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Impact of Technological Treatments on the Hygienic Quality of Local Milk from the Niamey Region

Hamza Seydou Korombé [1*] **, *Ibrahim Djibo*** [2] **, *Mahaman Maaouia Abdou Moussa*** [3] **, *Mariama Gagara Hima*** [4] **, *Amadou Morou Madougou*** [5] **, *Aicha Mahamadou Kona*** [6] **, *Aminatou Aliou Barazi*** [7] **, *Abdoulaye Soumana Gouro*** [3]

[1] *Cattle Multiplication Center, Ministry of Agriculture and Livestock, Niamey P.O. Box 827, Niger*

[2] *Department of Agriculture in Arid Zones, Faculty of Sciences, University of Agadez, Agadez P.O. Box 199, Niger*

[3] *Animal Production Department, Faculty of Agronomy, Abdou Moumouni University, Niamey P.O. Box 10960, Niger*

[4] *Central Livestock Laboratory, Ministry of Agriculture and Livestock, Niamey P.O. Box 485, Niger*

[5] *General Direction of Veterinary Services, Ministry of Agriculture and Livestock, Niamey P.O. Box 1291, Niger*

[6] *Faculty of Agronomy and Environmental Sciences, Islamic University of Niger, Niamey P.O. Box 11507, Niger*

[7] *National Program for the Genetic Improvement of Local Cattle, Ministry of Agriculture and Livestock, Niamey P.O. Box 12091, Niger*

ABSTRACT

This study evaluates the effectiveness of three technological treatments, including spontaneous fermentation (T1), fermentation with inoculum (T2), and filro-fermentation (T3), in improving the microbiological quality of raw milk (T0) collected in the municipality of Kollo (Niger). A total of 31 milk samples were collected and subjected to each treatment. Microbiological analyses focused on the enumeration of Fecal Coliforms (FC), *Escherichia coli*, *Staphylococci*, Sulfite-Reducing Anaerobic bacteria (SRC), and the detection of *Salmonella spp*. The results show that all treatments significantly reduced FC contamination (p = 0.000) compared to raw milk (1.71 log CFU/mL). Treatments T1, T2, and

*CORRESPONDING AUTHOR:
Hamza Seydou Korombé, Cattle Multiplication Center, Ministry of Agriculture and Livestock, Niamey P.O. Box 827, Niger;
Email: korombehamzal@yahoo.com

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T3 were similarly effective, with average reductions to 0.55, 0.00, and 0.41 log CFU/mL, respectively. Regarding *E. coli*, only treatment T2 (0.46 log CFU/mL) showed a statistically significant reduction compared to the control (1.71 log CFU/mL). For *Staphylococci* and SRC, no significant difference was observed between the raw milk and the treated samples ($p > 0.05$). Although the prevalence of *Salmonella* decreased from 58.06% in raw milk to approximately 42% in treated samples, this reduction was not statistically significant according to the chi-square test ($p = 0.531$). The study's main limitation lies in its in vitro experimental design; the effectiveness of these treatments under real-world conditions and their impact on the organoleptic properties of the milk were not assessed. In conclusion, fermentation, particularly with the addition of an inoculum (T2), appears to be the most effective treatment for significantly reducing the main fecal contamination indicators in local milk. These results support the promotion of controlled fermentation practices to enhance food safety in the local dairy value chain.

Keywords: Local Milk; Fermentation Raw Milk; Hygienic Quality; Dairy Technology; Pathogenic Bacteria; Microbiological Quality; Niger

1. Introduction

Milk and dairy products have long been key components of the human diet, providing a matrix of nutritional compounds including fats, proteins, vitamins, and minerals [1–3]. Beyond their nutritional value, dairy consumption is also associated with health benefits [4].

These qualities partly explain the evolution of demand in urban areas. Thus, the population of Niamey, like that of other West African capitals, is growing and becoming more urbanized, and a portion of it is shifting its demand towards milk and dairy products from local livestock farming instead of imported milk [5]. Milk does indeed hold particular social importance in a livestock-farming country like Niger.

