





Microbiological Profile and Health Risks of Artisanally Processed Animal Products in the State of Mato Grosso


Perfil Microbiológico e Risco Sanitário de Produtos de Origem Animal Processados Artesanalmente no Estado de Mato Grosso

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Abstract

This study assessed the prevalence of pathogenic microorganisms in artisanal foods products of animal origin in Mato Grosso between 2019 and 2024 and identified potential public health risks. We conducted a retrospective review of analyses performed at the Laboratory of Molecular Food Microbiology (LABMMA) of the Faculty of Nutrition at the Federal University of Mato Grosso. We analyzed quantitative counts of *Escherichia coli*; coagulase-positive *Staphylococcus* spp. and *Staphylococcus* enterotoxins; *Bacillus cereus*; sulfite-reducing clostridia; molds and yeasts; *Enterobacteriaceae*; and *Listeria monocytogenes* and conducted qualitative detection of *Salmonella* spp. Records for 145 samples - dairy products, meat products, fish, honey, lard, and animal meal - were reviewed. Thirty-three samples (22.4%) failed because they contained at least one microorganism exceeding the limits established by Normative Instruction 161/2022 of the National Health Surveillance Agency – (ANVISA – Brazil). Notably, two fish samples were positive for *Salmonella* spp., and *Escherichia coli* was detected in fish (07), meat (06), and dairy products (11), with median *E. coli* counts of 10^4 CFU/g in fish and 10^2 CFU/g in meat and dairy products. High counts of coagulase-positive *Staphylococcus* spp., were also observed, with median populations of 10^4 in dairy products and 10^5 CFU/gram in fish. These findings underscore the need for targeted measures to mitigate these pathogens in artisanal foods produced in Mato Grosso, thereby improving product safety and protecting public health.

Keywords: Food Safety. Artisanal Foods. *Salmonella* spp. *Staphylococcus* spp. *Escherichia coli*.

Resumo

Este estudo avaliou a prevalência de microrganismos patogênicos em produtos alimentícios artesanais de origem animal do Mato Grosso entre 2019 e 2024, identificando potenciais riscos à saúde pública. Foi realizada uma pesquisa retrospectiva das análises realizadas no Laboratório de Microbiologia Molecular de Alimentos (LABMMA) da Faculdade de Nutrição da Universidade Federal de Mato Grosso. Foram analisados dados de determinações quantitativas de *Escherichia coli*, *Staphylococcus* spp. coagulase positiva e suas enterotoxinas, *Bacillus cereus*, clostrídios redutores de sulfito, bolores e leveduras, *Enterobacteriaceae* e *Listeria monocytogenes*, bem como a determinação qualitativa de *Salmonella* spp. Registros de 145 amostras de laticínios, produtos cárneos, peixes, mel, banha e farinhas animais foram analisados. 33 (22,4%) das amostras falharam por conter pelo menos um microrganismo fora dos limites indicados na Instrução Normativa 161/2022 da Agência Nacional de Vigilância Sanitária - Brasil. Vale destacar a falha de duas amostras de peixes com a presença de *Salmonella* spp., bem como *Escherichia coli* presente em peixes (07), carnes (06) e laticínios (11), com contagens medianas de *E. coli* de 10^4 UFC/grama em peixes e 10^2 UFC/grama em carnes e laticínios. Além de contagens elevadas de *Staphylococcus* spp. coagulase positiva com populações de 10^4 e 10^5 UFC/grama observadas em laticínios e peixes, respectivamente. Os resultados revelam a necessidade de ações para mitigar a presença desses importantes patógenos em alimentos artesanais produzidos em Mato Grosso, garantindo sua segurança e, conseqüentemente, preservando a saúde pública local em termos de nutrição adequada.

Palavras-chave: Segurança Alimentar. Alimentos Artesanais. *Salmonella* spp. *Staphylococcus* spp. *Escherichia coli*.

1 Introduction

Several microorganisms can be transmitted through food and affect human health (Abebe; Gugsá; Ahmed, 2020). Bacteria are the main causative agents of foodborne toxoinfections, whether due to the presence of vegetative cells or toxins produced by these microorganisms (Abebe; Gugsá; Ahmed, 2020). The World Health Organization (WHO) reports that among foodborne diseases, 32 are caused by 31 agents, including 11 diarrheal disease agents (1 virus, 7 bacteria, 3 protozoa), 7 agents of invasive infectious diseases (1 virus, 5 bacteria, 1 protozoan), 10 helminths, and 3 chemical products (WHO, 2015).

Since bacteria are the main group of microorganisms responsible for foodborne diseases, the World Health Organization (WHO) lists those considered a priority for monitoring, classifying them as diarrheal disease agents (*Campylobacter* spp., *Escherichia coli* [enteropathogenic *E. coli*, enterotoxigenic *E. coli*, and Shiga toxin-producing *E. coli*], non-typhoidal *Salmonella*, *Shigella* spp., and *Vibrio cholerae*), agents of invasive infections (*Brucella* sp., *Listeria monocytogenes*, *Mycobacterium bovis*, *Salmonella Paratyphi*, and *Salmonella Typhi*), as well as *Bacillus cereus*, *Clostridium botulinum*, *Clostridium perfringens*, and *Staphylococcus aureus*, which are classified as agents of enteric intoxication (Abebe; Gugsá; Ahmed, 2020; WHO, 2015).

Foodborne diseases can be classified into three types: intoxication (food poisoning caused by toxins produced by pathogens in food), infection (ingestion of food contaminated with pathogens), and toxoinfection (toxin production by microorganisms that grow in the human intestine) (Abebe; Gugsá; Ahmed, 2020; WHO, 2015).

