# Assessment of the microbiological quality of beef marketed in commune I of Bamako district


## ABSTRACT

**Aims:**
To assess the microbiological quality of beef marketed in commune I of Bamako district to determine its level of contamination and identify the main pathogens present. This study is based on the hypothesis that the microbiological quality of meat sold in the markets studied is influenced by storage conditions, hygiene practices and the infrastructure of the points of sale. Therefore, a thorough assessment of these factors could identify the main sources of microbiological contamination and propose practical solutions to improve the quality and safety of meat products.

**Study design**
A descriptive and analytical study was conducted between [from July to November 2023]. It involved meat samples collected from different points of sale in commune I.

**Methodology:**

Beef samples were collected randomly from markets, butcher shops and street stalls. Microbiological analyses were performed according to standardized protocols to enumerate total mesophilic flora, total coliforms, fecal coliforms, as well as to detect specific pathogens such as *Salmonella* spp., Escherichia coli and *Staphylococcus aureus*.

**Results:**
The results showed high microbiological contamination in [65,68%] of the samples analyzed, exceeding the thresholds set by food safety standards. Total and faecal coliforms were present in [23,35%]. Pathogens such as *Escherichia coli*, *Salmonella* spp., and *Staphylococcus aureus* were isolated in [26,39%]. Contamination rates were higher in informal outlets compared to licensed butchers.

**Conclusion:**
Beef marketed in Commune I has a worrying microbiological quality, constituting a potential risk to public health. There is an urgent need to strengthen hygiene measures throughout the production and sales chain, as well as to increase awareness of food safety among stakeholders.



*Keywords: Microbiological quality, Fresh meat, Bovine, Market*


***Introduction***

Mali has the largest cattle herd in West Africa, with an estimated national population of 12,111,128 heads (Teno, 2022; FAO, 2013). This potential place the country as the second largest livestock-producing nation in ECOWAS (Economic Community of West African States), after Nigeria, and first in UEMOA (West African Economic and Monetary Union)

(Gning, 2021). Livestock farming plays a major role in the Malian economy, accounting for 30% of the primary sector's contribution to Gross Domestic Product (GDP) and 9% of national GDP (Samaké et al., 2008).
In Bamako, the capital of Mali, two large refrigerated slaughterhouses and seven other regional slaughterhouses serve the city and its surroundings with a total annual production capacity of around 12,000 tons (Samaké et al., 2008; Santara et al., 2019). Beef, particularly in its fresh and unprocessed form, is an essential component of the local diet due to its richness in proteins and essential amino acids such as lysine and histidine. It plays a key role in human development, both physically and cognitively (Oumokhtar et al., 1998).
However, meat is also a favorable substrate for microbial proliferation due to its nutrient composition(Phillips et al., 2001). Failures to comply with good hygiene practices at different stages of the supply chain (slaughter, transport, storage, and marketing) constitute a potential source of contamination and food poisoning. These gaps may result from poor operator training, inadequate hand washing, the use of non-sterile equipment, or the conditions in which meat is displayed on shelves (Boubaker Fattoum, 2021).

Contamination of meat by pathogenic microorganisms is a major issue for public health and the quality of food products. Indeed, these microorganisms can cause serious illnesses in consumers while degrading the organoleptic properties of meat. In addition to pathogens, some spoilage microorganisms, although harmless to health, compromise the quality of products through visible changes, such as a repulsive appearance or unpleasant odors. These spoilage phenomena are well documented in recent literature (Ellies-Oury, 2016; Bellés et al., 2017; Hamaidia, 2019; Toldrá and Reig, 2021).

This study aims to assess the microbiological quality of meat by analyzing the presence of different microbial groups, including total mesophilic aerobic flora (TMAF), total and fecal coliforms, *Escherichia coli*, *Salmonella/Shigella*, *Staphylococcus aureus*, as well as yeasts and molds. These microorganisms were chosen for their relevance as indicators of the quality and safety of meat products. The standards chosen for this study are based on international standards, including the Codex Alimentarius and the recommendations of the World Health Organization (WHO), in order to ensure comparison with global data.

## II. MATERIAL AND METHODS

### 2.1. Materials

#### 2.1.1 Sampling Sites

This study was conducted in three different markets located in Commune 1 on the Right Bank. These markets, designated as Market 1 (M1), Market 2 (M2) and Market 3 (M3), were selected to represent beef sales areas within the commune.

