Journal of Animal and Feed Sciences, 27, 2018, 97–104 *https://doi.org/10.22358/jafs/90015/2018*
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The relationship between somatic cells and milk traits, and their variation in dairy sheep breeds in Slovakia

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KEY WORDS: ewes, decadic logarithm, somatic cell count, milk yield, milk composition

Received: 15 June 2017
Revised: 5 December 2017
Accepted: 1 June 2018

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ABSTRACT. The objective of this study was to analyse milk traits (milk yield from morning milking, and fat, protein and lactose contents) and somatic cell count (SCC) in dairy sheep breeds in Slovakia: Tsigai (TS), Improved Valachian (IV) and Lacaune (LC), and their crosses (IV × LC and TS × LC). Milk performance testing was performed between 2010 and 2013. Mixed model for milk traits included fixed factors: SCC class (low, medium high), lactation number, month in milk, year-month of measurement, genotype, lactation number × month in milk interaction, lactation number × SCC class interaction, and random effects of ewe and residual error. Mixed model for $\log_{10}$SCC (decadic logarithm of SCC) included the same factors except for SCC class and lactation number × SCC class interaction. Instead, covariates of milk yield and milk components were considered. Milk yield and lactose content decreased ($P \leq 0.05$ and $P \leq 0.01$, respectively), whereas fat and protein contents increased ($P \leq 0.05$ and $P \leq 0.01$, respectively) with increasing SCC. Similar trends were revealed when relationships between $\log_{10}$SCC and milk yield and milk components were investigated through linear regressions and correlations (however, not all regressions were statistically significant, also correlations between $\log_{10}$SCC and milk yield and between $\log_{10}$SCC and fat content were very weak). To ensure the effectiveness of mastitis control programmes, further research is needed to understand an importance of somatic cells function as an indicator of health status which may affect ewe udder, milk yield and milk components.

Introduction

Dairy sheep sector is a traditional branch of livestock sector in Slovakia. Local breeds: Tsigai (TS) and Improved Valachian (IV) are the most numerous breeds. Highly productive specialized dairy breeds: East Friesian and Lacaune (LC) were launched in the 1970s and 1990s, respectively. In order to increase milk yield of local breeds, two- and three-breed crossbred composite populations (either on base of TS or IV) were formed during two last decades. Daily milk yield, fat and protein contents and factors affecting their variation in dairy sheep were studied in detail (Oravcová et al., 2006, 2007). Not only daily milk yield, fat and protein contents are good determinants of the quality of sheep milk, but also somatic cell count (SCC) is an important udder health indicator (Abdelgawad et al., 2016). Mastitis is a costly health problem in dairy ewes (Arias et al., 2012); mammary infections damage udder tissue

(Burriel, 1997) and increase SCC (Pengov, 2001). Somatic cells and their relationship with milk yield and milk components were studied in sheep recently (e.g., Gonzalo et al., 1994; Olechnowicz et al., 2009; Vršková et al., 2015). Also, studies investigating associations between SCC and bacterial pathogens in ovine and goat milk were published (Hariharan et al., 2004; Bagnicka et al., 2011).

In Slovakia, the analysis of occurrence of somatic cells in sheep milk is not involved in regular milk recording due to its high cost (Tančin et al., 2017). Nevertheless, a distribution of somatic cells and factors affecting SCC (Margetín et al., 1995; Idriss et al., 2015) as well as relationship between SCC and milk traits (Vršková et al., 2015; Tančin et al., 2017) were analysed. Field study analysing 1086 bulk milk samples revealed only 7.3% of the bulk samples in the category below 0.5×10^6 cells · ml^{-1} and 49% of samples above 1×10^6 cells · ml^{-1} (Tomáška et al., 2015). It means that more detailed research on mastitis control in dairy practice in Slovakia is needed.

Thus, the objective of the study was to analyse and compare milk traits (milk yield from morning milking, and fat, protein and lactose contents) and $\log_{10}$SCC (decadic logarithm of SCC) and its relationships with the most important factors affecting these traits in purebred (TS, IV and LC) and crossbred (TS × LC and IV × LC) dairy ewes in Slovakia.

