foods

MDPI

*Article*

# The Effects of Milking and Cleaning Procedures on the Quality and Microbiome of Raw Goat Milk

**Alyssa Thibodeau [1,†], Eiseul Kim [1,†], Seung-Min Yang [1], Lisbeth Goddik [1], Hae-Yeong Kim [2] and Si Hong Park [1,2,*]**

[1] Department of Food Science and Technology, Oregon State University, Corvallis, OR 97331, USA; alyssa.thibodeau@oregonstate.edu (A.T.); eskim89@khu.ac.kr (E.K.); ysm9284@gmail.com (S.-M.Y.); lisbeth.goddik@oregonstate.edu (L.G.)
[2] Department of Food Science and Biotechnology, Kyung Hee University, Yongin 17104, Republic of Korea; hykim@khu.ac.kr
* Correspondence: sihong.park@oregonstate.edu; Tel.: +1-541-737-1684
† These authors contributed equally to the work.

## Abstract

The rising popularity of raw goat milk has heightened concerns about its safety. This study examined how differences in milking and cleaning practices influence the quality and microbiota of goat milk from small-scale Oregon farms during July and August. Milk quality was assessed through somatic cell counts (SCCs) and components, while microbiota was evaluated using viable counts and 16S rRNA sequencing. Sequencing revealed a diverse microbial community, dominated by genera such as *Staphylococcus*, *Escherichia-Shigella*, and *Pseudomonas*, with pathogenic taxa like *Salmonella* and *Campylobacter* largely absent or detected at negligible levels. Alpha diversity varied significantly among sample types but not across farms, and beta diversity indicated considerable dissimilarity in microbial composition. Importantly, regression models identified significant associations between hygiene practices and bacterial abundance: the absence of glove use and hand sanitation was linked to increased levels of *Escherichia-Shigella*, *Kocuria*, *Enterococcus*, and *Corynebacterium*, while the use of bleach-chlorhexidine sanitizer was associated with higher *Deinococcus*. These findings highlight the role of rigorous hygiene protocols in shaping the microbiota of raw goat milk and emphasize the need for targeted practices to minimize contamination risks.

**Keywords:** raw goat milk; quality; microbiome; food safety

check for updates

Academic Editors: Golfo Moatsou, Ekaterini Moschopoulou, Agostino Sevi and Lambros Sakkas

Received: 4 September 2025
Revised: 30 September 2025
Accepted: 16 October 2025
Published: 20 October 2025

**Citation:** Thibodeau, A.; Kim, E.; Yang, S.-M.; Goddik, L.; Kim, H.-Y.; Park, S.H. The Effects of Milking and Cleaning Procedures on the Quality and Microbiome of Raw Goat Milk. *Foods* **2025**, *14*, 3563. https://doi.org/10.3390/foods14203563

**Copyright:** © 2025 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

## 1. Introduction

Milk provides an ideal environment for microbial growth due to its nearly neutral pH, high water activity, and rich nutrient profile [1]. Although milk within the udder of a lactating animal is considered sterile, it becomes exposed to contaminants from the air, milking equipment, or residual microbes on the teat surface during milking [2,3]. This exposure, combined with milk's nutrient-rich nature, facilitates rapid microbial growth and potential degradation, influenced by factors such as feeding practices and animal handling during milking [4]. Effective pre- and post-milking procedures are essential for maintaining the quality and microbiological safety of raw milk.

The demand for goat dairy products has been rising globally, with goat milk production projected to increase by more than 50% by 2030 [5,6]. In the U.S., over 35,000 farms were raising dairy goats in 2017, and the vast majority were small-scale operations, with

nearly all having fewer than 500 goats and more than half maintaining fewer than 10 [7]. As consumer interest in goat milk and derived products grows, often driven by perceptions of health benefits, ensuring product safety and consistency has become increasingly important [8].

Raw goat milk harbors a diverse microbiota, including lactic acid bacteria such as *Lactobacillus* and *Lactococcus*, along with genera like *Pseudomonas* and *Streptococcus* [9,10]. The safety and quality of goat milk are shaped by animal health, hygiene during milking, and equipment sanitation [3,11]. Previous studies have shown that poor milking hygiene and inadequate cleaning of equipment can elevate bacterial contamination, reducing both shelf life and safety [12,13]. Goat milk quality is commonly assessed by parameters such as chemical composition, somatic cell count (SCC), microbial load, and sensory properties [14,15]. These attributes vary according to breed, lactation stage, and milking time, underscoring the complexity of maintaining consistent quality [16–19].

Recent research has highlighted the nutritional and functional attributes of goat milk, including its digestibility, lower allergenicity, and probiotic potential [20,21]. Advances in microbial profiling tools such as 16S rRNA sequencing and metagenomics have revealed the complexity of the goat milk microbiome and its implications for food safety and functionality [22,23]. Studies have also investigated pathogen prevalence and antimicrobial resistance in raw goat milk, emphasizing the need for rigorous hygiene and monitoring [22]. In practice, small-scale producers typically adopt basic but critical measures such as pre- and post-milking teat sanitation, cleaning equipment with hot water and sanitizers, and rapid cooling of milk [24]. However, these approaches are largely adapted from bovine systems and may not fully suit goats, highlighting the need for species-specific best practices.

Despite the perception of raw milk as "risky," consumer interest continues to grow, particularly among small-scale farm markets. In the U.S., the Food and Drug Administration (FDA) prohibits interstate raw milk sales, but individual states establish their own rules [25]. In Oregon, for instance, farms with fewer than nine goats may sell raw milk directly on-site under defined conditions (O.R.S. § 621.012 and O.R.S. § 621.117) [26]. Yet, small producers often lack the resources to systematically validate their practices, and the absence of goat-specific standards creates inconsistencies. This study therefore aims to evaluate how variations in milking and cleaning practices influence the microbiome and overall quality of raw goat milk, with the goal of identifying best practices that minimize contamination while ensuring safe, high-quality production.

## 2. Materials and Methods

### *2.1. Study Design*

To participate in this study, farms had to meet two criteria: (1) milking fewer than 9 goats and (2) producing raw milk for direct human consumption. Small-scale goat farmers and homesteaders within a 60-mile radius of Corvallis, Oregon, who met these criteria were invited to join. Four farms (A, B, C, and D) were recruited, and samples were collected twice a week during the 2nd, 3rd, and 4th weeks of July and August 2021 (Table 1). This involved a total of six visits to each farm, resulting in 24 visits overall. During the initial visit to each farm, a comprehensive assessment was conducted to document operating practices and logistics. Information gathered included milking and cleaning procedures, frequency and types of cleaning agents, milking frequency (once or twice daily), maintenance routines for the milking parlor and barn, and details about milking equipment replacement. Additionally, farm-specific details such as goat breed(s), stage of lactation, parity, and age were recorded. To qualitatively assess hygiene conditions in a consistent manner, a structured visual assessment was performed by the same trained researcher during farm visits. A checklist was used to evaluate barn/parlor layout, barn/parlor

cleaning routine, glove or hand sanitizer use, udder preparation steps, and equipment cleaning practices. Each criterion was coded on a 0–2 scale as described in Table 2.

