Journal of Dairy Research

cambridge.org/dar

Pathogens in milk of goats and their relationship with somatic cell count

Kristína Tvarožková[1], Vladimír Tančin[1,2], Michal Uhrinčať[2], Marta Oravcová[2], Lukáš Hleba[3], Barbora Gancárová[1], Lucia Mačuhová[2], Martin Ptáček[4] and Pierre-Guy Marnet[5]

[1]Faculty of Agrobiology and Food Resources, Slovak University of Agriculture in Nitra, Nitra, Slovak Republic; [2]National Agricultural and Food Centre, Research Institute for Animal Production Nitra, Lužianky, Slovak Republic; [3]Faculty of Biotechnology and Food Sciences, Slovak University of Agriculture in Nitra, Nitra, Slovak Republic; [4]Faculty of Agrobiology, Food & Natural Resources Czech University Life Sciences Prague, Prague, Czech Republic and [5]Institut Agro Rennes-Angers, Animal and food Sciences department, 35000 Rennes, France

Research Article

Cite this article: Tvarožková K, Tančin V, Uhrinčať M, Oravcová M, Hleba L, Gancárová B, Mačuhová L, Ptáček M and Marnet P-G (2023). Pathogens in milk of goats and their relationship with somatic cell count. *Journal of Dairy Research* **90**, 173–177. https://doi.org/10.1017/S0022029923000237

Received: 25 May 2022
Revised: 27 February 2023
Accepted: 6 March 2023
First published online: 25 May 2023

Keywords:
Goats; milk composition; pathogens; somatic cell count

Corresponding author:
Vladimír Tančin;
Email: vladimir.tancin@uniag.sk

Abstract

We evaluated the presence of bacterial pathogens in the milk of goats and their relationship with somatic cell count (SCC) and milk composition. The study was performed on a dairy farm in northern Slovakia. Half udder milk samples were collected from goats in June and July. The samples were divided on the basis of SCC into 4 bands (SCC1 lowest to SCC4 highest). Bacterial pathogens were only detected in 13% of samples. SCC3 and SCC4 had 15 and 25% positive samples respectively compared with SCC1 (2%) and SCC2 (14%). Coagulase-negative staphylococci (CNS) were the most common isolates (73%), of which *Staphylococcus caprae* was the most frequently isolated (65%). In samples with $\geq 1000 \times 10^3$ cells ml^{-1} (SCC3, SCC4) there was higher somatic cell score (SCS) in the presence of a pathogen (7.48 ± 0.11) than without a pathogen (7.16 ± 0.05, $P < 0.01$). Statistically significant but weak negative correlations were observed between SCS and lactose, dry matter and non-fat dry matter. In conclusion, a higher percentage of bacteriologically positive milk samples was observed in both SCC3 and SCC4 groups but this does not explain the aetiology of high SCC in the milk of goats that are apparently free of bacteria. As a diagnostic tool, SCC is probably less useful in goats than in cows.

The breeding of goats has a rich tradition and history in Slovakia. The majority are dairy goats, predominantly the White Shorthaired, then the Brown Shorthaired breeds and finally the dual-purpose Anglo-Nubian breed (Oravcová, 2013). Recently, the demand for goat milk and its products has increased, so attention is paid to the best nutritional, techno-functional and sanitary qualities of dairy goat products, all of them depending on the udder health (Kováčová *et al.*, 2021). Mastitis, an intramammary inflammation mostly resulting of bacterial infection, is the most important disease of the udder in dairy animals. The health of the udder is critical for dairy farms and is correlated with milk yield, quality of milk and food safety (Spuria *et al.*, 2017; Zigo *et al.*, 2022). Mastitis in goats is responsible for a drop in milk production and protein, lactose and fat contents (Novac and Andrei, 2020) as also observed in dairy ewes (Tvarožková *et al.*, 2019). Intramammary infection is also the main cause of somatic cell count (SCC) increase in milk (Raynal-Ljutovac *et al.*, 2007) which is used for mastitis detection in goats as in other ruminants. However, other factors that also affect SCC in goat milk include parity, stage of lactation, oestrus cycle and breed (Paape *et al.*, 2007; Persson *et al.*, 2014). Udder and teat morphologies, milking frequency, grazing management, milking machine equipment and settings (Marnet *et al.*, 2018) and viral co-infection with CAEV (Sanchez *et al.*, 2001) can all influence SCC, making high SCC difficult to interpret in goats, compared with cows and ewes (Persson and Olofsson, 2011). Further, subclinical mastitis is a problem in goats where prevalence rates are important (reported as 35% to 70%: Leitner et al. 2004a; Hall and Rycroft, 2007). The major types of pathogens causing subclinical mastitis in dairy goats are coagulase-negative staphylococci (CNS) (Bergonier *et al.*, 2003; Dore *et al.*, 2016), in particular *Staphylococcus caprae* and *Staphylococcus epidermidis* (Leitner *et al.*, 2004b). However, the main pathogens affecting goats in Slovakia and their effects on udder inflammation are still unknown.