Material and methods

Data on dairy ewes were collected from the experimental farm of the National Agricultural and Food Centre – Research Institute for Animal Production Nitra located in western Slovakia during the period of four consecutive years (2010 to 2013). Morning milking data were only taken into account. Milk was recorded once per month after lambs weaning (40 ± 10 days). Milk samples were also collected monthly; milk components (fat, protein and lactose content) were calculated using a MilkoScan FT120 (Foss, Hillerød, Denmark) and somatic cells were counted using a Fossomatic 90 (Foss Electric, Hillerød, Denmark) after heat treatment at 40 °C for 15 min. SCC were divided into three groups according to number of SCC in individual milk samples: low class (SCC under 3×10^5 cells · ml^{-1}), middle class (SCC between 3×10^5 and 6×10^5 cells · ml^{-1}) and high class (SCC above 6×10^5 cells · ml^{-1}). Since there is an absence of normal distribution of SCC, the transformation and decadic logarithms of SCC, i.e. $\log_{10}$SCC, were used. In total, the analyses comprised 2623 test-day records of 435 ewes that were either purebred: Tsigai (TS, n = 34), Improved Valachian (IV, n = 10) and Lacaune (LC, n = 103) or crossbred TS × LC (n = 139) and IV × LC (n = 149). Ewes were on their first (n = 285), second (n = 228) and third (n = 200) lactation. Thus, on average, 3.679 monthly measurements per lactation were done, i.e. lactations with at least 3 milk samples were involved. According to the day of lambing, ewes were on their first to fifth month in milk (MIM): MIM1 (up to day 45 after parturition) – 288 observations, MIM2 (days 46–75) – 885 observations, MIM3 (days 76–105) – 901 observations, MIM4 (days 106 and 135) – 539 observations and MIM5 (from day 136) – 10 observations. Observations from MIM4 and MIM5 were joined together because insufficient number of observations was available for the latter. Therefore, in the study were used MIM1, MIM2, MIM3 and MIM4 classes. Lambing occurred between January and April; most frequent lambing months slightly fluctuated in individual years, depending on Easter. Majority of test-day records was done between April and August.

Statistical analyses were performed using statistical programme SAS 9.2 (2009). Correlation analysis was done in order to reveal relationships between $\log_{10}$SCC and milk traits, regardless of purebred or crossbred origin of ewes. Correlation coefficients between $\log_{10}$SCC and milk traits: milk yield, fat, protein and lactose contents were calculated using CORR procedure. The mixed model methodology using MIXED procedure was applied in order to study the influence of factors affecting variation of studied traits. Two different models were employed.

For milk yield, fat, protein and lactose content, the following model equation (1) was used:

$$y_{ijklmno} = \alpha + C_i + L_j + MIM_k + YM_l + G_m + L_j MIM_k + C_i L_j + u_n + e_{ijklmno} \quad (1)$$

where:

- $y_{ijklmno}$ – individual observations of milk yield, fat, protein and lactose contents
- α – intercept
- C_i – fixed effect of SCC class (low, middle, high); $\sum_i C = 0$
- L_j – fixed effect of lactation number (1, 2, 3); $\sum_j L = 0$
- MIM_k – fixed effect of month in milk (1, 2, 3, 4); $\sum_k MIM = 0$
- YM_l – fixed effect of year-month of measurement (1, 2 to 19); $\sum_l YM = 0$
- G_m – fixed effect of genotype (TS, IV, LC, TS × LC, IV × LC); $\sum_m G = 0$

$L_j MIM_k$ – fixed effect of interaction between lactation number and MIM; $\sum_{jk}$ $LMIM = 0$

$C_i L_j$ – fixed effect of interaction between lactation number and SCC class; $\sum_{ij}$ $CL = 0$

u_n – random effect of ewe (1, 2 to 435); $u_n \sim N(0, I\sigma_e^2)$

$e_{ijklmno}$ – random error $e_{ijklmno} \sim N(0, I\sigma_e^2)$.