**Table 1.** Sampling information for raw milk and environmental sample collection.

| Farm | Farm Location | Breed | No. of Milking Does |
|---|---|---|---|
| A | Silverton, OR, USA | American Alpine, La Mancha | 6 |
| B | Monroe, OR, USA | Alpine, Oberhasli, Nigerian Dwarf | 4 |
| C | Sherwood, OR, USA | American Alpine, La Mancha, Saanen | 8 |
| D | Dallas, OR, USA | French and American Alpines | 3 |

**Table 2.** Visual assessment criteria and coding scheme for farm hygiene conditions.

| Criterion | Coding Scheme |
|---|---|
| Barn/parlor layout | 0 = milking in barn, 1 = semi-enclosed, 2 = separate enclosed parlor |
| Barn/parlor cleaning | 0 = only occasional sweeping, 1 = regular sweeping, 2 = sweeping and mopping routine |
| Glove/hand sanitizer use | 0 = none, 1 = occasional, 2 = consistent |
| Udder preparation | 0 = minimal (wipes), 1 = moderate (wipes + dip or soap), 2 = intensive (multi-step with agents) |
| Equipment cleaning | 0 = inconsistent/short, 1 = regular but limited, 2 = thorough (hot water or sanitizer with contact) |

### 2.2. Sample Collection

During each visit, raw milk and environmental samples were collected. Milk samples were taken in quadruplet, using 50 mL conical tubes, while environmental samples were collected in duplicate using PUR-Blue Swabs (World Bioproducts LLC, Woodinville, WA, USA). Environmental samples included swabs from the bulk tank interior surface, teat cup liners, and the milking stanchion. Each area (approx. 10 × 10 cm) was swabbed for ~10 s using sterile cotton swabs moistened with buffered peptone water. Sampling was performed immediately before milking under ambient barn conditions, and swabs were placed into sterile tubes and transported on ice to the laboratory for microbiological analysis. All collected samples were immediately stored in an ice-filled cooler and transported to the lab. Samples were either processed the same day or stored in a −20 °C freezer for further analysis.

### 2.3. Microbial Enumeration

Raw milk samples were collected once a week for three consecutive weeks in both July and August from each farm and processed on the day of collection. Microbial enumeration was performed according to internationally recognized methods [27–31]. Samples were serially diluted in sterile deionized water. For the preparation of the first decimal dilution, 1 mL of raw milk was added to 9 mL of sterile deionized water. For each diluted sample, 1 mL was plated on aerobic plate count (APC, Peel Plate AC, Charm Sciences Inc., Lawrence, MA, USA), coliform count (CC, Peel Plate CC, Charm Sciences Inc.), and yeast and mold count plates (YM, Peel Plate YM, Charm Sciences Inc.). The APC plates were incubated at 35 °C for 24 h, the CC plates at 35 °C for 24 h, and the YM plates at 30 °C for 72 h. Colony-forming units (CFU/mL) were enumerated from triplicate plates for each dilution, averaged to obtain a representative value, and $\log_{10}$-transformed prior to statistical analysis.

### 2.4. SCC and Milk Component Analysis

SCC and milk component analysis were conducted on the same raw milk samples that were also used for microbiological counts. To prevent microbial growth and ensure sample integrity, raw milk was immediately treated with a bronopol and natamycin preservative tablet (Broad Spectrum Microtabs II, Norwood, MA, USA) and stored at 4 °C for up to

one week before analysis. For somatic cell counts, 50 mL of raw milk was used with the flow cytometry (SomaScope Smart, Delta Instruments BV, Drachten, The Netherlands). Milk components, including true protein, fat, lactose, and blood non-esterified fatty acids (NEFA), were analyzed using 50 mL of raw milk with the fourier-transform infrared spectroscopy (FTIR) milk analyzer (LactoScope, Delta Instruments BV). Each SCC measurement was performed in duplicate, and the two values were averaged to yield a representative value per week. SCC values were $\log_{10}$-transformed prior to statistical analysis.

### 2.5. Milk Microbiome Analysis

#### 2.5.1. DNA Extraction

For raw milk samples, 1 mL of milk was homogenized by vortexing and then centrifuged at 13,000× *g* for 15 min at 4 °C. The supernatant was discarded, and the pellet was washed with 500 µL of phosphate-buffered saline (PBS). DNA was then extracted from the pellet using the Qiagen Power Foods DNA extraction kit (Qiagen, Hilden, Germany), following the manufacturer's instructions. Environmental samples (bulk tank, teat cup liner, and milking stanchion) were collected in 1 mL increments. The samples were then centrifuged at 1000× *g* for 2 min at room temperature. The pellets were processed for DNA extraction using the Qiagen Blood & Tissue Kit (Qiagen) with the protocol for Gram-positive bacteria. DNA concentrations from both raw milk and environmental samples were measured using a Qubit 3.0 fluorometer (Thermo Fisher Scientific, Waltham, MA, USA).

#### 2.5.2. Microbiome Sequencing

Following DNA extraction, an amplicon library of the V4 region of the 16S rRNA gene was created for both milk and environmental samples using the protocol described by previous study [32]. DNA fragments were amplified using AccuPrime™ Pfx SuperMix (Thermo Fisher Scientific), and successful amplification was confirmed via gel electrophoresis on a 1.5% agarose gel. PCR products were normalized with the SequalPrep™ Normalization Plate Kit (Thermo Fisher Scientific), following the manufacturer's instructions. A 5 µL aliquot of each normalized sample was pooled to create a sequencing library, which was then sequenced at the Oregon State University Center for Quantitative Life Sciences (CQLS) using an Illumina MiSeq Reagent Kit v2 (2 × 250 bp, 500 cycles; Illumina Inc., San Diego, CA, USA).

### 2.6. Statistical Analysis

#### 2.6.1. Statistical Analysis of APC, CC, YM, and SCC Data

Due to the small sample size, normality and homogeneity of variance were not formally tested, and non-parametric statistical methods were applied. Differences among farms were assessed using the Kruskal–Wallis test, followed by Dunn's post hoc test. Multiple testing correction was applied using both the Bonferroni and Benjamini–Hochberg (FDR) procedures. All analyses were performed in R version 4.3.2 using the Dunn test and FSA packages. Statistical significance was defined as $p < 0.05$.

#### 2.6.2. Metagenomic Analyses

Raw sequencing data were analyzed using QIIME 2 (version 2021.4), the latest stable release at the time of analysis (2021–2022) [33]. Demultiplexed paired-end reads were processed with the DADA2 plugin for quality filtering, denoising, and chimera removal. Taxonomy was assigned using the q2-feature-classifier plugin with a Naive Bayes classifier pre-trained on the SILVA 138 database. Alpha diversity was assessed with the Shannon index, and beta diversity with Bray–Curtis dissimilarity, followed by Analysis of Similarities (ANOSIM) to compare group-level differences. Relative abundances of dominant genera were calculated from the feature table using QIIME 2 and further processed in Mi-

crosoft Excel. Differences in genus-level abundance among farms were analyzed using the Kruskal–Wallis test with Dunn's post hoc test and multiple testing correction (Bonferroni and Benjamini–Hochberg).

To examine associations between milking hygiene practices and bacterial genera, linear regression analyses were conducted in R (stats package). The relative abundance (arcsine square-root transformed) of selected genera was modeled as the outcome variable, with predictor variables including glove use, hand sanitation between animals, and sanitizer type. All categorical predictors were coded as factors, with reference levels set to "Yes" (glove use, hand sanitation) and "Bleach-Iodine" (sanitizer type). Farm identity was treated as a blocking variable and checked in sensitivity analyses. Model assumptions (linearity, normality of residuals, and homoscedasticity) were verified through residual diagnostics. Statistical significance was defined as $p < 0.05$.

## 3. Results

### 3.1. Cleaning Intensity Based on Farm Assessment

Based on the structured visual assessment, hygiene practices were coded for each farm according to barn/parlor layout, barn/parlor cleaning, glove or hand sanitizer use, udder preparation, and equipment cleaning (Table 3). Farm A consistently received the highest codes across categories, with semi-enclosed facilities, regular sweeping and mopping, consistent glove use, multi-step udder preparation using iodine and bleach, and thorough equipment sanitation with hot water and bleach. Farm B scored lowest overall, with a separate enclosed parlor. Although barn/parlor cleaning was performed regularly, this farm showed limited overall hygiene due to the absence of glove or sanitizer use, minimal udder preparation (wipes only), and inconsistent equipment cleaning with lukewarm water and short contact times. Farm C showed mixed practices: although the barn cleaning score was lowest (occasional sweeping only), this farm employed moderate udder preparation with wipes and dip, occasional glove or sanitizer use, and thorough equipment cleaning through a dishwasher cycle with boiling hot water. Farm D achieved high codes for barn/parlor cleaning and regular soap-bleach steps in udder preparation but did not use gloves or hand sanitizers and relied on short contact times for equipment sanitation.