The hypothesis of this work was that the high level of somatic cells in the milk of goats is caused by mastitis pathogens and that the increased SCC changes milk composition. Therefore, the aim of this study was to describe the frequency of distribution of SCC from half udder milk samples, identify causative bacteria of mastitis and evaluate effects on milk composition in dairy goats.

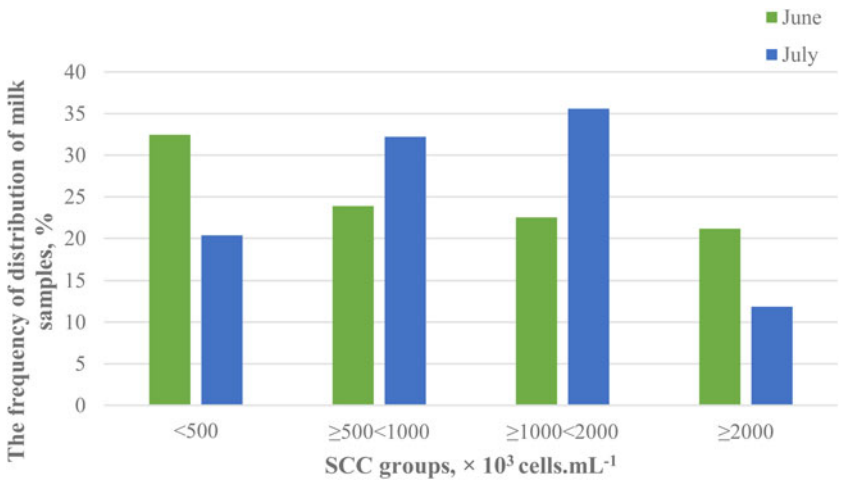

Figure 1. Frequency of distribution of half udder milk samples for four SCC groups ($\times 10^3$ cells ml^{-1}) in June and July.

Material and methods

Sampling

The study was carried out on a goat dairy farm in northern Slovakia on dairy goats of the White Shorthaired breed. A total of 458 half udder milk samples from 129 goats (44 goats in their first lactation, 61 in second and 24 in third and higher lactations) were collected during evening milking in June (222) and July (236 samples). The goats had kidded from mid-February to mid-March, so the samples were from mid- to late lactation. Only 22 animals were not sampled in both months. Only clinically healthy goats without any visual abnormalities in udder or milk were included. The first squirts of milk from teats were discarded and subsequently the teat end was cleaned with 70% alcohol. Then the milk samples were collected for bacteriological cultivation using sterile tubes (5 ml) and followed by sampling for determination of SCC and milk composition (50 ml). Samples were frozen at −20°C until thawing and cultivation (Sánchez *et al.*, 2003).