For $\log_{10}$SCC, the following model equation (2) was used:

$$y_{ijklmn} = \alpha + L_i + MIM_j + YM_k + G_l + L_i\,MIM_j + b_1 x_{1ijklmn} + b_2 x_{2\,ijklmn} + b_3 x_{3\,ijklmn} + b_4 x_{4\,ijklmn} + u_m + e_{ijklmn} \quad (2)$$

where:

y_{ijklmn} – individual decadic logarithm of SCC, i.e. $\log_{10}$SCC

α – intercept

L_i – fixed effect of lactation number (1, 2, 3); $\sum_i L = 0$

MIM_j – fixed effect of month in milk (1, 2, 3, 4); $\sum_k MIM = 0$

YM_k – fixed effect of year-month of measurement (1, 2 to 19); $\sum_l YM = 0$

G_l – fixed effect of genotype (TS, IV, LC, TS × LC, IV × LC); $\sum_l G = 0$

$L_i MIM_j$ – fixed effect of interaction between lactation number and MIM; $\sum_{ij}$ LMIM = 0

$b_1 x_{1\,ijklmn}$ – linear regression coefficient of $\log_{10}$SCC on milk yield

$b_2 x_{2\,ijklmn}$ – linear regression coefficient of $\log_{10}$SCC on fat content

$b_3 x_{3\,ijklmn}$ – linear regression coefficient of $\log_{10}$SCC on protein content

$b_4 x_{4\,ijklmn}$ – linear regression coefficient of $\log_{10}$SCC on lactose content

u_m – random effect of ewe (1, 2 to 435); $u_n \sim N(0, I\sigma_u^2)$

e_{ijklmn} – random error; $e_{ijklmn} \sim N(0, I\sigma_e^2)$.

Fixed factors included in the models (1) and (2) were estimated using the Least Squares Means (LSM) method. Statistical significances of fixed factors were tested by Fischer's F-test, and statistical significances of individual differences between estimated levels of fixed factors – by Scheffe's multiple-range tests. Differences were considered statistically significant when $P \leq 0.05$. Ewe and residual error variances were estimated using the Restricted Maximum Likelihood (REML) method. Estimated variances were used to estimate repeatability of studied traits that can be interpreted as the proportion of total variance attributable to among-individual variance: (model 1) and (model 2), respectively.

Results and discussion

Negative correlation coefficients between $\log_{10}$SCC and milk yield (−0.07), and between $\log_{10}$SCC and lactose content (−0.24), whereas positive correlation coefficients between $\log_{10}$SCC and fat content (+0.05), and between $\log_{10}$SCC and protein content (+0.13) were estimated (Table 1). However, correlations between $\log_{10}$SCC and fat content and between $\log_{10}$SCC and milk yield were very weak. The same pattern was found by Serrano et al. (2003) and Riggio et al. (2007), however these authors considered somatic cell score (SCS = $\log_2$(SCC/100) + 3) in analyses. Correlation coefficients between transformed SCC and milk traits obtained in our study differed from literature (Riggio et al., 2007; Olechnowicz et al., 2009): slightly stronger relationships were found for Valle del Belice ewes (correlations between SCS and daily milk yield, between SCS and fat content, and between SCS and protein content, equalled −0.12, +0.14 and +0.25, respectively) and for Polish Line 05 ewes (correlations between logSCC and fat content, between log SCC and protein content, and between logSCC and lactose content were +0.24, +0.18 and −0.49, respectively). Similarly, slightly stronger correlations were found for Manchega ewes by Serrano et al. (2003). These authors investigated lactation data; correlation between SCS and cumulative milk yield equalled −0.13, and correlation between SCS and protein content was +0.22. Othmane et al. (2002) reported stronger correlation between lnSCC (natural logarithm) and daily milk yield (−0.16) and weaker correlations between lnSCC and fat content (+0.01), and between lnSCC and protein content (+0.09) for Churra sheep. Baro et al. (1994) reported weaker correlation between lnSCC and daily milk yield (−0.05) and the same correlation between lnSCC and protein content (+0.13) for Churra sheep in earlier study. Arias et al. (2012), who analysed correlations between individual test-day (test-days 1 to 4) SCS and milk yield in Manchega breed, reported values oscillating around correlation coefficient estimated in this study (from −0.04 to −0.15). Correlation between average lactation SCS and cumulative milk yield was almost the same (−0.09). According to Monardes et al. (1984) and Baro et al. (1994), estimates of correlations between somatic cells and protein content might be controversial because somatic cells vary with protein fraction and thus rely on the laboratory method.