**Table 3.** Coded results of visual assessment of farm hygiene practices.

| Farm | Layout | Barn/Parlor Cleaning | Gloves/Hand Sanitizer | Udder Preparation | Equipment Cleaning |
|---|---|---|---|---|---|
| A | 1 | 2 | 2 (gloves + sanitizer) | 2 (iodine/bleach) | 2 (bleach + hot wash) |
| B | 2 | 2 | 0 (none) | 0 (wipes only) | 0 (lukewarm, short) |
| C | 2 | 0 | 1 (gloves/sanitizer, irregular) | 1 (wipes + dip) | 2 (dishwasher hot water) |
| D | 0 | 2 | 0 (none) | 1 (wipes + soap + bleach) | 1 (hot water + bleach, short) |

### 3.2. Microbiological Analyses

Mean and standard deviation values for APC, YM, and CC are illustrated in Figure 1A for both July and August. Nonparametric analysis (Kruskal–Wallis with Dunn's post hoc test) indicated significant differences in APC between farms in July ($p = 0.025$) and August ($p = 0.031$) (Table 4). In July, farm A had significantly lower APC compared with farms B and C. In August, APC in farm A was again significantly lower than in farm B ($p = 0.010$). No significant differences were observed in YM and CC in July. In August, YM showed a marginal trend ($p = 0.072$), and post hoc comparison revealed a significant difference only between farms A and B ($p = 0.036$). CC values did not differ among farms in August. The relatively large standard deviations observed in some groups likely reflect inherent

biological variability among farms and animals, as well as week-to-week variation within each month, since three weekly samples were collected.

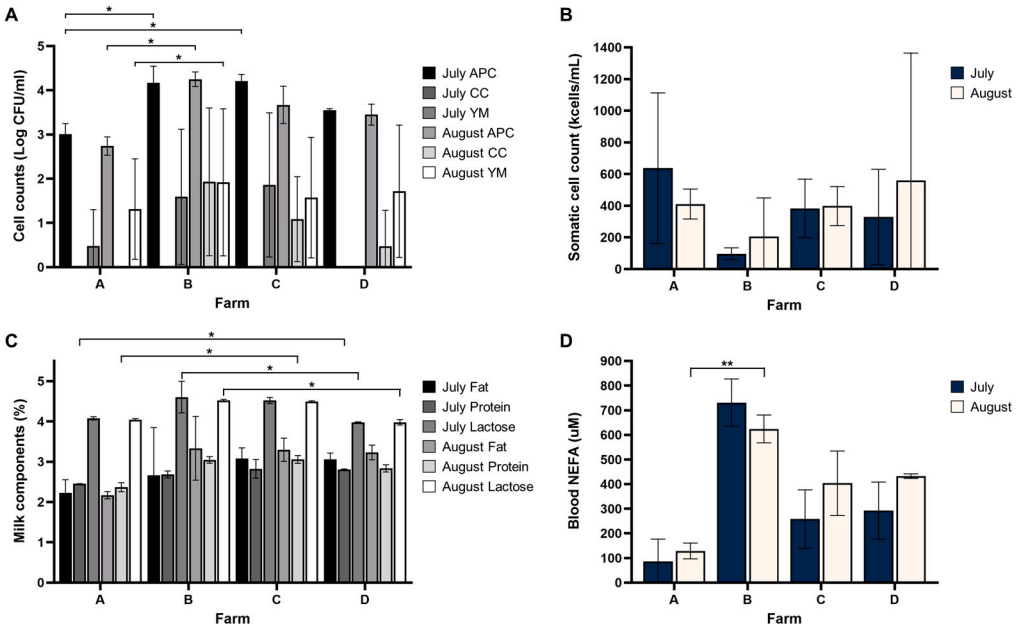



**Figure 1.** Microbiological and quality assessments of raw milk samples collected from farms A, B, C, and D in July and August. (**A**) Plate counts, including aerobic plate count (APC), coliform count (CC), and yeast and mold (YM), for each farm. (**B**) Somatic cell counts (SCC), showing variations between July and August for each farm. (**C**) Milk components, including true protein, fat, and lactose levels. (**D**) Blood non-esterified fatty acids (NEFA) concentrations in raw milk. Error bars represent the standard deviation of triplicate measurements. Asterisks indicate significant differences between farms based on Kruskal–Wallis tests followed by Dunn's post hoc test with multiple comparison adjustment. *, $p < 0.05$; **, $p < 0.01$.

**Table 4.** Summary of Kruskal–Wallis and Dunn's post hoc test results for microbiological and compositional parameters in goat milk across farms.

| Parameter | Month | Kruskal–Wallis $\chi^2$ | $p$ Value | Significant Pairwise Differences | |
|---|---|---|---|---|---|
| | | | | Adjusted $p$ (Bonferroni) | Adjusted $p$ (FDR: Benjamini–Hochberg) |
| APC | July | 9.36 | 0.025 | A vs. B (0.038), A vs. C (0.028) | A vs. B (0.020), A vs. C (0.028) |
| APC | August | 8.90 | 0.031 | A vs. B (0.010) | A vs. B (0.010) |
| YM | July | 4.11 | 0.250 | None | None |
| YM | August | 7.00 | 0.072 | A vs. B (0.036) * | A vs. B (0.036) * |
| CC | August | 4.11 | 0.250 | None | None |
| SCC | July | 5.15 | 0.161 | None | None |
| SCC | August | 1.97 | 0.578 | None | None |
| Fat | July | 4.33 | 0.228 | None | None |
| Fat | August | 6.28 | 0.099 | None | None |
| Protein | July | 8.08 | 0.045 | A vs. D (0.020) | A vs. D (0.020) |
| Protein | August | 9.46 | 0.024 | A vs. C (0.020) | A vs. C (0.020) |
| Lactose | July | 9.46 | 0.024 | B vs. D (0.020) | B vs. D (0.020) |
| Lactose | August | 8.95 | 0.030 | B vs. D (0.028) | B vs. D (0.028) |
| Blood NEFA | July | 2.59 | 0.459 | None | None |
| Blood NEFA | August | 9.46 | 0.024 | A vs. B (0.007) | A vs. B (0.007) |

* Marginal significance in overall test ($p = 0.072$), but pairwise comparison reached significance.

### *3.3. Results of SCC and Milk Component Analysis*

Mean and standard deviation values for SCC, milk components, and blood NEFA are illustrated in Figure 1 for both July and August. SCC did not differ significantly among farms in July ($p = 0.161$) or August ($p = 0.578$) (Table 4). Pairwise comparisons also confirmed no significant differences. For milk fat, no significant differences were detected in either July ($p = 0.228$) or August ($p = 0.099$). Blood NEFA concentrations did not differ in July ($p = 0.459$) but there were significantly different in August ($p = 0.024$), with farm A showing lower values than farm B ($p = 0.007$). Protein content varied among farms in July ($p = 0.045$), with farm A lower than farm D ($p = 0.020$). In August, protein also differed ($p = 0.024$), with farm A lower than farm C ($p = 0.020$). Lactose content showed significant variation in both July ($p = 0.024$) and August ($p = 0.030$). In July, farms B and D differed marginally ($p = 0.020$), and in August, the difference between farms B and D was significant ($p = 0.028$).