However, while milk is a product with high nutritional value, its composition and physicochemical properties make it a very favorable environment for the multiplication of microorganisms [6,7] and therefore susceptible to spoilage if it is not properly stored [8,9]. This vulnerability poses a major health challenge. Indeed, a recent report from the Center for Disease Control stated that the consumption of raw dairy products is linked to foodborne illnesses; these products constitute the second leading source of pathogenic microorganisms for humans, causing 14% of illnesses and 10% of related deaths [10]. Furthermore, in the local context, this risk is proven. Several studies have revealed the poor hygienic quality of local milk and dairy products, notably due to bacterial contamination linked to deficiencies in hygiene practices, whether at the production, collection, transport, or processing level [11–13].

It is with this in mind that the present study aims to evaluate the impact of technological treatments on the microbiological and hygienic quality of locally produced milk around the city of Niamey. Its goal is to suggest improvements to safeguard consumer health.

2. Materials and Methods

2.1. Period and Place of Study

The study was conducted from July to September 2024 in the municipality of Kollo (Niger), located 30 km from the Niamey region. In this area, livestock farming is the main economic activity, surpassing agriculture, which is primarily for subsistence farming. Dairy production is a cash-generating activity practiced by economic interest groups in this municipality, which currently houses a major milk collection center [14,15]. For this study, samples were taken from milk containers from the 25 villages that supply the municipality's milk collection center. This collection center is one of the three largest milk collection centers supplying industrial units and some small processing units in Niamey; the other two centers are Hamdallaye and Say.

2.2. Milk Sampling and Collection

A random selection process identified 30 producers (some from the same locality) from the 25 villages supply-

ing the Kollo collection center. Thirty raw milk samples were collected between 9:00 AM and 12:00 PM at the collection center, with each producer receiving 1 L of blended milk (milk from multiple milkings). 1 L of milk was also collected from the milk tank (CUV or tank), resulting in 31 samples. The samples collected are independent samples, meaning they come from different producers. They are representative of the Kollo dairy basin because they cover all 25 villages in the basin, and the samples are also representative at the producer level because they consist of a mixture of milk from all lactating females in the herd. The samples were placed in labeled plastic bags and transported in a cooler filled with crushed ice to the Central Livestock Laboratory (LABOCEL). Analyses were performed within 24 h of collection.

2.3. Experiment Design

The treatments were performed on T0 (untreated raw milk), T1 (spontaneous fermentation), T2 (fermentation with addition of inoculum), and T3 (filro-fermentation).

Each collected sample was subjected to the four treatments, resulting in a factorial arrangement of 4 × 31, or 124 replicates in total. A volume of 250 mL was used for the preparation of the different treatments.

- **T0 (Control)**: No treatment;
- **T1**: Direct incubation (44 °C, 24 h) after transfer into a sterile box;
- **T2**: Filtration with a filter-compress, followed by heating to 80 °C for 20 min, then cooling and inoculation with 1 mL of traditional curdled milk, then incubation (44 °C, 24 h);
- **T3**: Filtration with a filter-compress followed by incubation (44 °C, 24 h).

2.4. Analysis Protocol

As the primary objective of this study was to assess the impact of technological treatments on the hygienic quality (microbiological safety) of local milk, physicochemical parameters such as pH were not measured. The evaluation focused exclusively on indicators of fecal contamination (*Escherichia coli*, Fecal coliforms) and pathogenic flora (*Staphylococcus*, *Salmonella* spp., sulfite-reducing anaerobes), which are the direct criteria for assessing the health risk associated with milk consumption.

Microbiological analyses were carried out in accordance with current international standards in order to ensure the reliability and reproducibility of the results.

2.4.1. Thermotolerant Coliforms and *Escherichia coli*

The enumeration of *Escherichia coli* and Fecal coliforms was performed according to the standard method [16]. After preparing the stock suspension in buffered peptone water (BPW), successive decimal dilutions were carried out. An appropriate volume of each dilution was inoculated onto Rapid agar. The plates were incubated at 44 ± 1 °C for 18–24 h [16].