The effect of SCC class, considered in the model for milk yield and milk components, was highly significant (Table 2). Also, the effects of year-month of

Table 1. Estimates of Pearson's phenotypic correlations between decadic logarithm of somatic cell count (log_{10}SCC) and milk traits

Variables	Milk yield, ml	Fat content, %	Protein content, %	Lactose content, %
log_{10}SCC · ml^{-1}	−0.07^{++}	0.05^{+}	0.13^{++}	−0.24^{++}

$^{++}$ – $P \leq 0.01$, $^{+}$ – $P \leq 0.05$

Table 2. Analyses of variance (statistical significance of Fisher F-test) for milk traits and decadic logarithm of somatic cell count (log_{10}SCC)

Trait	Fixed effect						
	SCC class	Lact	MIM	Year-Month	Genotype	Lact × MIM	Lact × SCC class
Milk yield*, ml	++	NS	++	++	++	++	NS
Fat content, %	++	+	++	++	++	++	NS
Protein content, %	++	+	++	++	++	NS	+
Lactose content, %	++	++	NS	++	+	++	+
log_{10}SCC · ml^{-1}	N.C.	++	NS	++	++	+	N.C.

Lact – lactation number; MIM – month in milk; N.C. – not considered; NS – no significance, $P > 0.05$; * – milk yield per milking; $^{++}$ – $P \leq 0.01$, $^{+}$ – $P \leq 0.05$

measurement and genotype were significant in analyses of milk traits. The effect of MIM was not significant only in the analysis of lactose content; the effect of lactation number (Lact) was not significant only in the analysis of milk yield. Interactions (Lact × MIM and Lact × SCC class) were either significant or insignificant in analyses of milk traits. All fixed factors considered in the model for log_{10}SCC (except for MIM) were significant. Differences in studied traits in accordance to individual levels of considered factors are discussed below. With increasing SCC, milk yield and lactose content significantly decreased and milk fat and protein contents significantly increased (Table 3). The class with highest number of SCC was least numerous (22% of samples with SCC above 6×10^5 cells · ml^{-1} and only 15% of samples with SCC above 1×10^6 cells · ml^{-1}). Contrariwise, 60% of samples had SCC less than or equal to 2×10^5 cells · ml^{-1}. These findings may reflect the fact that most ewes had healthy udders when comparing with thresholds between healthy and infected udders presented by Green (1984), Hahn et al. (1992) and Gonzalo et al. (1994), who recommended SCC values ranging from 5×10^5 to 1×10^6 cells · ml^{-1}, and when comparing with reports of de la Cruz et al. (1994), González-Rodríguez et al. (1995) and El-Saied et al. (1998), who recommended SCC values ranging from 2.5×10^5 to 3×10^5 cells · ml^{-1}. The same trends for milk yield and milk components were revealed by Vršková et al. (2015) for TS breed. Linear regression coefficient of milk yield on logSCC estimated by Gonzalo et al. (1994) as negative value for Churra ewes agreed with an influence of effect of SCC class on milk yield reported in this study. Also, decreasing trend in lactose content as compared with increasing SCC class (from 4.54 to 4.41%) agreed with findings of Nudda et al. (2001) reported for Sarda ewes (from 4.55 to 4.14%), though SCC classes were chosen in a slightly different way.

Trends in least squares means of milk yield and milk components for the first, second and third lactation (Table 4) partly agreed with previous studies of Oravcová et al. (2006, 2007) where TS, IV and LC breeds were analysed separately. However, no general pattern of these traits with increasing milk yield and decreasing milk components and increasing lactation number was found, maybe, due to fact that purebred and crossbred ewes were analysed jointly (although effect of genotype was considered). No differences in relationship between lactation number and milk yield were found. In the case of log_{10}SCC, the effect of lactation number (higher lactation number, higher log_{10}SCC) resulted

Table 3. Least squares means and standard errors for milk traits by somatic cell count (SCC) class