### *3.4. Microbial Diversity*

#### 3.4.1. Alpha Diversity

Alpha diversity differed significantly among sample types ($p < 0.0001$). Milking stanchion and raw milk samples showed significantly higher diversity than bulk tank samples ($p < 0.001$). Teat cup liner samples did not differ significantly from bulk tank samples but exhibited lower diversity than both milking stanchion and raw milk samples ($p < 0.01$). No significant difference was observed between milking stanchion and raw milk samples ($p = 0.509$) (Figure 2A). In contrast, alpha diversity did not significantly differ among farms ($p = 0.112$) (Figure 2B). Although Farm C tended to show higher diversity and farm D lower, none of the pairwise comparisons reached statistical significance after multiple testing correction ($p > 0.058$). We also compared the alpha diversity of raw milk samples between months. No significant differences were found among farms in either July ($p = 0.10$) or August ($p = 0.079$). In July, farm D tended to show lower diversity than farm A ($p = 0.052$), and in August, farm C tended to be more diverse than farm A ($p = 0.052$), but these differences were not statistically significant after multiple testing correction (Figure 2C).

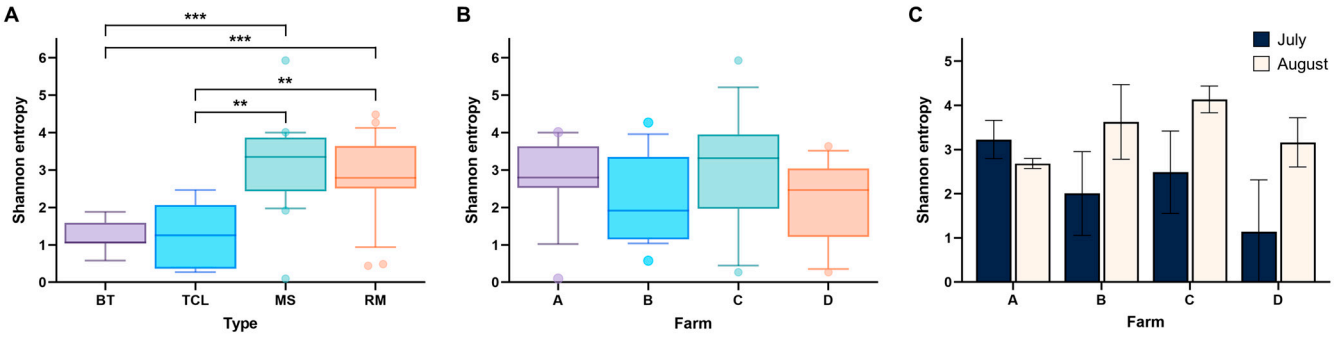



**Figure 2.** Alpha diversity (Shannon index) of microbial communities across various sample types, locations, and collection periods. (**A**) Alpha diversity across different sample types: bulk tank (BT), teat cup liner (TCL), milking stanchion (MS), and raw milk (RM), highlighting variation in microbial richness and evenness among these categories. (**B**) Alpha diversity comparison between locations, including all samples (raw milk and environmental samples combined). (**C**) Alpha diversity of raw milk samples collected in July and August, illustrating seasonal variations in microbial diversity. Error bars represent standard deviations, indicating variability within each category. Asterisks indicate significant pairwise differences among sample types based on Kruskal–Wallis tests followed by Dunn's post hoc test with multiple comparison adjustment. **, $p < 0.01$; ***, $p < 0.001$.

#### 3.4.2. Beta Diversity

Beta diversity was initially evaluated using pairwise comparisons, revealing statistically significant differences among all samples. However, these differences did not distinctly separate the farms. To further analyze beta diversity, an ANOSIM test was performed to assess the similarity or dissimilarity of the microbiota among samples. The Unweighted UniFrac metric was used, which measures the fraction of unshared microbial groups between samples. R-values closer to 1 indicate greater dissimilarity, while values closer to 0 indicate greater similarity [34]. For both July and August, R-values for the raw milk samples ranged from 0.44 to 0.67, suggesting considerable dissimilarity in microbial communities, though the data were not strong enough to draw definitive conclusions.

### *3.5. Taxonomic Analysis*

#### 3.5.1. Farm-Level Microbiota Composition

A total of 611 taxonomic groups were identified at the genus level across all raw milk and environmental samples. Farm A's microbiota was dominated by *Staphylococcus* and *Escherichia*, with no presence of *Pseudomonas*. In contrast, farm B had a higher abundance of *Pseudomonas* along with notable amounts of *Yersiniaceae*, *Lactococcus*, and other taxa. Farm C exhibited significant proportions of *Staphylococcus* and *Escherichia*, with smaller amounts of *Acinetobacter* and *Corynebacterium*. Farm D was characterized by a large proportion of *Pseudomonas* and *Staphylococcus*, with fewer additional taxa (Figure 3A).

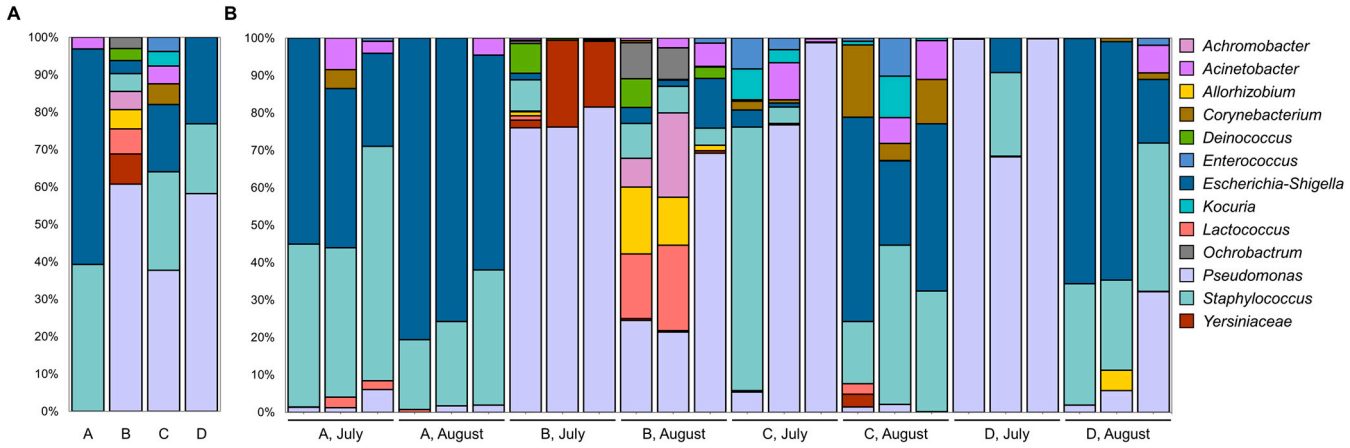



**Figure 3.** Microbiome composition across different farms (A, B, C, and D) based on relative abundance at the genus level. (**A**) Microbial community structure in combined samples (raw milk and environmental samples) from each farm, illustrating the overall microbial diversity and distribution across different farm types. (**B**) Microbial community structure specifically in raw milk samples from each farm, highlighting the dominant genera present in raw milk alone. Each color represents a different genus, and the varying heights of color blocks indicate the relative abundance of each microbial group within the samples.

#### 3.5.2. Raw Milk Samples

When focusing specifically on raw milk samples, the dominant microbial groups were *Staphylococcus*, *Escherichia-Shigella*, and *Pseudomonas*, showing considerable variation between samples (Figure 3B). *Pseudomonas* was particularly abundant in certain samples from farms B and D, whereas *Staphylococcus* and *Escherichia-Shigella* were prevalent across multiple raw milk samples from all farms. Some taxa, like *Yersiniaceae* and *Lactococcus*, appeared sporadically with low relative abundance. Importantly, the pathogenic genus *Salmonella* was not detected in any of the samples, and *Campylobacter* was found in only one milk sample from farm B in August, with a very low relative abundance of 0.014%. The microbial composition varied distinctly between farms.

