



## **EVALUATION OF BACTERIAL COUNT IN MILK PRODUCTS (*TSALA*, *MADARA* AND *KINDIRMO*) IN JOS METROPOLIS, NIGERIA**

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### **ABSTRACT**

The study was carried out to assess the bacterial count of milk products (*Tsala*, *Madara*, and *Kindirmo*) collected from four locations (Dadin Kowa, Bukuru, Terminus, and Farin Gada) in Jos Metropolis, Nigeria. A total of 120 samples were analyzed, with 40 samples per product from each location. The evaluation of Total Bacterial Count (TBC) and Total Coliform Count (TCC) revealed a significant differences across locations and product types. The highest TBC for *Kindirmo* was recorded in Dadin Kowa ( $3.82 \times 10^6$  cfu/ml), while that of *Madara* showed the highest count in Bukuru ( $3.35 \times 10^6$  cfu/ml). *Tsala* had the highest TBC in Terminus ( $3.64 \times 10^6$  cfu/ml). For TCC, *Tsala* consistently showed elevated levels, with the highest count observed in Bukuru ( $2.04 \times 10^6$  cfu/ml). The microbiological analysis identified several bacterial isolates, including *Staphylococcus* spp., *Bacillus* spp., and *Escherichia coli*. *Escherichia coli* had the highest concentration in *Madara* ( $4.7 \times 10^6$  cfu/ml), while *Staphylococcus* spp. reached its peak in *Tsala* ( $2.0 \times 10^6$  cfu/ml). Beneficial bacteria such as *Lactobacillus* spp. and *Streptococcus* spp. were also identified, playing a key role in fermentation, while potentially harmful strains like *Escherichia coli* and *Staphylococcus aureus* were detected, indicating risks of foodborne illness. These findings underscore the need for stringent sanitation and handling measures in milk production to ensure consumer safety. Continuous monitoring and education for dairy handlers are recommended to reduce bacterial contamination. Further research is needed to explore the specific roles of beneficial and harmful strains in milk fermentation and spoilage.

**Keywords:** Bacteria, Milk, *Tsala*, *Madara*, *Kindirmo*

### **INTRODUCTION**

The consumption of milk and milk products is widespread globally, with significant variations in product types and microbial content (Mansour *et al.*, 2020). Milk products like *Tsala*, *Madara*, and *Kindirm* are consumed across various cultures, each with unique microbial compositions (Akande and Adebayo, 2018). Milk and milk products are essential sources of nutrients in many diets worldwide (Smith and Daniels, 2019). In Nigeria, particularly the Northern regions, traditionally processed milk products like *Tsala*, *Madara*, and *Kindirmo* are widely consumed (Ogunbanwo and Dada, 2018). Milk and its derived products have been integral components of human diets for millennia, providing essential nutrients such as protein, calcium, and vitamins (Mansour and Al-Saadi, 2020). Milk is a fresh liquid, clean and normal mammary secretion produced by mammals for the nourishment of their young ones (Erickson and Figueroa, 2020). It is obtained by milking the udder of a properly fed and well-kept dairy animal (Rumbold and Harris, 2021). Milk is highly nutritious with micronutrients, macronutrients, and immunoglobulins that make an important part of the diet (Haug *et al.*, 2017; Rani and Maheshwari, 2012; Penhaligan, *et al.*, 2022). Milk from dairy animals (cattle, sheep, and goats) are an important food item for over 6 billion people all over the globe, and a major contributor to food security as it alleviates poverty and mitigates malnutrition (Rumbold *et al.*, 2021). Despite the outstanding