Trait	SCC class[1]			Scheffe's test
	low (1) N = 1763	middle (2) N = 285	high (3) N = 575	
Milk yield*, ml	526.8 ± 9.9	503.8 ± 12.4	486.8 ± 11.6	1:2^{+},3^{++}
Fat content, %	6.91 ± 0.05	6.93 ± 0.07	7.08 ± 0.07	1:3^{+}; 2:3^{+}
Protein content, %	5.52 ± 0.03	5.58 ± 0.03	5.66 ± 0.03	1:2^{+},3^{++}; 2:3^{+}
Lactose content, %	4.54 ± 0.01	4.50 ± 0.02	4.41 ± 0.02	1:2,3^{++}; 2:3^{++}

[1] SCC class: low – SCC under 3×10^5 cells · ml^{-1}, middle – SCC between 3×10^5 and 6×10^5 cells · ml^{-1}, high – SCC above 6×10^5 cells · ml^{-1}; N – number of observations; * – milk yield per milking; $^{++}$ – $P \leq 0.01$, $^{+}$ – $P \leq 0.05$

Table 4. Least squares means and standard errors for milk traits and decadic logarithm of somatic cell count (log_{10}SCC) by lactation number

Trait	Lactation number first (1) N = 1032	 second (2) N = 864	 third (3) N = 727	Scheffe's test
Milk yield*, ml	510.7 ± 12.1	507.8 ± 11.6	499.0 ± 11.5	NS
Fat content, %	6.95 ± 0.07	6.92 ± 0.06	7.05 ± 0.06	2:3^{+}
Protein content, %	5.62 ± 0.03	5.26 ± 0.03	5.58 ± 0.03	1:2^{+}
Lactose content, %	4.54 ± 0.02	4.47 ± 0.02	4.44 ± 0.02	1:2,3^{++}
log_{10}SCC · ml^{-1}	5.04 ± 0.04	5.11 ± 0.04	5.38 ± 0.04	1:2^{+}3^{++}; 2:3^{++}

N – number of observations; * – milk yield per milking; ++ – $P \leq 0.01$, + – $P \leq 0.05$; NS – no significance, $P > 0.05$

Table 5. Least squares means and standard errors for milk traits and decadic logarithm of somatic cell count (log_{10}SCC) by month in milk (MIM)

Trait	MIM first (1) N = 288	 second (2) N = 885	 third (3) N = 901	 fourth (4) N = 549	Scheffe's test
Milk yield*, ml	594.2 ± 16.6	523.3 ± 12.8	462.4 ± 11.6	443.3 ± 14.0	1:2,3,4^{++}; 2:3,4^{++}
Fat content, %	6.76 ± 0.10	6.84 ± 0.07	7.08 ± 0.07	7.22 ± 0.08	1:3^{+},4^{++}; 2:3^{+},4^{++}
Protein content, %	5.43 ± 0.04	5.55 ± 0.03	5.66 ± 0.03	5.70 ± 0.04	1:2,3,4^{++}; 2:3,4^{++}
Lactose content, %	4.51 ± 0.02	4.49 ± 0.02	4.47 ± 0.02	4.47 ± 0.02	NS
log_{10}SCC · ml^{-1}	5.14 ± 0.06	5.16 ± 0.05	5.21 ± 0.04	5.19 ± 0.05	NS

N – number of observations; * – milk yield per milking; ++ – $P \leq 0.01$, + – $P \leq 0.05$; NS – no significance, $P > 0.05$

in significantly different estimates (log_{10}SCC · ml^{-1} equalled 5.04, 5.11 and 5.38 for the first, second and third lactation, respectively) .