3.5.3. Genera of Interest

Seven genera of interest for comparison included *Bacillus*, *Pseudomonas*, *Escherichia-Shigella*, *Staphylococcus*, *Lactococcus*, *Listeria*, and the family *Yersiniaceae* (Figure 4). Except for *Lactococcus*, all these groups are considered non-beneficial microorganisms. Among the bacterial genera analyzed, *Pseudomonas* and *Escherichia-Shigella* exhibited significant differences in relative abundance across farms during August ($p = 0.048$ and 0.038, respectively). In August, *Escherichia-Shigella* abundance was significantly higher in farm A than in farm B ($p = 0.014$). While *Pseudomonas* abundance showed a significant overall difference, post hoc comparisons revealed a marginal difference between farms C and B ($p = 0.052$). In July, *Escherichia-Shigella* and *Pseudomonas* showed a trend toward significance ($p = 0.066$ and 0.086, respectively), but no pairwise comparisons reached statistical significance after correction. Other genera such as *Bacillus*, *Staphylococcus*, *Lactococcus*, *Yersiniaceae*, and *Listeria* did not show statistically significant differences among farms at either time point ($p > 0.05$). The Kruskal–Wallis test could not be performed for *Listeria* in August due to uniform values across groups.

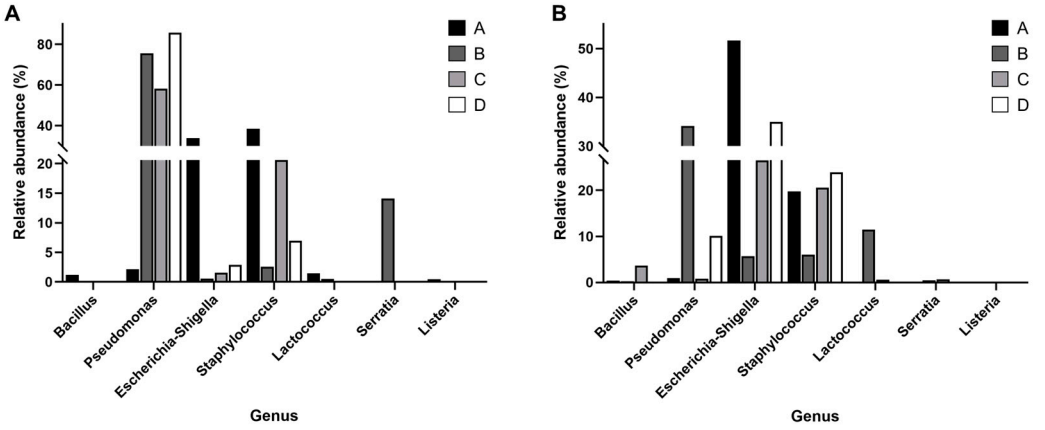



**Figure 4.** Relative abundance of seven major pathogenic bacteria identified in raw milk samples from different farms during (**A**) July and (**B**) August. Each bar represents the percentage of a specific pathogenic bacterial group within the sample, illustrating seasonal and farm-level variations in microbial composition.

*3.6. Association Between Milking Hygiene Practices and Bacterial Abundance*

Linear regression models were constructed to assess the association between hygiene-related practices and the relative abundance of dominant bacterial genera. The reference level (intercept) for all categorical variables was set as glove use = "yes", hand sanitation = "yes", and sanitizer type = "bleach iodine". Among the taxa analyzed, *Escherichia_Shigella* showed the strongest association ($R^2 = 0.526$, $p = 0.002$) (Table 5). Specifically, its intercept was highly significant ($p = 9.32 \times 10^{-7}$). *Deinococcus* abundance was significantly influenced by both the absence of hand sanitation ($p = 0.005$) and the use of bleach chlorhexidine sanitizer ($p = 0.005$) ($R^2 = 0.428$, $p = 0.010$). *Kocuria* ($R^2 = 0.435$, $p = 0.009$) and *Enterococcus* ($R^2 = 0.365$, $p = 0.026$) were both significantly elevated in conditions where gloves were not used and hand sanitation was not performed. Likewise, *Corynebacterium* ($R^2 = 0.351$, $p = 0.032$) showed significant increases under the same conditions ($p = 0.026$ and $p = 0.010$, respectively). *Staphylococcus* exhibited a significant intercept ($p = 5.59 \times 10^{-5}$). The remaining taxa did not show statistically significant associations ($p > 0.05$).

**Table 5.** Associations between hygiene practices and microbial abundance.

| Taxa | $R^2$ | *p* Value | Key Interpretation |
|---|---|---|---|
| *Pseudomonas* | 0.305 | 0.059 | Not significant |
| *Yersiniaceae* | 0.307 | 0.058 | Not significant |
| *Lactococcus* | 0.259 | 0.105 | Not significant |
| *Allorhizobium* | 0.298 | 0.065 | Not significant |
| *Achromobacter* | 0.212 | 0.180 | Not significant |
| *Staphylococcus* | 0.330 | 0.042 | Intercept ($p = 5.59 \times 10^{-5}$) |
| *Escherichia_Shigella* | 0.526 | 0.002 | Intercept ($p = 9.32 \times 10^{-7}$), Glove use no ($p = 0.004$) |
| *Deinococcus* | 0.428 | 0.010 | Hand sanitation no, Bleach chlorhexidine sanitizer ($p = 0.005$) |
| *Ochrobactrum* | 0.308 | 0.057 | Not significant |
| *Corynebacterium* | 0.351 | 0.032 | Glove use no ($p = 0.026$), Hand sanitation no ($p = 0.010$) |
| *Acinetobacter* | 0.130 | 0.415 | Not significant |
| *Kocuria* | 0.435 | 0.009 | Glove use no, Hand sanitation no ($p = 0.004$) |
| *Enterococcus* | 0.365 | 0.026 | Glove use no ($p = 0.010$), Hand sanitation no ($p = 0.012$) |

The intercept represents the condition where glove use = yes, hand sanitation = yes, and sanitizer type = bleach iodine.

## 4. Discussion

This study aimed to investigate how variations in milking and cleaning practices influence the quality and microbiome of raw goat milk. The findings demonstrate that farms with more rigorous cleaning protocols generally have lower counts of spoilage-specific microorganisms, which aligns with the research objective of identifying best practices for minimizing contamination.

APC, CC, and YM results showed that farms implementing multiple kill steps and frequent sanitization had fewer microbial contaminants. For example, farm A, which followed the most intensive cleaning procedures, including specified sanitizer concentrations, frequent milk parlor cleaning, and regular sanitation of equipment, consistently had coliform counts below the detection limit (<10 CFU/mL). This supports the established link between thorough hygiene practices and lower microbial contamination, as noted by Pantoja et al. (2011), who emphasized the importance of udder hygiene and bulk tank sanitation [35]. Farm D, despite not using precise sanitizer concentrations or gloves, had comparable microbial counts to farm A, suggesting that frequency and method of cleaning may outweigh specific product usage in some cases. Interestingly, despite overall rigorous cleaning, farm A exhibited significantly higher YM levels than farm B in August ($p = 0.036$), suggesting that fungal contamination may be influenced by environmental or equipment-related factors. As Vacheyrou et al. (2011) noted, fungal species in milk are often linked to the milking environment [36]. Farm A's less frequent replacement of equipment, such as gaskets and hoses, may have contributed to the persistence of YM, despite thorough cleaning practices. This highlights the importance of regularly replacing equipment, in addition to cleaning. Furthermore, the absence of acid or caustic wash steps at farm A suggests that incorporating these agents could help further reduce yeast and mold levels [37].

