeding conditions (Barnouin et al., 2005; Bujko et al., 2018a), also play a crucial role.
Focusing on evaluating milk production traits, milk component content, reproduction, SCC, and the relationships between these factors, as well as the influence of various determinants in Montbéliarde cattle and their crossbreeds, several studies have been published by authors such as Barnouin et al. (2005), Borkowska and Januś (2010), Koç (2011), Kuczyńska et al. (2012), Zółkiewski et al. (2018), Karamfilov and Nikolov (2020), and Sadek et al. (2021).
The objective of this paper was to evaluate the milk components and somatic cell count in a selected herd of Montbéliarde cattle.

MATERIAL AND METHODS

The data for the assessment of milk components and somatic cell count (SCC) in the herd of Montbéliarde dairy cows considered were obtained from the database of the Slovak Breeding Services (B.S. SR, S.E.). A total of 1,015 dairy cows (8,001 control samples) from the years 2019 to 2022 were observed during the evaluation of the following parameters: daily milk yield (DMY) in kg, fat content (FC) in %, protein content (PC) in %, lactose content (LC) in %, and SCC in ml^{-1}.
The dairy cows were grouped by lactation order as follows: "1" - first lactation, "2" - second lactation, "3" - third lactation, "4" - fourth lactation, "5" - fifth lactation, and "6" - sixth lactation and higher. According to the genetic proportion, the cows were classified by breed-type as MO 0 (the dairy cows with a genetic proportion of pure Montbéliarde blood ≥ 87.5%), MO 1 (the dairy cows with a genetic proportion of pure Montbéliarde blood from 75% to 87.4%), and MO 2 (the dairy cows with a genetic proportion of pure Montbéliarde blood from 50% to 74.9%). On the basis of the SCC values, the cows were divided into the following five groups: I: < 100,000 cells/ml, II: 100,000–400,000 cells/ml, III: 401,000–500,000 cells/ml, IV: 501,000–1,000,000 cells/ml, and V: > 1,000,000 cells/ml. According to the DMY, the cows were classified into 3 groups: M1: < 17.44, M2: 17.44–36.74, and M3: > 36.74.
Basic statistical and variable characteristics were evaluated using the Statistical Analysis System (SAS, 2016). The correlation analysis (procedure CORR) was applied to reveal the relationship between SCC and milk traits: daily milk yield (DMY), fat (FC), proteins (PC), and lactose (LC) content, respectively. The linear procedure (One-Way Analysis and GLM) was used for the final analysis. The statistical significance (P-value), F-test value, and the coefficient of determination (R^2) for the milk components (DMY, FC, PC, and LC) and SCC were evaluated in relation to the following factors: the year and month of control, lactation order, herd, breeding type, and sire. The following linear model with fixed effects was used for the computations:

$$Y_{ijklmno} = \mu + H_i + YM_j + b_k + c_l + d_m + f_n + e_{ijklmno}$$

where:
μ = mean value, H_i = effect of herd (A, B, C), YM_j = effect of years and month of control (1 to 48), b_k = sire (1 to 56), c_l = breeding type (1, 2, 3), d_m = parity (1, 2, 3, 4, 5, 6^+), f_n = cod_DMY (1, 2, 3), or f_n =cod_SCC (I., II., III., IV., V.), $e_{ijklmno}$ = residual error.

RESULTS AND DISCUSSION

The basic traits of milk components (DMY, FC, PC and LC) and somatic cell count (SCC) in the Montbéliarde dairy cows were as follows: 27.09 ± 9.65 kg daily milk yield (DMY), 3.99 ± 0.82% fat content (FC), 3.63 ± 0.35% protein content (PC), 4.83 ± 0.32% lactose content (LC), and 380.28 ± 919.39 x 10^3 somatic cell count in ml^{-1} (SCC). In the evaluation year of 2019, a total of 791 samples were analysed, showing an average of 26.24 ± 8.55 kg daily milk yield, 3.95 ± 0.75 % fat content, 3.67 ± 0.39% proteins content, 4.75 ± 0.29% lactose content, and 366.86 ± 1,076.92 x 10^3 cells x ml^{-1} SCC. The values for DMY (in kg) and SCC (somatic cell count/ml x 10^3) in the evaluated

population exhibited high variability, with coefficients of variation of 35.61% for DMY and 241.77% for SCC (Table 1). In the years 2020, 2021 and 2022, higher average values for the daily milk yield, milk components, and SCC were observed. These results are consistent with the findings of Borkowska and Januś (2010), Koç (2011), Kuczyńska et al. (2012), and Zółkiewski et al. (2018). Borkowska and Januś (2010) reported that Montbéliarde dairy cows produced milk of high cytological quality, with an average somatic cell count of 465,000 cells/ml, and 76.3% of the samples had the SCC up to 400,000 cells/ml, which is in line with our results and the European Commission's regulation (EC, 2004).