Microbiological analysis

Milk samples (10 µl) were incubated aerobically on blood agar plates (MkB Test a.s., Rosina, SR) for 24 h at 37°C. Bacterial colonies were identified by haemolysis, a catalase test, aesculin hydrolysis, Gram staining and cell morphology. Presumptive *Staphylococcus aureus* were identified with the clumping factor test (DiaMondiaL Staph Plus Kit, Germany). Aesculin-positive streptococci were subcultured to identify *Streptococcus uberis* or *Enterococcus* sp. on modified Rambach agar (Watts *et al.*, 1993). Aesculin negative streptococci were characterised by Lancefield serotyping (DiaMondiaL Strept Kit, Germany). Gram and catalase positive small colonies were identified as coryneform bacteria. Large colonies, Gram and catalase positive, capable of forming endospores were identified as *Bacillus* sp. All Gram positive and Gram negative colonies were classified using MALDI-TOF MS (Bruker Daltonics, Bremen, Germany) (Tvarožková *et al.*, 2021). Presence of contagious pathogens (*Staphylococcus aureus, Streptococcus agalactiae*) was reported as positive if one or more colonies were found. Presence of other pathogens was reported as positive if at least five colonies were found. Samples were considered contaminated and removed from data analysis if more than two different colony types were isolated on blood agar.

Somatic cell analysis

SCC were determined using a Somacount 150 (Bentley Czech, USA). Milk composition was determined using MilkoScan FT 120 (Foss Electric, Hillerød, Denmark).

Statistical analysis

Milk samples were divided into four SCC groups on the basis of half udder SCC. Group SCC1 comprised samples of less than 500×10^3 cells ml^{-1}. SCC2 ranged from 500 to 1000, SCC3 from 1000 to 2000 and SCC4 comprised samples above 2000, all $\times$ 10^3 cells ml^{-1}. For statistical evaluation SCC were recalculated to SCS: LOG_2 (SCC/100 000) + 3.

Relationships among traits were analysed using Pearson's correlation coefficients. Statistical analysis was performed using the GLM procedure in SAS9.2 (2009). The resulting models, based on preliminary analysis of possible sources of variability of investigated traits, are specified in the online Supplementary File. Results are presented as LSmeans ± standard error. The effects in the models were tested using the *F*-test. Differences between LSmeans were tested using multiple ranging Sheffes tests. The differences were considered statistically significant at $P \leq 0.05$.

Results

The overall mean SCC was $1250 \pm 1265 \times 10^3$ cells mL^{-1} (SCS 6.10 ± 1.30). Classification by SCC groups is shown in Figure 1. More than 50% of individual samples were below 10^6 cells mL^{-1} and 32.43 and 20.34% of samples were classified in SCC1 group ($< 500 \times 10^3$ cells ml^{-1}) in the months June and July, respectively (Fig. 1). Bacteria presence was detected from 12.88% of milk samples, none of which were contaminated. The most common bacteria found were CNS (72.88%). The most common CNS was *Staphylococcus caprae* (65.12%) (Table 1). *Staphylococcus aureus* was isolated from 6.90% and 6.66% of samples taken in June and July, respectively (Table 1). Seven goats had the same pathogen in both halves of udder and four goats had different species of pathogens in the two udder halves. Bacterial positive samples were found only in 1.67%, 13.95%, 14.93% and 25.33% in SCC1, SCC2, SCC3 and SCC4, respectively.

We compared bacteria positive and negative milk samples within the SCC3 and SCC4 groups. In total we observed significantly higher SCS in milk samples with a pathogen (7.48 ± 0.11)

https://doi.org/10.1017/S0022029923000237 Published online by Cambridge University Press

Table 1. The incidence of pathogens in goat milk samples taken in June and July

	Month *n*, (%) positive samples	
Pathogens	June	July
Citrobacter braakii	1 (3.45)	
Enterobacter cloacae	2 (6.90)	
Enterobacter kobei	8 (27.59)	
Staphylococcus aureus	2 (6.90)	2 (6.66)
Staphylococcus caprae	10 (34.48)	18 (60)
Staphylococcus epidermidis	6 (20.69)	8 (26.67)
Staphylococcus xylosus		1 (3.33)
Steptococcus. pluranimalium		1 (3.33)
All positive samples, n (% of all samples)	29 (13.06)	30 (12.71)

compared with no pathogen (7.16 ± 0.05, $P < 0.001$: model 2). We found no effect of the month of sampling on SCC (online Supplementary Table S1), with more milk samples in SCC2 and SCC3 and fewer in SCC1 in July compared to June (Fig. 1). However, the mean SCS when only SCC3 and SCC4 were analysed (model 2) dropped significantly ($P < 0.05$) from June (7.49 ± 0.09) to July (7.15 ± 0.08). Parity significantly influenced SCS, where SCS significantly increased from first (5.82 ± 0.10) to second (6.17 ± 0.08) and third and higher lactation (6.54 ± 0.16: $P < 0.05$, online Supplementary Table S2).