The "MARKETS" mentioned in this study correspond to different types of outlets, including traditional markets, supermarkets and street stalls. Each site has distinct characteristics in terms of storage conditions, hygiene and temperature control. These factors directly influence the microbial load of the products and were taken into account during sample collection.

#### 2.1.2 Meat Sample Collection

Samples were collected in the morning, around 8 am, after post-mortem inspection of bovine carcasses. Thirty (30) samples were collected per market according to ISO 17604 (2003), for a total of ninety (90) samples collected randomly. Samples were collected three times a week over a period of four months.
Each sample was packaged in sterile bags and hermetically sealed, then labeled with information regarding the sample code, date, time and place of collection. The bags were transported in a cooler to the laboratory and stored at 4 °C before analysis.

## 2.2 Methods

### 2.2.1 Preparation of stock suspensions and decimal dilutions

Twenty-five grams (25 g) of each sample were homogenized in 225 mL of sterile physiological water to obtain a stock suspension. Decimal dilutions were then performed: 1 mL of the stock suspension was added to 9 mL of physiological water to obtain a $10^{-1}$ dilution, then repeated to achieve dilutions up to $10^{-}$□.

### 2.2.2 Inoculation and counting of germs

#### 2.2.2.1 Total mesophilic aerobic flora (FMAT) (Standard NF EN ISO 4833-1:2013)

For the analysis of total mesophilic aerobic flora (TMAF), Plate Count Agar culture medium was used, as recommended by ISO 4833-1:2013 standards. This precision is essential to ensure the reproducibility of the results.Briefly, one milliliter (1 mL) of each dilution was inoculated in masse in Petri dishes containing an appropriate agar medium. The dishes were incubated at 37 ± 1 °C for 72 ± 3 hours. The colonies developed were counted and expressed in colony-forming units per gram (CFU/g), retaining only the dishes containing between 30 and 300 colonies.

#### 2.2.2.2 Total and faecal coliforms (NF V08-050:2009 Standard)

The samples were inoculated on Deoxycholate Agar and incubated at 37 °C for total coliforms (24 h) and at 44 °C for faecal coliforms (48 h). The red colonies observed were counted and expressed in CFU/g

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#### 2.2.2.3 *Staphylococcus aureus* (NF EN ISO 6888-2:1999 Standard)

The samples were inoculated on Chapman agar and incubated at 37 °C for 48 hours. The bright yellow colonies were counted and expressed in CFU/g.

#### 2.2.2.3 *Salmonella* sp. (Standard NF EN ISO 6579/A1:2012)

The Salmonella search included four steps:

**1. Pre-enrichment:** 25 g of meat in 225 mL of buffered peptone water, incubated at 37 °C for 8 to 24 hours.

**2. Enrichment:** 0.1 mL of pre-enrichment in 10 mL of Rappaport-Vassiliadis broth, incubated at 42 °C for 18 to 24 hours.

**3. Isolation**: Inoculation on Hektoen agar, incubated at 37 °C for 24 hours. Blue-green colonies with or without black center were presumed positive.

**4. Identification:** Biochemical test with TSI medium. After incubation incubated at +36.0 °C ± 1.0 °C, for 24 hours; Table 1 was used to identify Salmonella.

**Tableau 1.** Lecture des tests sur gélose triple sucre-fer (TSI)

| | Lactose | Glucose | Saccharose | $H_2S$ | Gaz |
|---|---|---|---|---|---|
| ***S.Typhi*** | - | + | + | + | - |
| ***S.ParatyphiA*** | - | + | + | - | + |
| **Other *Salmonella*** | - | + | + | + | + |

#### 2.2.2.4 *Escherichia coli* (AFNOR SDP 07/1-07/93 method)

The samples were inoculated on TBX agar, incubated at 44 °C for 48 hours. The characteristic colonies of E. coli were counted directly in CFU/g.

#### 2.2.2.5 Yeasts and molds (NF ISO 21527-2:2008 standard)

The samples were inoculated on Sabouraud Dextrose Agar and incubated at 37 °C for 48 hours. The colonies were counted and expressed in CFU/g.

#### Data analysis

The results were expressed in CFU/g and compared to international microbiological criteria in accordance with Regulation 2073/2005/EC. Data were analyzed using Excel pivot tables to calculate means, standard deviations, and covariances of the studied parameters.