Table1. Descriptive statistics for the milk components and SCC in the Montbéliarde cows considered (2019–2022)

Trait	n[1]	Mean[2]	SD[3]	CV[4]	Min.	Max.	Mode[5]	Median[6]
DMY (kg)		27.09	9.65	35.61	3.3	68.6	16.6	26.3
FC (%)		3.99	0.82	20.43	1.54	8.97	3.80	3.95
PC (%)	8,001	3.63	0.35	9.78	2.24	6.54	3.59	3.61
LC (%)		4.83	0.32	6.70	1.99	5.66	4.92	4.89
SCC (cells/ ml.10^3)		380.28	919.39	241.77	1.0	1,4602	10.0	92.0

Legend: DMY - daily milk yield; FC - fat content; LC - lactose content; PC - protein content; SCC - somatic cells count; n[1] - Number of observation; [2]Mean; SD[3] - Standard deviation; CV[4] - Coefficient of variation; Min. – Minimum; Max. – Maximum; [5]Mode - the value that appears most often; [6]Median - the value separating the higher half from the lower half of the data

The correlation analysis between the traits of daily milk yield (DMY), fat content (FC), protein content (PC), lactose content (LC), and SCC by Pearson's coefficient is summarized in Table 2. The correlations between SCC and daily milk yield (DMY), and between SCC and lactose content, were low to moderate and negative (r = -0.106 and r = -0.366, P < 0.001). Conversely, the correlations between SCC and fat content (FC) and SCC and protein content (PC) were low and positive (r = 0.043 and r = 0.065, P < 0.001). These findings are consistent with those of several other authors (Koç, 2011; Dadpasand et al., 2013; Alhussien and Dang, 2018; Barbosa et al., 2019). The published data by De Freitas et al. (2017) showed similar correlation coefficients between the daily milk yield (kg), fat content (%), protein content (%), and lactose content (%) with SCC: r = -0.18116, r = -0.16943, r = -0.37156, and r = 0.39230, respectively.

Table 2. Pearson's correlation coefficients between the SCC and milk production traits

Traits	DMY (kg)	Fat (%)	Proteins (%)	Lactose (%)	SCC (cells/ ml.10^3)
DMY (kg)	…….	-0.17202***	-0.33119***	0.42151***	-0.10600***
Fat (%)		……..	0.31569***	-0.00708***	0.04392***
Proteins (%)			……..	-0.21204***	0.06548***
Lactose (%)				……..	-0.36628***

Legend: DMY - daily milk yield; SCC - somatic cells count; Significant differences: $^{***}P < 0.001$

The effect of herd, years and months of control, sire, parity, and genetic coding (cod_DMY or cod_SCC) were found to be statistically significant for the SCC and DMY (Table 3).

Table 3. Analysis of variance for the DMY, SCC, and selected traits in the Montbéliarde dairy cows (2019–2022)

Traits	SCC			DMY		
	DF[1]	F-value	R -Square[2]	DF[1]	F-value	R -Square[2]
Herd	3	7.55***	0.001887	3	792.77***	0.165445
Years_month_control	48	2.60***	0.015177	48	7.13***	0.040427
Sire	56	3.43***	0.023260	56	14.54***	0.091477
Breeding_type	3	2.87***	0.000720	3	18.27***	0.004547
Parity	6	62.95***	0.037955	6	46.75***	0.028404
Cod_DMY or Cod_SCC	3	39.14***	0.009713	5	144.66***	0.067618
All factors	**118**	**18.72*****	**0.078742**	**120**	**830.94*****	**0.330070**

Legend: DMY - daily milk yield; SCC - somatic cells count; DF[1] - Degrees of freedom; R-Square[2] - Coefficient of determination; Significant differences: *** $P < 0.001$

In the linear model, the highest coefficient of determination for the SCC was related to the order of lactation (R^2 = 0.037955), followed by the sire (R^2 = 0.023260). For the DMY and milk components, the highest effect for fat

content (%) was from the sire (R^2 = 0.024929), whereas the highest effect for lactose content (%) was also from the sire (R^2 = 0.144237). The highest effect for protein content (%) was attributed to the herd (R^2 = 0.042148). All the effects observed were statistically significant (P < 0.0001). These results align with those of Borkowska and Januś (2010), Tančín et al. (2018), Bujko et al. (2018b, 2019), Marinov et al. (2019), and Sahin (2023). According to Borkowska and Januś (2010), Ivanov et al. (2017), and Marinov et al. (2019), somatic cell count is significantly influenced by factors such as sire, parity, and herd.

CONCLUSION

In conclusion, the analysis of the years 2020, 2021, and 2022 revealed higher average values for the daily milk yield (DMY), milk components (fat content (FC), protein content (PC), and lactose content (LC)), and somatic cell count (SCC) compared to 2019. The highest coefficient of determination for the SCC was attributed to the lactation order, followed by the sire. For the milk components, the sire had the most significant effect on the daily milk yield, fat content, lactose content, and protein content.

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Data availability statement (optional): The datasets analyzed in the current study are not publicly available but can be obtained from the corresponding author upon reasonable request.

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