Significantly less protein, NFDM and lactose were found in July than in June, whereas fat content was the reverse (online Supplementary Table S1). Milk composition was not influenced by parity but SCS significantly increased with parity (5.82 ± 0.10, 6.17 ± 0.08 and 6.54 ± 0.16 for first, second and greater parities, online Supplementary Table S2). Milk composition in the four SCC groups is presented in Table 2. Statistically significant negative correlations were found between SCS and lactose content (−0.37), dry matter (−0.19) and non-fat dry matter (−0.30) ($P < 0.001$). The correlations between SCS and fat or protein were not significant.

Discussion

Our data confirm the presence of high SCC in goat milk samples, comparable to those of Moroni *et al.* (2005), Gosselin *et al.* (2020) and Podhorecká *et al.* (2021) but almost twice that reported by Persson and Olofsson, (2011). We observed more than 50% samples with SCC less than 10^6 cells ml^{-1} which we interpret as probably without infection. Albenzio *et al.* (2015) reported SCC of 700×10^3 cells mL^{-1} as a threshold which represents changes in leucocyte distribution as a reflection of the immune status of the udder.

Persson and Olofsson (2011) and Bagnicka *et al.* (2011) reported the presence of pathogens in 18% and 35% of milk samples respectively, compared to our overall value of 15% and 25% in the highest SCC groups (SCC3 and SCC4, respectively). In our study CNS were the most common bacteria isolated. Our results also confirm the results of Leitner *et al.* (2004b) and Persson and Olofsson (2011) who reported that CNS were the most frequent pathogens in milk of goats. Among these pathogens Koop *et al.* (2012) and Gosselin *et al.* (2020) found *Staphylococcus caprae* as the second more frequent pathogen when we detected *S. caprae* as the most common pathogen. *Staphylococcus aureus* is considered the most important contagious pathogen in dairy goats, ranging from 4% to 40% of bacteriologically positive samples (Min *et al.*, 2007; Marogna *et al.*, 2010; Persson and Olofsson, 2011; Dore *et al.*, 2016). Our data were at the bottom end of this range (7%). The number of same infection (7/129 goats) or dual pathogen infections (4/129 goats) in both half udder in our study is low, in agreement with Persson and Olofsson (2011) (9 and 3/111).

One of the main reasons for a high SCC in milk is the presence of mastitis pathogens, whether it be cows (Holko *et al.*, 2019) or goats. Our findings confirm this result and seem to be different from a previous study done in dairy ewes in which we did not find effect of different pathogens on SCS over the range 6.68 ± 0.41 to 8.11 ± 0.63 (Tvarožková *et al.*, 2020). Various observations have reported the effect of different pathogens on SCC in milk of goats (Moroni *et al.*, 2005; Koop *et al.*, 2012; Gosselin *et al.*, 2020). *Staphylococcus caprae* was associated with higher SCC compared to other CNS (Moroni *et al.*, 2005). Koop *et al.* (2012) recorded a higher SCC in milk samples with *S. aureus* compared to milk samples infected by CNS. The low number of *S. aureus* infections meant that we could neither confirm nor refute this observation. In another study *S. caprae, S. epidermidis, S. simulans* and *S. xylosus* were associated with higher SCC than other CNS species (Gosselin *et al.*, 2020). We have considered the possibility that our high SCC values might indicate infection by microorganisms other than those we could detect using the methods employed (*Mycoplasma*, for example). Given the high number of such samples (high SCC in the absence of an identified pathogen) we consider this unlikely. Accordingly, it may be that the diagnostic value of SCC is lower