Although no statistically significant differences in SCC were observed among farms, considerable week-to-week fluctuations were detected, often coinciding with reported health issues in the herds. This observation is consistent with previous studies in goats, which emphasized that SCC are more strongly influenced by herd health status, stage of lactation, and parity than by milking hygiene alone [38,39]. Similar findings have been reported in dairy cows, where SCC variation largely reflected udder health and physiological factors rather than external management practices [40]. In our study, extreme weekly values likely contributed to the even distribution of mean SCC across farms, underscoring the multifactorial nature of this trait. Thus, while SCC remains an important indicator of

udder health, its interpretation requires consideration of multiple interacting factors. In contrast, milk composition parameters such as protein and lactose showed clearer farm-level differences, with farm A consistently exhibiting lower levels than farms C or D.

In our study, the dominant bacterial genera in raw goat milk were *Staphylococcus*, *Escherichia-Shigella*, and *Pseudomonas*, with occasional detection of *Lactococcus*, *Corynebacterium*, and *Yersiniaceae*. Previous studies of goat milk microbiota have similarly identified *Staphylococcus* and *Escherichia* as prevalent taxa, largely reflecting contamination from teat skin, fecal matter, or the farm environment [41,42]. By contrast, *Pseudomonas* has been more consistently highlighted as a major psychrotrophic genus in bovine raw milk [43]. These observations suggest that goat and cow milk share certain core taxa, but the relative contribution of spoilage-associated bacteria differs, potentially due to host physiology, teat canal morphology, and farm management practices [44]. Seasonal and lactation-related shifts in milk microbiota have also been documented, which may explain fluctuations in the abundance of dominant taxa [9,45,46]. Notably, some genera reported as dominant in other goat milk studies, such as *Enterococcus*, *Lactococcus*, and *Clostridium* [42,47], were only sporadically detected in our samples. Such discrepancies likely reflect differences in geographic origin, feeding systems, or methodological approaches, and highlight the diversity of goat milk microbiota across production contexts.

Regarding specific microbial genera, *Pseudomonas* species are well known for causing spoilage due to their proteolytic and lipolytic enzyme production and ability to grow at refrigeration temperatures. While *Pseudomonas* is consistently highlighted as dominant in bovine raw milk, in our goat milk samples it was not always abundant; rather, its prevalence appeared strongly influenced by cooling efficiency. Farm A had the lowest relative abundance of *Pseudomonas*, likely due to rapid cooling (to 4 °C in <2 h with an ice bath), whereas the other farms required 2–4 h using standard refrigeration. This pattern supports previous findings that inadequate cooling favors *Pseudomonas* proliferation and accelerates spoilage [48]. Thus, while *Pseudomonas* may not dominate goat milk under all conditions, it can become problematic when cooling is delayed. *Escherichia-Shigella* was also frequently detected, consistent with its status as a common genus in goat milk. *Escherichia-Shigella* multiplication is often linked to poor hygiene and the presence of feces or organic matter [49], and in our study its relative abundance varied substantially depending on hygiene conditions. In July, farm A had the highest counts, while in August farm B had the lowest. These differences may be explained by parlor design: farm A's parlor was only partially enclosed, allowing environmental contamination, whereas farm B's parlor was fully enclosed. This highlights that although *Escherichia-Shigella* is often present, its levels are strongly modulated by hygiene and facility characteristics [50].

*Staphylococcus aureus* was detected in higher relative abundance at farm A compared to farms B and D. This genus is widely recognized as one of the dominant taxa in goat milk [51], but our results indicate that specific farms may show particularly elevated levels. Such variation could be related to handler-associated contamination or subclinical mastitis, though our data do not allow firm conclusions [49,52]. Farm B also showed a relatively higher abundance of *Lactococcus* in August. While this genus was only sporadically detected overall, its increased abundance in Farm B at a specific time point suggests a farm- or feed-related effect. Although generally considered beneficial, *Lactococcus* can also drive rapid acidification and cause undesirable flavors [53]. The elevated levels observed here may reflect feed composition or lactose availability, as SCC values were not consistent with mastitis. Similarly, *Serratia* species were more abundant at farm B in July, though without accompanying udder health issues. *Listeria* species were detected at farm A in July, underscoring the potential role of environmental sources such as soil or manure.

Finally, our regression analysis indicated that hygiene practices significantly shaped the abundance of certain genera. The absence of glove use and hand sanitation was associated with increased levels of *Escherichia-Shigella*, *Kocuria*, *Enterococcus*, and *Corynebacterium*, all of which are typically considered fecal- or skin-associated bacteria. Similar associations between poor hygiene and elevated contamination have been reported in dairy cow studies [54,55]. In contrast, several groups, including the genus *Pseudomonas* and the family Yersiniaceae, showed little or no association with hygiene variables, suggesting that they may persist in the farm environment regardless of routine sanitation and are more strongly influenced by factors such as equipment condition or water quality.

This study has several limitations that should be acknowledged. First, the number of farms included was small ($n = 4$) and the sampling period was restricted to July and August. As a result, the findings may not be generalizable across seasons, and further studies covering more diverse farms and longer timeframes are required to validate these observations. Second, the visual assessment of hygiene practices was conducted by a single trained researcher. Although a structured checklist and coding system were applied to minimize subjectivity, the potential for observer bias cannot be excluded. Incorporating multiple independent assessors or inter-rater validation in future studies would strengthen the reliability of such qualitative evaluations. Finally, the week-to-week variability observed in several parameters suggests that additional longitudinal sampling across multiple lactation stages and herd health conditions would be valuable for capturing the full spectrum of variability in raw goat milk microbiota and quality. Beyond these limitations, it is also important to consider how these findings can be implemented across broader contexts. While the present results highlight the role of hygiene and equipment cleaning in shaping milk microbiota, differences in management systems, herd size, and regional practices may influence the applicability of these recommendations in other production settings. Future research should therefore not only validate the findings in larger and more diverse cohorts but also assess strategies for adapting best practices to varying farm infrastructures.

## 5. Conclusions

This study evaluated the milking and cleaning practices of goat dairy farms to understand their impact on the quality and microbiota of raw goat milk. The findings indicate that differences in cleaning and milking procedures both between and within farms affect bacterial counts and the types of microorganisms present in the milk. The results also suggest that practices related to udder and equipment cleaning, as well as the location of the milking parlor relative to the barn, play crucial roles in shaping the milk's microbiota. Future research should expand to include a larger number of goat dairy farms, investigate the populations of beneficial microorganisms in raw milk, and explore additional milking practices and farm logistics that may influence milk quality. Additionally, testing the implementation of optimized procedures across different farms could provide further insights, such as examining how consistent practices affect milk quality and microbial communities.

**Author Contributions:** Conceptualization, A.T. and S.H.P.; methodology, S.H.P.; validation, S.-M.Y.; investigation, A.T.; data curation, E.K.; writing—original draft preparation, A.T. and E.K.; writing—review and editing, L.G., H.-Y.K. and S.H.P.; visualization, E.K.; supervision, S.H.P. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research is partially funded by ER Jackman Friends and Alumni at the College of Agricultural Sciences, Oregon State University, and supported by the Oregon Agricultural Experiment Station with funding from the Hatch Act capacity funding program (award number NI21HFPXXXXG047) through the USDA National Institute of Food and Agriculture (NIFA).

**Institutional Review Board Statement:** Not applicable.

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** The sequencing data have been deposited in the NCBI Sequence Read Archive (SRA) under accession number SRP584650.