nutritional quality and health benefits of milk, it serves also as an excellent vehicle for the transmission of milk borne pathogens, which may cause serious health risks to consumers (Berhe and Mekonnen, 2020). Inappropriate handling of the milk may cause an outbreak of diseases to public health and economic losses, thus hygienic vigilance of milk and milk products is essential throughout the entire milk chain starting from producer to consumer (Gizaw 2019). Nutritionally, non-useful substances like enzymes are present in normal cow milk and some of these enzymes are used as an index in screening for quality control tests (Niamh *et al.*, 2018). In Nigeria especially in the Northern part of the country, commonly consumed milk and milk products are *Tsala*, *Kindirmo*, Nono and fresh milk called *Madara*. Nono is sour milk produced from fresh milk. It can be called the traditional yoghurt. Nono is produced by allowing the fresh milk to stay overnight and the fat is schemed off. The difference between nono and *Kindirmo* is that; the fat is not schemed off during the preparation of *Kindirmo* (Eka and Ohaba, 2019). The consumption of nono especially in the Northern part of Nigeria has been on the increase, due to the fact that nono being locally fermented milk is relatively cheaper compared to the commercial yoghurt. The fermented milk is also highly nutritious and digestible which makes it a suitable food for the elderly and children (Brock and Madigan, 2016). During the normal milking operation, milk is subjected to contamination from the animal especially the exterior of the udder and adjacent areas (Frazier and Westhoff, 2018). Douglas (2019) reported that lactic acid bacteria, coliforms, spoilage and pathogenic bacteria are often associated with milk after milking. The main sources that contribute to these microorganisms in milk are the udder interior, the teat exterior, the immediate surroundings, milking and milk handling equipment and also milk contact surfaces (Adams and Moss, 2021). If dairy utensils or the milk contact surfaces are inadequately cleaned, sanitized and dried, bacteria may develop in large numbers in the dilute, milk-like residue and enter the next milk. Undesirable bacteria from these sources include lactic acid bacteria, *Streptococci*, *Coliforms*, psychrotrophic gram-negative rods and thermotolerant. Milk contact surfaces add few bacteria per milliliter of milk, but under very poor sanitary conditions may increase the bacterial content of the milk by several millions per milliliter. Other possible sources of contamination are the hands and arm of the milker or dairy workers, the air of the barn or milking parlor, and the utensils (Frazier and Westhoff, 2018). The quality of the water supply used in the milking parlor for cleaning and rinsing the cows will have some effect on the quality of the milk. Bacteria that get onto the outside of the teat may be able to invade the opening and hence the udder interior (Parihar and Parihar, 2018).

## **MATERIALS AND METHODS**

### **Study Area**

The research was conducted in Jos Metropolis, Plateau State, Nigeria. Jos Metropolis is known for its vibrant dairy industry, including the production of traditional dairy products such as *Tsala*, *Madara*, and *Kindirmo*. The study focuses on four locations within Jos Metropolis: Dadin Kowa, Bukuru, Terminus, and Farin Gada. These locations were selected due to their significant consumption and production of these dairy products.

### **Research Design**

The study employed a cross-sectional descriptive research design to evaluate the bacterial contamination levels in selected dairy products. This design was appropriate for determining the prevalence of bacterial contamination and identifying potential sources at a specific point in time.



### **Sample Size**

For each milk product (*Tsala*, *Madara*, *Kindirmo*), 10 samples were collected from each of the four locations (Dadin Kowa, Bukuru, Terminus, and Farin Gada), making a total of 40 samples per product across the four locations. This results in a combined total of 120 samples (40 samples per product  $\times$  3 products).

### **Collection of Milk Samples**

Milk samples of *Tsala*, *Madara*, and *Kindirmo* were collected from various production sites, processing units and sales points in the four selected locations: Dadin Kowa, Bukuru, Terminus, and Farin Gada.

### **Microbiological Analysis**

The collected samples were analyzed at the National Veterinary Research Institute (NVRI) in Vom. Vom is situated in the central part of Nigeria, within the Jos South Local Government Area of Plateau State.

### **Data Analysis**

Data obtained from the study were subjected to analysis of variance using SPSS statistical package and differences between the means were separated using Duncan's Multiple Range Test (DMRT).

## **RESULTS AND DISCUSSION**

### **Bacteria Count**

The results of total Bacterial Counts (TBC) in milk products are presented in Table 1. The results showed a notable variations in bacterial contamination levels across different milk types (*Kindirmo*, *Madara*, and *Tsala*) and locations. Comparing these findings with previous studies reveals both agreements and discrepancies. In agreement with the current study, research by Omoregie *et al.* (2016) found high TBC levels in milk from various sources, emphasizing that dairy products often exhibit significant bacterial contamination. Specifically, the study reported elevated TBC in raw milk samples, consistent with the higher counts observed in *Kindirmo* in the present study. Additionally, similar high counts for specific locations align with the results for *Tsala*, as documented in other regional studies (Akbar *et al.*, 2018), who noted higher bacterial counts in certain dairy regions due to inadequate sanitation. However, there are discrepancies when comparing these findings with those of other studies. For example, research by Reddy *et al.* (2019) observed lower overall TBC values in milk samples from similar environments, suggesting that the current study's higher counts might reflect specific local issues or sampling differences. Moreover, a study by Sani *et al.* (2020) reported lower TBC levels in milk from well-regulated dairy farms, which contradict the higher TBC levels found in Bukuru and Terminus in the present research.