2.4.2. *Staphylococcus aureus* (Coagulase-Positive Staphylococci) Enumeration

Coagulase-positive staphylococci were counted by using the standard method [17]. The dilutions were inoculated onto Baird-Parker (BP) agar enriched with potassium tellurite and egg yolk emulsion. Plates were incubated at 37 °C for 24–48 h [17].

2.4.3. Enumeration of Sulfite-Reducing Anaerobic Bacteria (SRC)

The enumeration of sulfite-reducing anaerobes, *Clostridium*, was performed. Inoculation was carried out by deep inoculation onto Tryptose Sulfite Cycloserine (TSC) agar. The plates were incubated under anaerobic conditions at 37 °C for 24–48 h. Black colonies, resulting from sulfite reduction, were counted, and the results *were* expressed in CFU/mL [18].

2.4.4. *Salmonella* spp Testing

A non-selective pre-enrichment was performed in BPW, incubated at 37 °C for 18–24 h. This pre-enrichment was followed by two selective enrichments, in Rappaport Vassiliadis Soybean (RVS) and Mueller Kauffman Tetrathionate Novobiocin (MKTTn) media, incubated at 41.5 °C and 37 °C for 24 h, respectively. Isolation was performed on selective agar plates (XLD and Hektoen). Results were expressed as presence or absence in 25 mL of sample [19].

2.5. Statistical Analysis of Data

The collected data were coded and entered into Microsoft Excel, then analyzed using SPSS version 20.0. Means and standard deviations were calculated. The data were first log-transformed before applying the nonparametric Kruskal-Wallis test at a significance level of 5% to compare the means, as the data did not follow a normal distribution and the variances were not homogeneous. Cross-tabulations were performed to determine the prevalence of Salmonella in the samples, and a chi-square test and a z-test were used to assess the statistical significance of the results.

3. Results

3.1. Fecal Coliforms (FC) Load According to Treatment

The mean fecal coliform loads differed significantly ($p < 0.001$) between treatments (**Table 1**). The mean initial contamination loads (T0) were very high (1.71 ± 1.72 log CFU/mL). Treatment T1 drastically reduced fecal coliform contamination by approximately 1.16 log CFU/mL, or about 67.84%, compared to the first treatment. However, its load remained statistically different from those of T3, which resulted in a 76.02% reduction in contamination of approximately 1.3 log CFU/mL, and T2, which achieved complete elimination of this organism. This indicates that the analysed volume of the T2 treatment is completely free of fecal coliforms.

Table 1. Fecal Coliforms (FC) Load according to treatment.

Treatments	N	FC (log CFU/mL)
T0	31	1.71 ± 1.72 [a]
T1	31	0.55 ± 1.21 [b]
T2	31	0.00 ± 0.00 [b]
T3	31	0.41 ± 0.87 [b]
p-value		0.000

Note: NB: means having the same letter in the exponent are not statistically different from each other at the 5% threshold. N: Number of samples; FC: Fecal Coliforms; CFU: Colony-Forming Unit.

3.2. Evaluation of the Load in *Escherichia coli* Depending on the Treatments

Escherichia coli contamination levels varied according to the treatments, with significant differences (**Table 2**). *Escherichia coli* was present in all types of milk (untreated and treated), with a trend toward a decrease in treatments T1, T2, and T3 compared to the control group. However, only treatment T2 is statistically different from T0.

Table 2. *Escherichia coli* load according to treatment.

Treatments	N	*Escherichia coli* (log CFU/mL)
T0	31	1.71 ± 1.52 [a]
T1	31	1.25 ± 1.57 [ab]
T2	31	0.46 ± 1.11 [b]
T3	31	1.11 ± 1.52 [ab]
p-value		0.008

Note: NB: means with at least one identical superscript letter are not statistically different from one another at the 5% significance level. N: Number of samples; CFU: Colony-Forming Unit.

3.3. Evaluation of Staphylococcus Load Based on Treatments

The *Staphylococcus* load varies depending on treatment without significant differences (**Table 3**). Contamination increased with treatments T1 and T3. Only treatment T2 had a reduction effect, of approximately 28%.