**Conflicts of Interest:** The authors declare no conflicts of interest.

## References


1. Duarte, R.V.; Pinto, C.A.; Gomes, A.M.; Delgadillo, I.; Saraiva, J.A. A microbiological perspective of raw milk preserved at room temperature using hyperbaric storage compared to refrigerated storage. *Innov. Food Sci. Emerg. Technol.* **2022**, *78*, 103019. [CrossRef]
2. Mullin, G.E.; Belkoff, S.M.; Box, R. Survey to determine why people drink raw milk. *Glob. Adv. Health Med.* **2014**, *3*, 19–24. [CrossRef] [PubMed]
3. Perin, L.M.; Pereira, J.G.; Bersot, L.S.; Nero, L.A. The microbiology of raw milk. In *Raw Milk: Balance Between Hazards Benefits*; Elsevier: Amsterdam, The Netherlands, 2018; pp. 45–64.
4. Dash, K.K.; Fayaz, U.; Dar, A.H.; Shams, R.; Manzoor, S.; Sundarsingh, A.; Deka, P.; Khan, S.A. A comprehensive review on heat treatments and related impact on the quality and microbial safety of milk and milk-based products. *Food Chem. Adv.* **2022**, *1*, 100041. [CrossRef]
5. Akshit, F.N.U.; Deshwal, G.K.; Sharma, H.; Kumar, P.; Maddipatla, D.K.; Singh, M.P.; Goksen, G. Technological challenges in production of goat milk products and strategies to overcome them: A review. *Int. J. Food Sci. Technol.* **2024**, *59*, 6–16. [CrossRef]
6. Pulina, G.; Milán, M.J.; Lavín, M.P.; Theodoridis, A.; Morin, E.; Capote, J.; Thomas, D.L.; Francesconi, A.H.D.; Caja, G. Invited review: Current production trends, farm structures, and economics of the dairy sheep and goat sectors. *J. Dairy Sci.* **2018**, *101*, 6715–6729. [CrossRef]
7. Miller, B.A.; Lu, C.D. Current status of global dairy goat production: An overview. *Asian-Australas. J. Anim. Sci.* **2019**, *32*, 1219–1232. [CrossRef]
8. Migeemanathan, S.; Bhat, R.; Min-Tze, L.; Wan-Abdullah, W.N. Effects of temperature abuse on the survival, growth, and inactivation of *Salmonella typhimurium* in goat milk. *Foodborne Pathog. Dis.* **2011**, *8*, 1235–1240. [CrossRef] [PubMed]
9. Lauková, A.; Micenková, L.; Grešáková, Ľ.; Mad'arová, M.; Simonová, M.P.; Focková, V.; Ščerbová, J. Microbiome associated with Slovak raw goat milk, trace minerals, and vitamin E content. *Int. J. Food Sci.* **2022**, *2022*, 4595473. [CrossRef]
10. Niyazbekova, Z.; Yao, X.T.; Liu, M.J.; Bold, N.; Tong, J.Z.; Chang, J.J.; Wen, Y.; Li, L.; Wang, Y.; Chen, D.K.; et al. Compositional and functional comparisons of the microbiota in the colostrum and mature milk of dairy goats. *Animals* **2020**, *10*, 1955. [CrossRef]
11. Park, Y.W. Improving Goat Milk. In *Improving the Safety and Quality of Milk*; Woodhead Publishing: London, UK, 2010; Volume 2, pp. 304–346.
12. Deddefo, A.; Mamo, G.; Asfaw, M.; Amenu, K. Factors affecting the microbiological quality and contamination of farm bulk milk by *Staphylococcus aureus* in dairy farms in Asella, Ethiopia. *BMC Microbiol.* **2023**, *23*, 65. [CrossRef]
13. Ntuli, V.; Sibanda, T.; Elegbeleye, J.A.; Mugadza, D.T.; Seifu, E.; Buys, E.M. Dairy production: Microbial safety of raw milk and processed milk products. In *Present Knowledge in Food Safety: A Risk-Based Approach Through the Food Chain*; Elsevier: Amsterdam, The Netherlands, 2022; pp. 439–454.
14. Nayik, G.A.; Jagdale, Y.D.; Gaikwad, S.A.; Devkatte, A.N.; Dar, A.H.; Dezmirean, D.S.; Bobis, O.; Ranjha, M.M.A.N.; Ansari, M.J.; Hemeg, H.A.; et al. Recent insights into processing approaches and potential health benefits of goat milk and its products: A review. *Front. Nutr.* **2021**, *8*, 789117. [CrossRef] [PubMed]
15. Zecconi, A.; Dell'orco, F.; Vairani, D.; Rizzi, N.; Cipolla, M.; Zanini, L. Differential somatic cell count as a marker for changes of milk composition in cows with very low somatic cell count. *Animals* **2020**, *10*, 604. [CrossRef]
16. Agnihotri, M.K.; Rajkumar, V. Effect of breed, parity and stage of lactation on milk composition of western region goats of India. *Int. J. Dairy Sci.* **2007**, *2*, 172–177. [CrossRef]
17. Park, Y.W.; Humphrey, R.D. Bacterial cell counts in goat milk and their correlations with somatic cell counts, percent fat, and protein. *J. Dairy Sci.* **1986**, *69*, 32–37. [CrossRef]
18. Wilson, D.J.; Stewart, K.N.; Sears, P.M. Effects of stage of lactation, production, parity and season on somatic cell counts in infected and uninfected dairy goats. *Small Rumin. Res.* **1995**, *16*, 165–169. [CrossRef]
19. Zeng, S.S.; Escobar, E.N. Effect of parity and milk production on somatic cell count, standard plate count and composition of goat milk. *Small Rumin. Res.* **1995**, *17*, 269–274. [CrossRef]
20. ALKaisy, Q.H.; Al-Saadi, J.S.; AL-Rikabi, A.K.J.; Altemimi, A.B.; Hesarinejad, M.A.; Abedelmaksoud, T.G. Exploring the health benefits and functional properties of goat milk proteins. *Food Sci. Nutr.* **2023**, *11*, 5641–5656. [CrossRef] [PubMed]
21. Verruck, S.; Dantas, A.; Prudencio, E.S. Functionality of the components from goat's milk, recent advances for functional dairy products development and its implications on human health. *J. Funct. Foods* **2019**, *52*, 243–257. [CrossRef]