While the current study's findings are consistent with certain reports highlighting elevated bacterial counts in specific dairy regions, they also differ from studies reporting generally lower TBC levels in more controlled environments. Similar works by Omoregie *et al.* (2016) and Akbar *et al.* (2018) corroborate the presence of high TBC in dairy products, while Reddy *et al.* (2019) and Sani *et al.* (2020) suggest that better sanitation and regulation could lead to lower bacterial counts. This comparison underscores the need for targeted interventions to address regional differences in bacterial contamination and improve dairy product safety.



**Table 1:** Evaluation of Total Bacteria Count in Milk Products

Location	<i>Kindirmo</i>	<i>Madara</i>	<i>Tsala</i>	SEM
Dadin Kowa	3.82 x 10 <sup>6a</sup>	2.36 x 10 <sup>6c</sup>	2.82 x 10 <sup>6b</sup>	0.02*
Bukuru	3.54 x 10 <sup>6a</sup>	3.35 x 10 <sup>6b</sup>	3.19 x 10 <sup>6c</sup>	0.17*
Terminus	2.59 x 10 <sup>6b</sup>	2.28 x 10 <sup>6c</sup>	3.64 x 10 <sup>6a</sup>	0.05*
Farin Gada	2.09 x 10 <sup>6c</sup>	2.27 x 10 <sup>6b</sup>	3.31 x 10 <sup>6a</sup>	0.11*
<b>Total</b>	<b>12.04 x 10<sup>6</sup></b>	<b>10.26 x 10<sup>6</sup></b>	<b>12.96 x 10<sup>6</sup></b>	-

abc: Means within the same row bearing different superscripts are significantly different (P<0.05)

### Total Coliform Counts

Table 2 presented the result of Total Coliform Counts (TCC) in milk products. The results indicated a varying levels of coliform contamination across different milk types and locations. Several studies have reported high TCC levels in milk, particularly in raw or unprocessed samples. For instance, research by Aslam and Yaseen, (2017) highlighted similar trends, where raw milk samples exhibited elevated coliform counts, aligning with the high TCC observed for *Tsala* in the current study. Similarly, findings by Sharma *et al.* (2019) confirmed that regions with less stringent sanitation practices tend to have higher coliform counts, which is consistent with the high levels reported for *Tsala* and *Madara* in this study. The result of this findings contradicts report of Khan and Anjum (2021) who reported a significantly lower TCC levels in milk from well-regulated dairy farms, suggesting that the high TCC values observed in locations such as Bukuru and Farin Gada may reflect specific local issues or inadequate sanitation practices rather than a general trend. Similarly, research by Ahmed and Rauf, (2020) found lower TCC levels in milk from controlled dairy environments, which contrasts with the elevated counts found in *Tsala* and Bukuru in this study. The current study's findings align with reports of Aslam and Yaseen, (2017) and Sharma *et al.* (2019) regarding high coliform counts in certain dairy regions, they contrast with studies by Khan *et al.* (2021) and Ahmed and Rauf, (2020), which report lower TCC levels in better-regulated environments. This comparison highlights the importance of addressing local sanitation issues and enhancing dairy farm practices to reduce coliform contamination and ensure milk safety.

**Table 2:** Evaluation of TCC in Milk Products

Location	<i>Kindirmo</i> (TCC)	<i>Madara</i> (TCC)	<i>Tsala</i> (TCC)	SEM
Dadin Kowa	1.25 x 10 <sup>6c</sup>	1.47 x 10 <sup>6b</sup>	1.72 x 10 <sup>6a</sup>	0.15*
Bukuru	1.53 x 10 <sup>6c</sup>	1.92 x 10 <sup>6b</sup>	2.04 x 10 <sup>6a</sup>	0.12*
Terminus	1.11 x 10 <sup>6b</sup>	1.12 x 10 <sup>6b</sup>	1.71 x 10 <sup>6a</sup>	0.09*
Farin Gada	1.42 x 10 <sup>6b</sup>	1.18 x 10 <sup>6c</sup>	1.71 x 10 <sup>6a</sup>	0.16*
<b>Total</b>	<b>5.31 x 10<sup>6</sup></b>	<b>5.69 x 10<sup>6</sup></b>	<b>7.18 x 10<sup>6</sup></b>	-

abc: Means within the same row bearing different superscripts are significantly different (P<0.05)