MIMs (Table 5) had significant effect on milk yield, fat and protein content. These findings agreed with studies of Oravcová et al. (2006, 2007) and Komprej et al. (2012) on dairy sheep in Slovakia and Slovenia. However, this effect on lactose content and log_{10}SCC, respectively, was not significant. Values of log_{10}SCC in dairy ewes in Slovakia partly agreed with the results of the study of Baro et al. (1994), who reported linear regression of age of ewe significantly different from zero, and linear regression of MIM not different from zero (however, quadratic regression of MIM was significantly different from zero) for Churra ewes. El-Saied et al. (1998) found both MIM and lactation number affecting SCS in Churra ewes. Findings for log_{10}SCC in dairy ewes in Slovakia partially disagreed with study of Othmane et al. (2002), who reported no effects of both stage of lactation and age of Churra ewes. The authors explained lack of influence of these effects on SCC by strict mastitis control measurements (teat dip after milking, selective dry therapy and culling of ewes with chronic mastitis) and high levels of husbandry applied to flocks investigated. Lower variation of SCS in comparison with variation of daily milk yield depending on the stage of lactation was reported for French LC ewes during their first lactation (Barillet et al., 2001). No influence of lactation number on log_{10}SCC was reported for TS (Margetín et al., 1995; Vršková et al., 2015) and IV (Margetín et al., 1995) previously. These studies, however, considered only seasonal effect of test-day measurements (no differentiation between stage of lactation and season of measurement), which was found either significant (Margetín et al., 1995) or not significant (Vršková et al., 2015). According to Margetín et al. (1995), log_{10}SCC was either the same or lower in TS as compared with IV ewes. Tančin et al. (2017), who studied influence of stage of lactation on log_{10}SCC in LC breed, found this factor not significant. In contrast, Arias et al. (2012), who implemented a more complicated model for analysis of Manchega ewes, found significant effects of age of ewe, lactation stage, flock-year of measurement, season and number of lambs born as well as of some interactions between these effects. Unfortunately, data on litter size in this study were mostly unavailable; therefore, an influence of this effect was not investigated and cannot be compared.

Although MIM had no influence on log_{10}SCC, Lact × MIM interaction affected log_{10}SCC. The dependence of log_{10}SCC on this interaction is shown in Figure 1. It agreed with pattern over individual lactations and is in partial agreement with trend of log_{10}SCC over individual MIM that increased up to MIM3 (first lactation) and MIM4 (second lactation). To our best knowledge, our study is the first research considering Lact × MIM interaction.

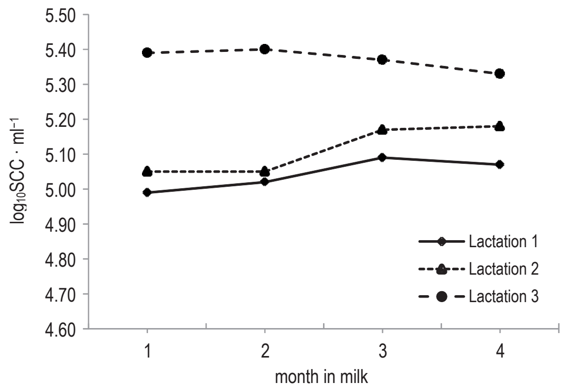

Figure 1. Least squares means for $\log_{10}$SCC (decadic logarithm of somatic cell count) by interaction between lactation number and month in milk

reported SCS (5.26) for Churra sheep, i.e. similar to values found for LC, TS × LC and IV × LC ewes. For Valle del Belice sheep, Riggio et al. (2007) reported the higher value of SCS (6.89).

Milk yield, protein and lactose contents included as covariates (Table 7) showed highly significant influence on $\log_{10}$SCC. Linear regression coefficients were negative for milk yield (−0.00023) and lactose content (−0.6489) and positive for protein content (+0.1015). For fat content, linear regression coefficient was slightly positive (+0.00073); however, no difference from zero was found. The pattern of linear regression coefficients was in agreement with the pattern of correlation coefficients: milk yield and lactose content decreased with increasing SCC; fat and protein contents tended to increase or increased with increasing SCC. To our best knowledge, no study aimed at investigations of dependence of SCC on covariates of milk yield and milk components in sheep was done. Only Pleguezuelos et al. (2015) performed similar study but on Murciano-Granadina goat breed. The authors reported higher estimates of linear regression coefficients of dependence of $\log_{10}$SCC on daily milk yield, and fat and protein contents when comparing with findings of this study. In cows, Strzałkowska et al. (2009) found influence of SCC class on daily milk yield, fat and protein content. However, Strzałkowska et al. (2010) found influence of SCC class on milk yield and protein content in goats.