22. Monareng, N.J.; Ncube, K.T.; van Rooi, C.; Modiba, M.C.; Mtileni, B. A systematic review on microbial profiling techniques in goat milk: Implications for probiotics and shelf-life. *Int. J. Mol. Sci.* **2025**, *26*, 5551. [CrossRef]
23. Praja, R.N.; Yudhana, A.; Saputro, A.L.; Hamonangan, J.M. The first study on antimicrobial resistance of Staphylococcus aureus isolated from raw goat milk associated with subclinical mastitis in Siliragung Subdistrict, East Java, Indonesia. *Vet. World* **2023**, *16*, 786–791. [CrossRef]
24. D'Amico, D.J.; Donnelly, C.W. Microbiological quality of raw milk used for small-scale artisan cheese production in Vermont: Effect of farm characteristics and practices. *J. Dairy Sci.* **2010**, *93*, 134–147. [CrossRef]
25. Code of Federal Regulations. Mandatory Pasteurization for All Milk and Milk Products in Final Package Form Intended for Direct Human Consumption. 2014. Available online: https://www.ecfr.gov/current/title-21/chapter-I/subchapter-L/part-1240/subpart-D/section-1240.61 (accessed on 24 September 2025).
26. Oregon Revised Statutes (ORS) § 621.012—License Required for Sale of Milk; Exceptions. Available online: https://oregon.public.law/statutes/ors_621.012 (accessed on 24 September 2025).
27. Park, S.H.; Kim, S.A.; Rubinelli, P.M.; Roto, S.M.; Ricke, S.C. Microbial compositional changes in broiler chicken cecal contents from birds challenged with different Salmonella vaccine candidate strains. *Vaccine* **2017**, *35*, 3204–3208. [CrossRef]
28. Middelbos, I.S.; Godoy, M.R.; Fastinger, N.D.; Fahey, G.C. A dose-response evaluation of spray-dried yeast cell wall supplementation of diets fed to adult dogs: Effects on nutrient digestibility, immune indices, and fecal microbial populations. *J. Anim. Sci.* **2007**, *85*, 3022–3032. [CrossRef]
29. *ISO 4833-1:2013*; Microbiology of the Food Chain: Horizontal Method for the Enumeration of Microorganisms—Part 1: Colony Count at 30° C by the Pour Plate Technique. International Organization for Standardization: Geneva, Switzerland, 2022.
30. *ISO 21528-2:2017*; Microbiology of the Food Chain—Horizontal Method for the Detection and Enumeration of Enterobacteriaceae—Part 2: Colony-Count Technique. International Organization for Standardization: Geneva, Switzerland, 2017.
31. *ISO 6611:2004*; Milk and Milk Products—Enumeration of Colony-Forming Units of Yeasts and/or Moulds—Colony-Count Technique at 25 °C. International Organization for Standardization: Geneva, Switzerland, 2004.
32. Kozich, J.J.; Westcott, S.L.; Baxter, N.T.; Highlander, S.K.; Schloss, P.D. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the miseq illumina sequencing platform. *Appl. Environ. Microbiol.* **2013**, *79*, 5112–5120. [CrossRef]
33. Bolyen, E.; Rideout, J.R.; Dillon, M.R.; Bokulich, N.A.; Abnet, C.C.; Al-Ghalith, G.A.; Alexander, H.; Alm, E.J.; Arumugam, M.; Asnicar, F.; et al. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat. Biotechnol.* **2019**, *37*, 852–857. [CrossRef]
34. Bray, J.R.; Curtis, J.T. An ordination of the upland forest communities of southern Wisconsin. *Ecol. Monogr.* **1957**, *27*, 325–349. [CrossRef]
35. Pantoja, J.C.F.; Reinemann, D.J.; Ruegg, P.L. Factors associated with coliform count in unpasteurized bulk milk. *J. Dairy Sci.* **2011**, *94*, 2680–2691. [CrossRef] [PubMed]
36. Vacheyrou, M.; Normand, A.C.; Guyot, P.; Cassagne, C.; Piarroux, R.; Bouton, Y. Cultivable microbial communities in raw cow milk and potential transfers from stables of sixteen French farms. *Int. J. Food Microbiol.* **2011**, *146*, 253–262. [CrossRef]
37. Kabak, B.; Dobson, A.D.W.; Var, I. Strategies to prevent mycotoxin contamination of food and animal feed: A review. *Crit. Rev. Food Sci. Nutr.* **2006**, *46*, 593–619. [CrossRef]
38. Kaskous, S.; Farschtschi, S.; Pfaffl, M.W. Physiological aspects of milk somatic cell count in small ruminants—A review. *Dairy* **2023**, *4*, 26–42. [CrossRef]
39. Alhussien, M.N.; Dang, A.K. Milk somatic cells, factors influencing their release, future prospects, and practical utility in dairy animals: An overview. *Vet. World* **2018**, *11*, 562–577. [CrossRef]
40. Smistad, M.; Inglingstad, R.A.; Sølverød, L.; Skeie, S.; Hansen, B.G. Somatic cell count in dairy goats I: Association with infectious and non-infectious factors. *BMC Vet. Res.* **2024**, *20*, 509. [CrossRef] [PubMed]
41. Polveiro, R.C.; Vidigal, P.M.P.; de Oliveira Mendes, T.A.; Yamatogi, R.S.; da Silva, L.S.; Fujikura, J.M.; Da Costa, M.M.; Moreira, M.A.S. Distinguishing the milk microbiota of healthy goats and goats diagnosed with subclinical mastitis, clinical mastitis, and gangrenous mastitis. *Front. Microbiol.* **2022**, *13*, 918706. [CrossRef]
42. Hoving-Bolink, R.A.H.; Antonis, A.F.G.; te Pas, M.F.W.; Schokker, D. An observational study of the presence and variability of the microbiota composition of goat herd milk related to mainstream and artisanal farm management. *PLoS ONE* **2023**, *18*, e0292650. [PubMed]
43. Kim, E.; Song, T.C.; Yang, S.M.; Kim, J.; Kim, H.Y. Comparative analysis of microbial diversity and fatty acids in raw milk from different production systems. *Food Chem.* **2025**, *493*, 145899. [CrossRef]
44. Addis, M.F.; Tanca, A.; Uzzau, S.; Oikonomou, G.; Bicalho, R.C.; Moroni, P. The bovine milk microbiota: Insights and perspectives from -omics studies. *Mol. Biosyst.* **2016**, *12*, 2359–2372. [CrossRef]

45. Celano, G.; Calasso, M.; Costantino, G.; Vacca, M.; Ressa, A.; Nikoloudaki, O.; De Palo, P.; Calabrese, F.M.; Gobbetti, M.; De Angelis, M. Effect of seasonality on microbiological variability of raw cow milk from apulian dairy farms in Italy. *Microbiol. Spectr.* **2022**, *10*, e00514-22. [CrossRef]
46. McInnis, E.A.; Kalanetra, K.M.; Mills, D.A.; Maga, E.A. Analysis of raw goat milk microbiota: Impact of stage of lactation and lysozyme on microbial diversity. *Food Microbiol.* **2015**, *46*, 121–131. [CrossRef] [PubMed]
47. Perin, L.M.; Nero, L.A. Antagonistic lactic acid bacteria isolated from goat milk and identification of a novel nisin variant Lactococcus lactis. *BMC Microbiol.* **2014**, *14*, 36. [CrossRef]
48. De Jonghe, V.; Coorevits, A.; Van Hoorde, K.; Messens, W.; Van Landschoot, A.; De Vos, P.; Heyndrickx, M. Influence of storage conditions on the growth of pseudomonas species in refrigerated raw milk. *Appl. Environ. Microbiol.* **2011**, *77*, 460–470. [CrossRef]
49. Suguna, M.; Bhat, R.; Wan, W.A. Microbiological quality evaluation of goat milk collected from small-scale dairy farms in Penang Island, Malaysia. *Int. Food Res. J.* **2012**, *19*, 1241–1245.
50. Oliver, S.P.; Jayarao, B.M.; Almeida, R.A. Foodborne pathogens in milk and the dairy farm environment: Food safety and public health implications. *Foodborne Pathog. Dis.* **2005**, *2*, 115–129. [CrossRef]
51. Anderson, K.L.; Kearns, R.; Lyman, R.; Correa, M.T. Staphylococci in dairy goats and human milkers, and the relationship with herd management practices. *Small Rumin. Res.* **2019**, *171*, 13–22. [CrossRef]
52. Kousta, M.; Mataragas, M.; Skandamis, P.; Drosinos, E.H. Prevalence and sources of cheese contamination with pathogens at farm and processing levels. *Food Control* **2010**, *21*, 805–815. [CrossRef]
53. Quigley, L.; O'Sullivan, O.; Stanton, C.; Beresford, T.P.; Ross, R.P.; Fitzgerald, G.F.; Cotter, P.D. The complex microbiota of raw milk. *FEMS Microbiol. Rev.* **2013**, *37*, 664–698. [CrossRef] [PubMed]
54. Mallet, A.; Guéguen, M.; Kauffmann, F.; Chesneau, C.; Sesboué, A.; Desmasures, N. Quantitative and qualitative microbial analysis of raw milk reveals substantial diversity influenced by herd management practices. *Int. Dairy J.* **2012**, *27*, 13–21. [CrossRef]
55. Lafarge, V.; Ogier, J.C.; Girard, V.; Maladen, V.; Leveau, J.Y.; Gruss, A.; Delacroix-Buchet, A. Raw cow milk bacterial population shifts attributable to refrigeration. *Appl. Environ. Microbiol.* **2004**, *70*, 5644–5650. [CrossRef] [PubMed]


**Disclaimer/Publisher's Note:** The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.