Table 2. Milk composition in the four SCC groups

	SCC group (× 10^3 cells ml^{-1})			
Component	<500	≥500 < 1000	≥1000 < 2000	≥2000
Fat, %	4.15 ± 0.09	4.23 ± 0.09	4.13 ± 0.09	3.90 ± 0.12
Protein, %	3.09 ± 0.03	2.99 ± 0.03	2.98 ± 0.03	3.10 ± 0.04
Lactose, %	4.69 ± 0.04^{a}	4.61 ± 0.03^{ac}	4.52 ± 0.03^{bc}	4.26 ± 0.04^{d}
DM, %	12.53 ± 0.11^{a}	12.42 ± 0.10^{a}	12.24 ± 0.10^{ac}	11.93 ± 0.14^{bc}
NFDM, %	8.45 ± 0.05^{a}	8.25 ± 0.05^{b}	8.15 ± 0.05^{bd}	8.02 ± 0.06^{cd}

Note: a,b,c,d LS Means and standard error within row with different letters are significantly different at $P < 0.05$, DM, dry matter; NFDM, non-fat dry matter.

https://doi.org/10.1017/S0022029923000237 Published online by Cambridge University Press

in goats than in cows. Our data could also be interpreted as indicating that animals with a SCC $\geq 10^6$ cells ml^{-1} have subclinical mastitis and those with a SCC $< 500 \times 10^3$ cells ml^{-1} indicate absence of infection, as suggested by Persson and Olofsson (2011) who reported that the SCC of uninfected udder halves had a mean SCC of 478×10^3 cells ml^{-1}. So far, the SCC threshold indicating mastitis in the udder of goats has not been agreed.

We did not observe an effect of month/stage of lactation on SCS contrary to other studies (Paape *et al.*, 2007; Persson *et al.*, 2017; Smistad *et al.*, 2021) but the relative proximity of our two samples, both in mid lactation when milk production was stabilized, could explain this observation. On the other hand, we detected a significant influence of parity on SCS, as did Smistad *et al.* (2021).

The milk composition of uninfected udder halves is similar to those described by Currò *et al.* (2019). Yakan *et al.* (2019) reported an increase in protein content in late lactation, which we did not observe at the earlier lactation stage we used. A statistically significant but weak negative correlation was observed between the content of lactose and SCS (−0.37, $P < 0.001$). Similar relationship between SCC and milk lactose content was reported by Ying *et al.* (2004) in goats and by Oravcová *et al.* (2018) in dairy ewes. Such a relationship is to be expected on the basis of tight junction integrity, 'leaky' tight junctions (as a consequence of infection and inflammation) allowing partial equilibration between plasma and milk such that somatic cells enter milk and lactose exits (Ben-Chedly *et al.*, 2009).

In conclusion, as in other goat studies, a high occurrence of milk samples with high somatic cell count at the half udder level was observed. Nevertheless, we also confirmed that only low percentage of samples with high somatic cell count were bacteriologically positive. Even if the bacteriologically positive samples had higher SCC in groups with high SCC (SCC3 and SCC4) we assume that SCC should not be regarded as a gold standard of infection in goats. More intensive study of the relationship between somatic cell count and caprine udder health status is needed.

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/S0022029923000237

Acknowledgement. The research was supported by the APVV-21-0134 'Subclinical mastitis in ewes and goats farms: pathogens, somatic cells and udder morphology' and by the VEGA 1/0597/22 'Aetiology of somatic cell counts changes in the mammary gland of goats: physiological and pathological aspects'.

References

Albenzio M, Santillo A, Kelly AL, Caroprese M, Marino R and Sevi A (2015) Activities of indigenous proteolytic enzymes in caprine milk of different somatic cell counts. *Journal of Dairy Science* **98**, 7587–7594.

Bagnicka E, Winnicka A, Jozwik A, Rzewuska M, Strzalkowska N, Kościuczuk E, Prusak B, Kaba B, Horbańczuk J and Krzyzewski J (2011) Relationship between somatic cell count and bacterial pathogens in goat milk. *Small Ruminant Research* **100**, 72–77.

Ben-Chedly H, Lacasse P, Marnet PG, Wiart-Letort S, Finot L and Boutinaud M (2009) Cell junction disruption after 36 h milk accumulation was associated with changes in mammary secretory tissue activity and dynamics in lactating dairy goats. *Journal of Physiology and Pharmacology*, **60**(suppl. S3), 105–111.