## 3. RESULTS

### 3.1 Total Mesophilic Aerobic Flora (TMAF), Total and Fecal Coliforms, *Escherichia coli*, Salmonella/Shigella, *Staphylococcus aureus,* and Yeasts and Molds in Marketed Beef

Meats from the markets studied were highly contaminated by microbial pathogens, with significant variability between markets (Table 2). However, with the exception of coliforms, contamination did not vary significantly between repeat samples collected from each market.

**Table 2.** Analysis of variance for Total Aerobic Mesophilic Flora (FAMT), total and fecal coliforms, *Escherichia coli*, *Salmonella/Shigella*, *Staphylococcus aureus*, yeasts and molds in commercial beef

| Sources of variation | Pathogenic microorganisms | | | | | | |
|---|---|---|---|---|---|---|---|
| | DF | FAMT | *E. coli* | CF | CT | Staph | Moisissures |
| Markets | 2 | 1213,58*** | 156,59*** | 28,69** | 6353419*** | 648,26*** | 35979.1*** |
| Repetitions | 2 | 1,12NS | 1,02NS | 1,03NS | 33,14** | 1,35NS | 1,32NS |

****. ***,** significant at p<0.01 and p<0.001 respectively, NS: not significant, DOF; degree of freedom.

Fisher's test shows that meat from market 3 is the most contaminated by total coliforms, fecal coliforms and molds. On the other hand, meat from market 2 has higher concentrations of FMAT, *Escherichia coli* and *Staphylococcus aureus*. Market 1 is distinguished by a particularly high contamination by fecal coliforms (Table 3).

**Table 3.** Comparison of the means of Total Aerobic Mesophilic Flora (FMAT), total and fecal coliforms, *Escherichia coli*, *Salmonella/Shigella*, *Staphylococcus aureus*, as well as yeasts and molds in beef marketed in the market

| **Markets** | **FMAT** | ***E. coli*** | **Fecal coliforms** | **Total coliforms** | **Staph** | **Yeasts and moulds** |
|---|---|---|---|---|---|---|
| **Market 1** | 10982.53b | 10285b | 8134.3a | 14939.3c | 5342.33b | 14939.3c |

| | | | | | | |
|---|---|---|---|---|---|---|
| **Market 2** | 8841.33a | 18847a | 6045.0b | 15668.0b | 9644a | 15668b |
| **Market 3** | 11218.67c | 7919c | 8734.0a | 18771.3a | 5010c | 18771.3a |

Apart from total coliforms, contamination by other microorganisms is not influenced by the repetition of sampling (Table 4). Contaminants appear to depend mainly on the specific conditions of each market (sources of supply, transport and hygiene at sale).

**Table 4.** Comparison of the means of total mesophilic aerobic flora (TMAF), total and faecal coliforms, *Escherichia coli*, *Salmonella/Shigella*, *Staphylococcus aureus*, as well as yeasts and moulds in beef marketed by repetitions

| Repetitions | FMAT | *E. coli* | Fecal coliforms | Total coliforms | Staph | Yeasts and moulds |
|---|---|---|---|---|---|---|
| **R1** | 10301.67a | 11814.3a | 7328.3a | 12147b | 16508.3a | 6647.67a |
| **R2** | 10371.93a | 12619.0a | 7791.3a | 12159.33a | 16515.0a | 6671.33a |
| **R3** | 10368.93a | 12617.7a | 7793.7a | 12162.67a | 16355.3a | 6677.33a |

**3.2 Microbiological quality of meat marketed in the markets studied**

The average microbial contents show that except for FMAT and faecal coliforms, the microbial loads of *Escherichia coli*, total coliforms, staphylococci and yeasts/moulds are higher than the standards (Table 5).

**Table 5.** Microbiological quality of meat marketed in the markets studied

| Microorganismes recherchés et quantifies (UFC/g) | | | | | | |
|---|---|---|---|---|---|---|
| **Markets** | **FMAT ($x10^4$)** | **E. coli ($x10^3$)** | **Fecal coliforms ($x10^4$)** | **Total Coliforms ($x10^4$)** | **Staph ($x10^3$)** | **Yeasts and moulds ($x10^3$)** |
| **Market 1** | 1.10 | 10.30 | 0.81 | 1.50 | 5.3 | 14.9 |
| **Market 2** | 0.88 | 18.90 | 0.61 | 1.57 | 9.6 | 15.7 |
| **Market 3** | 1.12 | 7.90 | 0.87 | 1.88 | 5.0 | 18.8 |
| **AFNOR Norms** | $5.10^6$ UFC/g | $10^3$ UFC/g | $10^4$ UFC/g | $10^4$ UFC/g | $10^3$ UFC/g | $10^3$ UFC/g |



## DISCUSSION

### Microbiological contamination

Of the 90 samples analyzed (30 per market), FMAT concentrations were below the standards of 5×10□ CFU/g, reflecting a good general state of preservation. These results are in agreement with those of Boukhenfar et al. (2019) and Hamaidia and Rouachdia (2019), who reported similar microbial loads on meats sampled in Algeria.