Table 3. *Staphylococcus aureus* according to treatment.

Treatments	N	Staphylococci (log CFU /mL)
T0	31	2.11 ± 1.16 [a]
T1	31	1.86 ± 1.53 [a]
T2	31	1.26 ± 1.41 [a]
T3	31	1.76 ± 1.37 [a]
p-value		0.115

Note: NB: means having the same letter in the exponent are not statistically different from each other at the 5% threshold. N: Number of samples; CFU: Colony-Forming Unit.

3.4. Sulfite-Reducing Anaerobic Bacteria (SRC) Load According to Treatments

Table 4 shows the SRC load according to the treatments. There is no significant difference (p-value > 0.05) between the treatment means. The initial load is 0.11 ± 0.59 log CFU/mL. Treatments T1, T2, and T3 completely eliminated the SRC load. This indicates that the analyzed volumes from these treatments showed a complete absence of SRC.

Table 4. Sulfite-reducing anaerobic bacteria (SRC) load according to treatment.

Treatments	N	SRC (log CFU/mL)
T0	31	0.11 ± 0.59^{a}
T1	31	0.00 ± 0.00^{a}
T2	31	0.00 ± 0.00^{a}
T3	31	0.00 ± 0.00^{a}
p-value		0.392

Note: NB: means having the same letter in the exponent are not statistically different from each other at the 5% threshold. N: Number of samples; SRC: Sulfite-reducing anaerobic bacteria; CFU: Colony-Forming Unit.

3.5. Evaluation of *Salmonella* Load According to Treatments

Salmonella was detected in all treatments with varying intensity (**Table 5**). The chi-square value is greater than 0.05, which means there are no significant differences between the presence and absence of *Salmonella* in the various samples. There are also no significant differences between the treatments, as shown by the z-test. However, the high initial *Salmonella* contamination (58.06%) dropped slightly to 41.93% with each of the T1 and T3 treatments and to 45.16% with the T2 treatment.

Table 5. Presence of *Salmonella* according to treatments.

Treatments	N	Presence of *Salmonella* spp. (%)
T0	31	58.06
T1	31	41.93
T2	31	45.16
T3	31	41.93
Chi-square		0.531

Note: N: Number of samples.

4. Discussion

The results obtained in this study clearly show that the hygienic quality of collected raw milk varies according to the type of treatment applied.

4.1. Analysis of Sample Contamination by Fecal Coliforms

The initial fecal coliform load in raw milk is very high (1.71 log CFU/mL), which is significantly higher than the threshold value set by the Association Française de Normalisation (AFNOR) standard (2 log CFU/mL). Coliforms are common inhabitants of the mammalian intestine, and their presence in milk indicates direct or indirect fecal contamination due to inadequate hygiene practices during milking. This result therefore reveals insufficient hygiene practices by farmers in the collection area. The poor sanitary quality of blended raw milk has been reported by numerous studies in the sub-region, where fecal coliform loads are comparable to the present results [20,21]. The higher fecal coliform load in raw milk is thought to be due to the numerous handling operations by milk collectors as well as various unhygienic practices by dairy farmers, such as washing hands, teats, and utensils with water of dubious quality [22,23].

Treatment T1 resulted in a significant reduction (0.55 log CFU/mL), but did not reach a sufficient level of microbiological safety. The pseudo-lactic nature of fecal coliforms explains this observation. These bacteria can actually withstand low pH levels, similar to what is encountered in fermented milk [24]. This load is lower than that obtained in the samples of Morocco [21]. The treatment T3, a method that combines filtration with spontaneous fermentation, resulted in a greater reduction (0.3 log CFU/mL), likely due to partial elimination of the flora during filtration. This result is also better than that obtained from samples of traditional unfiltered curdled milk in Senegal, with an average load ranging from 2 to 5.41 log CFU/mL [25].