Bergonier D, De Crémoux R, Rupp R, Lagriffoul G and Berthelot X (2003) Mastitis of dairy small ruminants. *Veterinary Research* **34**, 689–716.

Currò S, Manuelian CL, De Marchi M, Claps S, Rufrano D and Neglia G (2019) Effects of breed and stage of lactation on milk fatty acid composition of Italian goat breeds. *Animals* **9**, 764.

Dore S, Liciardi M, Amatiste S, Bergagna S, Bolzoni G, Caligiuri V, Cerrone A, Farina G, Montagna CO, Saletti MA, Scatassa ML, Sotgiu G and Cannas EA (2016) Survey on small ruminant bacterial mastitis in Italy, 2013–2014. *Small Ruminant Research* **141**, 91–93.

Gosselin BV, Dufour S and Middleton JR (2020) Association between species-specific staphylococcal intramammary infections and milk somatic cell score over time in dairy goats. *Preventive Veteterinary Medicine* **174**, 104815.

Hall SM and Rycroft AN (2007) Causative organisms and somatic cell counts in subclinical intramammary infections in milking goats in the UK. *Veterinary Record* **160**, 19–22.

Holko I, Tančin V, Vršková M and Tvarožková K (2019) Prevalence and antimicrobial susceptibility of udder pathogens isolated from dairy cows in Slovakia. *Journal of Dairy Research* **86**, 436–439.

Koop G, De Vliegher S, De Visscher A, Supré K, Haesebrouck F, Nielen M and van Werven T (2012) Differences between coagulase-negative *Staphylococcus* species in persistence and in effect on somatic cell count and milk yield in dairy goats. *Journal.of Dairy Science* **95**, 5075–5084.

Kováčová M, Výrostková J, Dudriková E, Zigo F, Semjon B and Regecová I (2021) Assessment of quality and safety of farm level produced cheeses from sheep and goat milk. *Applied Sciences* **11**, 3196.

Leitner G, Merin U, Glickman A, Weisblit L, Krifucks O, Shwimmer A and Saran A (2004a) Factors influencing milk quantity and quality in Assaf sheep and goat crossbreds. *South African Journal of Animal Science* **34**, 162–164.

Leitner G, Merin U and Silanikove N (2004b) Changes in milk composition as affected by subclinical mastitis in goats. *Journal of Dairy Science* **87**(1), 719–1726.

Marnet PG, Dzidic A, Le Caro L and Hubert A (2018) Review of old and new approaches to evaluate milking impact and milking ability in goats. ADSA, 24–27 June 2018, Knoxville USA, Abstract 123.

Marogna G, Rolesu S, Lollai S, Tola S and Leori G (2010) Clinical findings in sheep farms affected by recurrent bacterial mastitis. *Small Ruminant Research* **88**, 119–125.

Min BR, Tomita G and Hart SP (2007) Effect of subclinical intramammary infection on somatic cell counts and chemical composition of goats' milk. *Journal of Dairy Research* **74**, 204–210.

Moroni P, Pisoni G, Antonini M, Ruffo G, Carli S, Varisco G and Boettcher P (2005) Subclinical mastitis and antimicrobial sus-ceptibility of *Staphylococcus caprae* and *Staphylococcus epidermidis* isolated from two Italian goat herds. *Journal of Dairy Science* **88**, 1694–1704.

Novac C and Andrei S (2020) The impact of mastitis on the biochemical parameters, oxidative and nitrosative stress markers in goat's milk: a review. *Pathogens (Basel, Switzerland)* **9**, 882.

Oravcová M (2013) Pedigree analysis in white shorthaired goat: first results. *Archives Animal Breeding* **56**, 547–554.

Oravcová M, Mačuhová L and Tančin V (2018) The relationship between somatic cells and milk traits, and their variation in dairy sheep breeds in Slovakia. *Journal Animal Feed Science* **27**, 97–104.

Paape MJ, Wiggans GR, Bannerman DD, Thomas DL, Sanders AH, Contreras A, Moroni P and Miller RH (2007) Monitoring goat and sheep milk somatic cell counts. *Small Ruminant Research* **68**, 114–125.