The proportion of total variance of studied traits attributable to among-individual ewe variance

Table 6. Least squares means and standard errors for milk traits and decadic logarithm of somatic cell count ($\log_{10}$SCC) by genotype

Trait	Genotype					Scheffe's test
	TS (1) N = 194	IV (2) N = 49	LC (3) N = 577	TS × LC (4) N = 826	IV × LC (5) N = 977	
Milk yield*, ml	374.9 ± 21.0	438.7 ± 36.4	625.3 ± 12.3	516.9 ± 11.0	573.2 ± 10.5	1:3,4,5++; 2:3,5++; 3:4++,5+; 4:5++
Fat content, %	6.93 ± 0.11	6.89 ± 0.20	6.87 ± 0.07	7.17 ± 0.06	7.02 ± 0.06	3:4++
Protein content, %	5.56 ± 0.06	5.81 ± 0.10	5.43 ± 0.03	5.69 ± 0.03	5.44 ± 0.03	1:4+;2:3,5+; 4:5++
Lactose content, %	4.46 ± 0.03	4.45 ± 0.05	4.54 ± 0.02	4.48 ± 0.01	4.49 ± 0.01	3:4+
$\log_{10}$SCC · ml^{-1}	5.20 ± 0.07	4.71 ± 0.13	5.34 ± 0.04	5.31 ± 0.04	5.33 ± 0.04	1:2+; 2:3,4,5++

N – number of observations; TS – Tsigai, IV – Improved Valachian, LC – Lacaune; * – milk yield per milking; ++ – $P \leq 0.01$, + – $P \leq 0.05$

The effect of genotype (Table 6) on milk yield and milk components is in agreement with previous findings of Oravcová et al. (2006, 2007) and Tančin et al. (2011), who reported lower milk yields in purebred TS and IV ewes in comparison with purebred LC and crossbred TS × LC and IV × LC ewes. In contrast, fat and protein contents were lower in purebred LC ewes in comparison with purebred TS and IV ewes. SCC for purebred ewes (LC, IV and TS) were 5.34, 5.20 and 4.71 ($\log_{10}$SCC · ml^{-1}), respectively. SCC for crosses TS × LC and IV × LC were 5.31 and 5.33 ($\log_{10}$SCC · ml^{-1}), respectively. Least squares mean of $\log_{10}$SCC · ml^{-1} for TS was similar to the finding of Vršková et al. (2015) for the same breed. In contrast, respective values estimated by Margetín et al. (1995) for TS and IV ewes were more than two times lower. Olechnowicz et al. (2009) reported log SCC · ml^{-1} as 5.19 for Polish Line 05 dairy sheep which fell between values estimated in this study for IV and TS ewes. Similarly, Skapetas et al. (2017) estimated log SCC · ml^{-1} as 5.30 for Chios sheep which was almost the same as values found either for TS × LS or for IV × LC crossbred ewes. Tančin et al. (2017) reported $\log_{10}$SCC · ml^{-1} on more numerous data of LC ewes ranging between 5.27 and 5.80 (five-flock analysis). El-Saied et al. (1998)

Table 7. Estimates of linear regression coefficients for decadic logarithm of somatic cell count ($\log_{10}$SCC)

Covariate	Estimate ± Standard Error	Significance
Milk yield*, ml	−0.00023 ± 0.00008	++
Fat content, %	+0.00730 ± 0.01342	NS
Protein content, %	+0.10150 ± 0.03085	++
Lactose content, %	−0.64890 ± 0.04361	++

* – milk yield per milking; ++ – $P \leq 0.01$, NS – no significance, $P > 0.05$

(repeatability) was moderate (results not shown), ranging from 0.19 (lactose content) to 0.46 (protein content) for dairy sheep in Slovakia. It reflects the variation accounted for individual ewe effect varying with investigated traits.

Conclusions

The study confirmed negative relationship between somatic cells and milk yield in ewes, i.e. with increasing somatic cell count, milk yield decreased. Due to the fact that somatic cells are generally always present in ovine milk, further detailed research on their physiological level is needed. Since the number of somatic cells increases when infectious agents enter the udder, there is a need for further investigations of possible relations between somatic cells and microorganisms, and additional explanations of factors influencing occurrence of somatic cells. Moreover, management strategies must be studied in order to implement acceptable programs that reduce possible risk of mastitis in ewes.

Acknowledgement

This study was carried out within the Project No. APVV-15-0072 supported by the Ministry of Education, Science, Research and Sports of the Slovak Republic/the Slovak Research and Development Agency.

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