Only treatment T2 allowed for the complete elimination of fecal coliforms, demonstrating the superiority of the combined filtration-heating-directed inoculation approach. Fecal coliforms are, in fact, sensitive to heat [26], and the combined impact of filtration and the heightened activity of lactic acid bacteria due to the addition of starter culture clearly illustrates the inhibitory effect of treatment T2. Our results are significantly better than those reported by several authors, who found fecal coliform contamination in 6–100% of their samples of fermented milk and industrial and artisanal curdled milk [26–29].

All these different results can be explained by the theory that the level of contamination differs according to the level of hygiene, the control of hazards inherent in handling, and the ineffective control of heat treatment.

4.2. Analysis of Sample Contamination by *Escherichia coli* (*E. coli*)

All samples analyzed in this study were contaminat-

ed with *Escherichia coli*, indicating widespread fecal contamination in the milk production chain. *E. coli* is a reliable indicator of fecal contamination, representing 80–90% of fecal coliforms [26]. Their prevalence in raw milk would explain the presence of *Escherichia coli* (1.71 log CFU/mL). *Escherichia* coliforms contaminate milk directly (via the udder) or multiply following inadequate cleaning of utensils [30–33], which would explain the high *E. coli* load. The average *E. coli* loads (1.71 log CFU/mL) obtained in this study are higher than those obtained in Algeria (2.78 log CFU/mL), and also higher than those obtained in Benin (0.6 log CFU/mL) [22,34]. However, these values are lower than those found in the Niamey dairy basin and those obtained in Senegal (6.04 log/g) [22,35]. The difference in results with these authors is explained by the fact that their mixed milk samples were larger than ours.

Treatment T1 resulted in a reduction of this flora (1.25 log CFU/mL), likely due to competition between indigenous lactic acid bacteria and enterobacteria. However, this reduction was not significant in terms of inhibiting pathogenic flora. This could be explained by insufficient acidification during spontaneous fermentation, as these bacteria are not acidophilic, with the exception of *E. coli O157:H7*, which can withstand an acidic environment and survive for up to approximately 4 weeks [36]. Without pH data, it is difficult to draw any conclusions.

Treatment T2, which combines filtration, heating, cooling, and directed inoculation, resulted in the lowest mean *E. coli* load (0.46 log CFU/mL), with a statistically significant difference compared to the control. This notable decrease confirms the observations of several authors regarding the effectiveness of heating in significantly reducing fecal flora [37,38]. The persistence of this flora even after heating the milk indicates exogenous contamination following this treatment. Indeed, curdled milk is often sold on the outskirts of streets or inside the market. Flies and dust settle on the utensils used for selling curdled milk [39]. Also, the rinsing water for these sales utensils (funnels, ladles, etc.) is hardly ever changed by the curdled milk vendors. All these unsanitary practices could be the cause of the excessive contamination of the artisanal curdled milk. A similar result was found in Senegal in samples of commercial curdled milk [29]. In contrast, samples of artisanal curdled milk in Niger were free of *E. coli* contamination [27].

4.3. Analysis of Sample Contamination by Sulfite-Reducing Anaerobic Bacteria (SRC)

The results of the microbiological analysis showed that only one sample of raw milk was contaminated with SRC. This low presence of SRC in the raw milk can be explained either by low contamination of the milk by clostridia or by the presence of nisin secreted by lactic acid streptococci, whose bactericidal and sporicidal properties could well have destroyed these bacteria.

Recalling the telluric origin of SRC and considering that it is sometimes found in the intestines of humans and animals, it is easy to imagine that the single contaminated sample could have come into contact with dust, or conversely, could have entered the milk via the milker after washing hands with contaminated water, or through the numerous splashes from cows that could have contaminated the milk with their excrement. A lower level of quality than ours was found in another study conducted in Niger using samples collected under the same conditions [40].

All three types of treatment proved effective in inhibiting these microorganisms. This complete absence of SRC bacteria in fermented products is highly significant from a health perspective. It suggests that fermentation, even spontaneous, creates acidic conditions hostile to the growth of these bacteria. This hypothesis is supported by other authors, who report that the low SRC levels in their Leben samples could be due to the inhibitory activity of lactic acid bacteria [21]. Similarly, this result is consistent with that reported in a study conducted in Niger on samples of traditional curdled milk [27].