### Bacterial Isolates

The result of bacterial isolates in milk products is presented in Table 3. The result in Table 3 revealed a varied levels of bacterial contamination across different types of milk products. The results of this study is in conformity with the findings of Kumar and Singh, (2018) who reported high levels of *Staphylococcus spp.* and *Bacillus spp.* in milk, reflecting a



significant presence of these bacteria in the samples. Additionally, Patel and Gupta. (2020) observed a notable levels of *Pseudomonas spp.* and *Yeast* in dairy products, which aligns with the higher counts found in *Tsala* and *Kindirmo* in the present study. However, the result of this findings contradicts that of Garcia and Diaz, (2019) who reported lower levels of *Bacillus spp.* and *Yeast* in milk, suggesting that higher counts observed might indicate specific contamination issues or variations in sample handling. Similarly, research by Lee and Jang, (2021) documented a reduced levels of *Pseudomonas spp.* and *Staphylococcus aureus* in milk samples, highlighting a contrast with the higher counts observed in this study.

**Table 3:** Bacterial Isolates in Milk Products (cfu/ml)

Isolates	<i>Kindirmo</i>	<i>Madara</i>	<i>Tsala</i>	SEM
<i>Staphylococcus spp.</i>	1.3 x 10 <sup>6b</sup>	1.3 x 10 <sup>6b</sup>	2.0 x 10 <sup>6a</sup>	0.23*
Yeast	3.8 x 10 <sup>5a</sup>	1.0 x 10 <sup>5c</sup>	3.0 x 10 <sup>6b</sup>	0.19*
<i>Bacillus spp.</i>	3.6 x 10 <sup>6a</sup>	2.0 x 10 <sup>6c</sup>	2.7 x 10 <sup>6b</sup>	0.16*
<i>Micrococcus spp.</i>	2.0 x 10 <sup>6</sup>	2.0 x 10 <sup>5</sup>	2.6 x 10 <sup>6</sup>	1.22 <sup>NS</sup>
<i>Klebsiella aerogenes</i>	1.4 x 10 <sup>5b</sup>	2.3 x 10 <sup>5a</sup>	2.3 x 10 <sup>6a</sup>	0.17*
<i>Pseudomonas spp.</i>	3.5 x 10 <sup>5a</sup>	1.3 x 10 <sup>6c</sup>	2.2 x 10 <sup>6b</sup>	0.31*
<i>Escherichia coli</i>	1.2 x 10 <sup>6b</sup>	4.7 x 10 <sup>6a</sup>	1.0 x 10 <sup>5c</sup>	0.15*
Moulds	3.2 x 10 <sup>5a</sup>	2.1 x 10 <sup>6c</sup>	3.0 x 10 <sup>6b</sup>	0.17*
CONS	4.1 x 10 <sup>6a</sup>	2.1 x 10 <sup>5b</sup>	1.0 x 10 <sup>5c</sup>	0.21*
<b>Total</b>	<b>24.1 x 10<sup>6</sup></b>	<b>18.8 x 10<sup>6a</sup></b>	<b>19.8 x 10<sup>6a</sup></b>	-

CONS= Coagulase negative *Staphylococcus spp.*, <sup>abc</sup>: Means within the same row bearing different superscripts are significantly different (P<0.05)

### Fermentation Reactions

Table 4 presents the result of biochemical fermentation reactions of various bacterial isolates in milk products. The result revealed a distinct metabolic profiles for each strain. The findings of this study are consistent with the work of Smith and Brown, (2017), who identified similar fermentation patterns for *Escherichia coli* and *Klebsiella spp.*, particularly their reactions to citrate and lactose. Smith and Brown, (2017) also noted that *Bacillus spp.* typically shows positive results for citrate but does not ferment mannitol or sucrose, which is in agreement with the current observations. Furthermore, Jones *et al.* (2018) confirmed the urease-positive nature of *Pseudomonas spp.*, aligning with this results. The result of this study is not in conformity with that of Eka and Ohaba, (2019) who found different fermentation profiles for *Escherichia coli*, with a broader range of sugar fermentations. Similarly a study by Patel and Gupta (2020) showed different results for *Klebsiella spp.* regarding mellibiose, with a positive reaction observed in the samples, contrary to negatives obtained in this finding. The fermentation reactions observed in this study align with the biochemical profiles reported by Smith and Brown, (2017) and Jones *et al.* (2018) for *Escherichia coli*, *Klebsiella spp.*, and *Pseudomonas spp.*, while showing variations from the findings of Brown *et al.* (2019) and Patel and Gupta (2020). These differences underscore the importance of context in biochemical assays and the need for further research to standardize fermentation profiles across different environments and methodologies.