Persson Y and Olofsson I (2011) Direct and indirect measurement of somatic cell count as indicator of intramammary infection in dairy goats. *Acta Veterinaria Scandinavica* **53**, 15.

Persson Y, Larsen T and Nyman AK (2014) Variation in udder health indicators at different stages oflactation in goats with no udder infection. *Small Ruminant Research* **116**, 51–56.

Persson Y, Nyman AK, Söderquist L, Tomic N and Persson Waller K (2017) Intramammary infections and somatic cell count in meat and pelt producing ewes with clinically healthy udders. *Small Ruminant Research* **156**, 66–72.

Podhorecká K, Borková M, Šulc M, Seydlová R, Dragounová H, Švejcarová M, Peroutková J and Elich O (2021) Somatic cell count in goat milk: an indirect quality indicator. *Foods (basel, Switzerland)* **10**, 1046.

Raynal-Ljutovac K, Pirisi A, De Crémoux R and Gonzalo C (2007) Somatic cells of goat and sheep milk: analytical sanitary, productive and technological aspects. *Small Ruminant Research* **68**, 126–144.

Sánchez A, Contreras A, Corrales JC and Marco JC (2001) Relationships between infection with caprine arthritis encephalitis virus, intramammary bacterial infection and somatic cell counts in dairy goats. *The Veterinary Record* **23**, 711–714.

Sánchez A, Contreras A, Jiménez J, Luengo C, Corrales JC and Fernández C (2003) Effect of freezing goat milk samples on recovery of intra-mammary bacterial pathogens. *Veterinary Microbiology* **94**, 71–77.

Smistad M, Sølverød L, Inglingstad RA and Østerås O (2021) Distribution of somatic cell count and udder pathogens in Norwegian dairy goats. *Journal Dairy Science* **104**. 11878–11888.

Spuria L, Biasibetti E, Bisanzio D, Biasato I, De Meneghi D, Nebbia P, Robino P, Bianco P, Lamberti M, Caruso C, Di Blasi A, Peletto S, Masoero L, Dondo A and Capucchio MT (2017) Microbial agents in macroscopically healthy mammary gland tissues of small ruminants. *PeerJ* **5**, 3994.

Tvarožková K, Tančin V, Holko I, Uhrinčať M and Mačuhová L (2019) Mastitis in ewes: somatic cell counts, pathogens and antibiotic resistance. *Journal Microbiology and Biotechnology Food Science* **9**, 661–670.

Tvarožková K, Tančin V, Uhrinčať M, Hleba L and Mačuhová L (2020) Mastitis pathogens and somatic cell count in ewes milk. *Potravinarstvo, Slovak Journal of Food Science* **14**, 164–169.

Tvarožková K, Vašíček J, Uhrinčať M, Mačuhová L, Hleba L and Tančin V (2021) The presence of pathogens in milk of ewes in relation to the somatic cell counts and subpopulations of leukocytes. *Czech Journal of Animal Science* **66**, 315–322.

Watts JL, Salmon SA and Yancey Jr RJ (1993) Use of modified Rambach agar to differentiate *Streptococcus uberis* from other mastitis streptococci. *Journal of Dairy Science* **76**, 1740–1743.

Yakan A, Ozkan H, Sakar AE, Ates CT, Kocak O, Dogruer G and Ozbeyaz C (2019) Milk yield and quality traits in different lactation stages of Damascus goats: concentrate and pasture based feeding systems. *Veterinary Journal of Ankara University* **66**, 117–129.

Ying C, Yang CB and Hsu JT (2004) Relationship of somatic cell count, physical, chemical and enzymatic properties to the bacterial standard plate count in different breeds of dairy goats. *Asian-Austral Journal of Animal Science* **17**, 554–559.

Zigo F, Farkašová Z, Výrostková J, Regecová I, Ondrašovičová S, Vargová M, Sasáková N, Pecka-Kielb E, Bursová Š and Kiss DS (2022) Dairy cows' udder pathogens and occurrence of virulence factors in Staphylococci. *Animals* **12**, 470.

https://doi.org/10.1017/S0022029923000237 Published online by Cambridge University Press