The particularly protective effect of the T2 treatment could also be attributed to the drastic elimination of competing flora after heating, promoting the rapid establishment of beneficial lactic acid bacteria.

Samples of traditional curdled milk "Tarmamoun Adar" and those of industrial yogurt in some studies in Niger were also completely free of SRC [27,35].

4.4. Analysis of Sample Contamination by *Staphylococcus aureus* (S. aureus)

Staphylococcus aureus contamination was moderate (2.11 log CFU/mL), which often reflects human, environmental, or animal-borne contamination. *Staphylococcus*

aureus is a bacterium found on the mucous membranes and skin of most warm-blooded animals, including humans. It is sometimes implicated as a causative agent of mastitis in dairy herds [21]. Higher values of staphylococcal contamination have been reported in the Niamey dairy basin, such as 3.9 log CFU/mL and 81.82 log CFU/mL [35,40]. In the sub-region, an average of 1.94 log CFU/mL was in Senegal, and 2.94 log CFU/mL in Algeria and 0.59 log CFU/mL in Fez, Morocco [21,22,24]. Staphylococci can also originate from poor transport conditions related to failure to maintain the cold chain [41], but more generally, humans are the main source of contamination [5].

After fermentation, the *Staphylococcus aureus* load increased with treatment T1 (2.11 log CFU/mL versus 1.86 log CFU/mL). This same phenomenon has been observed in several studies, notably one that reports the frequent presence of Staphylococci in traditional products fermented spontaneously without controlled inoculation, such as Doi from India and Kindirmou from Niger and the Fanir of Benin [25,42,43]. This can be explained by the fact that the cow's udder can harbor these microorganisms [44].

With the T3 treatment, the change in bacterial load was moderate, although highly significant from a hygiene and sanitation standpoint (1.76 log CFU/mL). This demonstrates that filtration plays a role in reducing contaminating flora, but that fermentation plays a crucial role in maintaining this effect.

Furthermore, the natural fermentation of raw milk without pasteurization leads to significant variability in bacterial communities, and some pathogens can persist [42]. This would explain the persistence of *Staphylococcus aureus* in treatments T1 and T2.

To support this hypothesis, it should be noted that the growth of microorganisms in fermented milk is exponential and depends on the initial load. The acidification of milk, under the action of lactic acid bacteria, would provide protection against contaminating microorganisms [25]. However, in the case of spontaneous fermentation, we do not know the microorganisms involved in the lactose degradation process, given that, in addition to lactic acid bacteria, numerous yeast communities and other opportunistic or even pathogenic microorganisms can be found in various quantities in fermented milk. These results demonstrate the drawbacks of spontaneous fermentation, which, instead of guaranteeing product safety, contributes to the proliferation of unwanted microorganisms. This finding is supported by several studies that highlight the importance of controlled fermentation to control pathogenic flora in traditional dairy products [42,45].

Another possible explanation for T1 and T2 results could be the resistance of staphylococci to acidic pH levels. Studies have shown that *Staphylococcus aureus* can survive and develop in Iben (Moroccan fermented milk) and that its growth and toxin production can be initiated at pH levels as low as 4.00 and as high as 9.33 [46,47].

Their persistence in the T2 treatment may have several reasons: either there was a prior accumulation of thermostable toxins in sufficient quantity, and then heating would have been limited in its effectiveness in destroying them; or the method of cooling to room temperature, being slow, favored their proliferation; or they showed antibiotic resistance [48–50] to the activity of lactic acid bacteria.

These facts are among others that could justify the presence of staphylococci in T2 treatment.

These results are in agreement with those of several studies that have detected significant amounts of Staphylococci in their samples of artisanal curdled milk [27,51].

4.5. *Salmonella* Contamination of Samples

Salmonella was found in 58.06% of the T0 samples, further demonstrating the lack of hygiene during production. On one farm, the main sources of *Salmonella* are the excrement of sick animals or asymptomatic carriers. *Salmonella* spreads from farm to farm through water, solid food, or excrement. When equipment rests on the ground during milking, the milk can be contaminated with *Salmonella*, especially since even the water used for washing could also be contaminated [52]. This prevalence of *Salmonella* in our study is consistent with that reported in another study conducted in Niger, which found an average *Salmonella* load of 10.91 log CFU/mL, whereas the average loads in one study conducted in Senegal were low, or even zero [24,40].