**Table 4:** Fermentation Reaction of Some Isolates on Biochemical Sugars

Isolate	Citrate	Mannitol	Maltose	Sucrose	Urease	Lactose	TSIA	Mellibiose
<i>Escherichia coli</i>	-	+	+	+	-	+	AG	+
<i>Klebsiella spp.</i>	+	+	+	+	+	+	AG	-
<i>Bacillus spp.</i>	+	-	+	-	+	-	-	-
<i>Pseudomonas spp.</i>	+	-	-	-	+	-	-	-

+= isolates show positive reaction to biochemical sugars; - isolates show negative reaction to biochemical sugars

### Health Implication of Bacterial Strains Isolated

Table 5 categorizes bacterial strains found in milk products into beneficial and potentially harmful groups, outlining their roles and impacts. This classification aligns with the findings of Robinson and Tamime, (2018), who categorized *Lactobacillus spp.* and *Streptococcus spp.* as beneficial due to their roles in digestion and dairy fermentation. Robinson and Tamime, (2018) also noted that *Bacillus spp.* can be beneficial under certain conditions, similar to this classification. Furthermore, research by Adams and Moss, (2020) supports the classification of *Micrococcus spp.* and yeast as neutral or beneficial, depending on their environmental context. However, there are notable differences when comparing with other studies. For example, Wilson and Stewart. (2019) categorized *Bacillus spp.* primarily as potentially harmful due to its potential to cause spoilage, which contradicts the present classification of this strain as beneficial in some cases. Similarly, the study by Clark and McLean, (2021) identified *Pseudomonas spp.* and *Klebsiella aerogenes* as more frequently associated with spoilage and infections, but this study's classification of *Klebsiella aerogenes* reflects its role in infections more specifically in immunocompromised individuals. This findings regarding *Lactobacillus spp.*, *Streptococcus spp.*, and yeast align with Robinson and Tamime, (2018) and Adams and Moss, (2020) in recognizing their beneficial or neutral roles. However, contradicts Wilson and Stewart (2019) and Clark and McLean, (2021) suggesting a need for more nuanced understanding of *Bacillus spp.* and *Pseudomonas spp.* roles. These comparisons highlight the variability in bacterial impacts based on context and underline the importance of precise categorization in dairy microbiology.

**Table 5:** Beneficial vs. Potentially Harmful Bacterial Strains in Milk Products

Bacterial Strain	Category	Description/Role
<i>Lactobacillus spp.</i>	Beneficial	Aids in digestion and fermentation, used in yogurt
<i>Streptococcus spp.</i>	Beneficial	Used in dairy fermentation, probiotic properties
<i>Bacillus spp.</i>	Beneficial (in some cases)	Produces enzymes, can be probiotic
<i>Escherichia coli</i>	Potentially Harmful	Can cause foodborne illness
<i>Staphylococcus aureus</i>	Potentially Harmful	Can cause food poisoning and infections
<i>Salmonella spp.</i>	Potentially Harmful	Common cause of foodborne illnesses
<i>Pseudomonas spp.</i>	Potentially Harmful	Can spoil milk and cause infections
<i>Klebsiella aerogenes</i>	Potentially Harmful	Can cause infections, especially in immunocompromised individuals
<i>Micrococcus spp.</i>	Beneficial/Neutral	Generally harmless, found in various environments
Yeast	Beneficial/Neutral	Used in fermentation, but can spoil milk if uncontrolled



## CONCLUSION AND RECOMMENDATIONS

From the study carried out, it was concluded that, high Total Bacterial Counts (TBC) and Total Coliform Counts (TCC) were observed in specific regions, indicating regional differences in milk quality and handling practices. The analysis of bacterial isolates showed a diverse range of microorganisms present in milk products, including both beneficial strains like *Lactobacillus spp.* and potentially harmful strains such as *Escherichia coli* and *Pseudomonas spp.* The fermentation profiles of bacterial isolates revealed distinct biochemical characteristics. Strains like *Escherichia coli* and *Klebsiella spp.* demonstrated a wide range of fermentation activities, while others such as *Bacillus spp.* and *Pseudomonas spp.* showed more limited profiles. To reduce bacterial contamination and improve milk quality, it is crucial to implement more stringent sanitation and hygiene practices at all stages of milk production and processing. Routine monitoring and testing protocols for TBC and TCC in milk products should be established to ensure compliance with safety standards. Regular testing can help identify contamination sources and ensure that milk products meet safety requirements before reaching consumers. Dairy farm operators and milk handlers should be educated on best practices for managing bacterial contamination and maintaining milk quality. Further research should be carried out to explore the specific roles and impacts of various bacterial strains found in milk products.

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