The presence of total and fecal coliforms, although fecal coliforms were below the standard, indicates improvable hygiene conditions. Djabou and Rafai (2021) also reported similar levels, although compliant with AFNOR/CODINORM and FCD (2015) standards.

Il faut élargir la section discussion pour inclure des implications plus larges, telles que l'impact socio-économique de la mauvaise qualité microbiologique de la viande et des suggestions pour des recherches futures.

**Major pathogens**

*Escherichia coli* concentrations were above the standards in all markets, with a peak at M2 (18500 CFU/g). The high concentrations of microorganisms observed in some samples can be directly attributed to the precarious conditions of the collection sites. For example, street stalls exposed to high ambient temperatures and poor hygiene promote microbial proliferation. These observations corroborate the work of Sofos and Geornaras (2010), who showed the impact of storage conditions on the quality of meat products.
These results differ from those reported by Boukhenfar et al. (2019), who found compliant loads under similar conditions.

For *Staphylococcus aureus*, our results corroborate the observations of Chadli and Farricha (2017) on meat products in Morocco, highlighting the risks associated with improper handling of meat.

The presence of *Staphylococcus aureus* and *Escherichia coli* in significantly high concentrations in the samples analyzed represents a major health risk. S. aureus is known to produce enterotoxic toxins responsible for acute food poisoning, while some strains of E. coli produce shiga toxins that can cause serious complications, such as hemolytic uremic syndrome (WHO, 2022). These results highlight the need to improve hygiene practices throughout the production and distribution chain to minimize these risks.

**Fungal contamination**

Yeast and mold load largely exceed standards in all markets. These results are consistent with those of Boudjehem and Mazouni (2014), who reported high loads in similar products.

**Presence of *Salmonella* spp.**

The overall compliance with *Salmonella* spp. (92%) is satisfactory, but the 8% of non-compliant samples require increased monitoring. These results are consistent with those of Boukhenfar et al. (2019), who reported similar proportions.

**Socio-economic impact of meat contamination**

The impact of poor microbiological quality of meat goes well beyond health considerations. On the socio-economic level, foodborne infections caused by contaminated meat result in significant costs for health systems, reduce workforce productivity, and affect consumer confidence in food supply chains (Toldrá& Reig, 2021). Economic losses are amplified by the need to recall contaminated products, manage complaints and litigation, and rehabilitate affected markets (Barro et al., 2021).

Furthermore, in developing countries where health control infrastructures are often limited, increased exposure to pathogens in meat products compromises food safety and increases social inequalities (World Health Organization, 2022). The most vulnerable communities, often dependent on traditional markets, bear the brunt of these impacts.

**Suggestion for future research**

Looking ahead, further research is needed to: (i) develop affordable technologies for rapid detection and prevention of microbiological contamination in meat (Daube et al., 2020), (ii)

study the effectiveness of good hygiene practices and educational interventions among value chain actors, including producers, transporters and sellers (Toldrá& Reig, 2021), and assess the interactions between waste management, food safety and public health to better understand the drivers of pathogen spread (Barro et al., 2021).

These research avenues, combined with international collaboration and local capacity building, could significantly improve the quality of meat products and reduce negative health, economic and social consequences.

## CONCLUSION

This study highlights the importance of controlling storage conditions and hygiene practices in different types of outlets to reduce microbial contamination of meat. The results obtained, supported by standardized methods, reinforce the need to establish strict regulatory measures and to raise awareness among food industry stakeholders about the health risks associated with S. aureus and E. coli. Increased collaboration between health agencies and producers will help ensure better quality and safety of meat products intended for consumers.

## DISCLAIMER

The authors hereby declare that no generative AI technologies such as large language models (ChatGPT, COPILOT, etc.) and text-to-image generators were used in the writing or editing of this manuscript.



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