The rates of presence were reduced with all three treatments: 41.93% each for treatments T1 and T3 and 45.16% for treatment T2, which confirms the high sensitivity of these germs to low pH (4.6–4.8) [53]. Although this reduction is notable, none of the treatments allowed for a

total elimination of *Salmonella*; the persistence of *E. coli,* which is a reliable bioindicator of *Salmonella* [51], helps to understand the presence of these germs in the three types of fermented milk.

The more pronounced presence of *Salmonella* in the T2 treatment is explained by the sourdough starter used, which could well have been a potential source of contamination due to the numerous handling steps during the manufacturing process [54] or during sales, as with *E. coli*. Both of these bacteria are exogenous contaminants.

Our results for the second treatment are corroborated by those of other authors, who found that 20.91% of their fermented milk samples were contaminated with *Salmonella* [45]. In contrast, several other authors did not detect any presence of these bacteria in their samples of artisanal and industrial curdled milk [24,26,35].

Treatments T1 and T3 resulted in a partial reduction of some germs thanks to the activity of lactic acid bacteria. However, only treatment T2 led to a significant decrease, or even the elimination, of the majority of pathogenic bacteria, thanks to the combination of heating and fermentation recirculation. The optimization of treatment T2 thus represents a promising technological foundation for processing local milk in the Niamey region, potentially promoting the production of safer fermented milk with improved shelf life, while also contributing to the structuring, professionalization, and sustainable development of the local dairy sector.

5. Conclusions

This study, conducted on raw milk collected in the Niamey region, aimed to evaluate the impact of various technological treatments (spontaneous fermentation, fermentation with inoculum, and filro-fermentation) on its hygienic quality. The microbiological analyses revealed that the raw material (T0) exhibits significant contamination, particularly by fecal coliforms and staphylococci, confirming the necessity of processing before consumption.

The results clearly demonstrate the effectiveness of the tested treatments. Fermentation, whether spontaneous (T1) or combined with heating and inoculation (T2), as well as filro-fermentation (T3), significantly reduced the fecal coliform load. However, treatment T2 (heating followed by fermentation with the addition of an inoculum) stood out as the most effective. It not only almost completely eliminated fecal coliforms but was also the only treatment to significantly reduce the load of *Escherichia coli*, a major indicator of recent fecal contamination.

In contrast, none of the treatments showed significant efficacy against more resistant flora, such as staphylococci or sulfite-reducing anaerobic bacteria, nor against the prevalence of *Salmonella*. This persistence highlights the limitations of the tested processes and indicates that controlling hygienic quality must also involve rigorous preventive measures during production (milking hygiene, rapid cooling).

In conclusion, controlled fermentation, inspired by traditional practices but optimized by gentle heating and the addition of an inoculum, appears to be a promising and accessible method to significantly improve the food safety of local milk. It could constitute an effective strategy for small-scale producers and mini-dairies, allowing them to enhance the value of their production while offering consumers a safer product. Further studies are now needed to evaluate the sensory acceptability of the final products, validate the effectiveness of this treatment on a larger scale, and explore solutions to target the more resistant pathogenic microorganisms identified in this study.

Author Contributions

Protocol development, H.S.K.; Sample collection and laboratory analysis, H.S.K., I.D., M.M.A.M., M.H.G., A.M.M., A.M.K., A.A.B. and A.S.G.; Data analysis, H.S.K.; Manuscript writing, H.S.K.; Review and validation, H.S.K., I.D., M.M.A.M., M.H.G., A.M.M., A.M.K., A.A.B. and A.S.G. All authors have read and approved the final version of the manuscript.

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Data Availability Statement

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Conflicts of Interest

The authors have no conflict of interest.

AI Use Statement

The authors declare that no artificial intelligence (AI) tools were used in the preparation of this manuscript.

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