Monitoring these microorganisms is essential; therefore, regulatory government agencies and

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the food industry use groups, genera, and species of bacteria as indicator organisms of the quality and/or hygienic status of food, water, and the environment (Tortorello, 2003). Microbiological indicators can be those applied to food safety or quality indicators (Tortorello, 2003). Among safety indicators, *Escherichia coli* and *Salmonella Enteritidis* stand out; among common quality indicators are aerobic plate counts, coliforms, *Escherichia coli*, *Enterobacteriaceae*, *Listeria* spp., enterococci, *Staphylococcus* spp., lactic acid bacteria, and spore-forming bacteria (Silva *et al.*, 2024 ; Tortorello, 2003).

Microbiological analyses of foods are conducted to verify microbiological criteria, which may be established to assess both the quality and safety of foods (ICMSF, 2015). In this context, standards are part of international, national, and regional laws and regulations; specifications are agreements between buyers and sellers of a product, forming the basis for trade; and guidelines are internal criteria established by processors, trade associations, or, at times, by governmental bodies (ICMSF, 2015).

In Brazil, the quality of food products of both plant and animal origin marketed in raw or processed form is regulated by the Normative Instruction No. 161 of Anvisa/Ministry of Health (Brazil, 2022). This normative instruction establishes the requirement for the absence of staphylococcal enterotoxin, *Salmonella* spp., *Listeria monocytogenes*, and *Cronobacter* spp.; and the maximum acceptable count limits for potential toxin producers such as coagulase-positive *Staphylococcus* spp., sulfite-reducing clostridial spores, *Clostridium perfringens*, and *Bacillus cereus*. Indicators of fecal contamination include enterococci, *Escherichia coli*, and *Enterobacteriaceae*; and spoilage or hygiene indicators include *Pseudomonas aeruginosa*, total coliforms, mesophilic aerobic bacteria, molds, and yeasts (Brazil, 2022).

Numerous publications report the occurrence of foodborne disease outbreaks in Brazil. In a retrospective study of Foodborne Disease Surveillance data, Daeger *et al.* (2019) observed that over 11 years (2007–2017), 7,630 outbreaks were recorded, involving 134,046 individuals, of whom 19,394 were hospitalized and 127 died. There is disagreement in the literature regarding the number of FBD cases in Mato Grosso. Daeger *et al.* (2019) reported 614 cases with no deaths between 2007 and 2017, whereas Santana and Duarte (2022) reported 977 cases with two deaths between 2005 and 2017.

Additionally, another retrospective study covering a longer period (2000–2018) found that among the foods implicated in FBD outbreaks in Brazil, in descending order, were unidentified foods, followed by water, mixed foods, eggs and egg products, red meat, among others (Finger *et al.*, 2019). The most frequently incriminated bacteria were *Salmonella* spp., *Escherichia coli*, *Staphylococcus aureus*, *Bacillus cereus*, *Clostridium perfringens*, and *Shigella sonnei* (Finger *et al.*, 2019; Daeger *et al.*, 2019).

Data from microbiological analyses conducted by a food testing laboratory in the municipality

of Concórdia, Santa Catarina, based on one year of registry books, showed 856 samples analyzed: 643 meat and meat products, 170 milk and dairy products, and 43 eggs. Among the 139 positive samples, occurrences of *Salmonella* spp., coagulase-positive *Staphylococcus*, sulfite-reducing clostridia, and thermotolerant coliforms were observed (Rossi; Bampi, 2015).

According to Lima *et al.* (2023) the ‘main purpose of the microbiological analysis of a food is to obtain information about the hygienic conditions during its production, processing, storage, and distribution for consumption, about its shelf life, and about the risk it poses to health.

Therefore, the aim of this study was to describe the prevalence of pathogenic microorganisms in food products of animal origin in Mato Grosso through the analysis of retrospective data from artisanal food samples sent to the Laboratory of Microbiological and Molecular Analysis of the School of Nutrition at Universidade Federal do Mato Grosso, Brazil (UFMT), between 2019 and 2024.

2 Material and Methods

The present study was conducted by evaluating the reports of 145 samples of animal-derived products from different regions of the State of Mato Grosso, which were submitted to the Laboratory of Molecular Microbiological Analysis of Foods, Faculty of Nutrition, Universidade Federal do Mato Grosso, between 2019 and 2024, with the exception of the year 2021 due to the Coronavirus pandemic.

These samples were analyzed through activities related to the extension project of the Faculty of Nutrition, titled Food Analysis Service of the Center-West Region – CENTROLAB. The products were submitted by the manufacturers themselves and included milk and dairy products, meat products from cattle, swine, and fish, honey, and animal-origin flours. Manufacturers refer to their products as artisanal production, most of them registered under Municipal Inspection Services. The types of requests observed were self-monitoring and compulsory analyses.

The analyses were performed using methodological protocols from the International Organization for Standardization (ISO): ISO 6579:2002 for the detection of *Salmonella* spp., ISO 6888-1 for the enumeration of coagulase-positive staphylococci, ISO 7251 for the enumeration of *Escherichia coli*, ISO 7932 for the enumeration of *Bacillus cereus*, ISO 21527-1 and ISO 6611 for the enumeration of molds and yeasts, ISO 21528-2 for the enumeration of *Enterobacteriaceae*, and APHA 9:2015 for the most probable number of thermotolerant coliforms at 45°C.

The results obtained were evaluated according to Normative Instruction No. 161, issued on July 1, 2022, by the Brazilian Health Regulatory Agency (ANVISA), Ministry of Health, which provides in its Annex I the Microbiological Standards for Food, except for commercially sterile products (Brazil, 2022).

The data evaluated herein comprised information contained in the registry books of the samples analyzed by the Laboratory of Molecular Microbiology of Foods. Access to the data used in this assessment was granted with the authorization of the laboratory coordination and the CENTROLAB extension project.

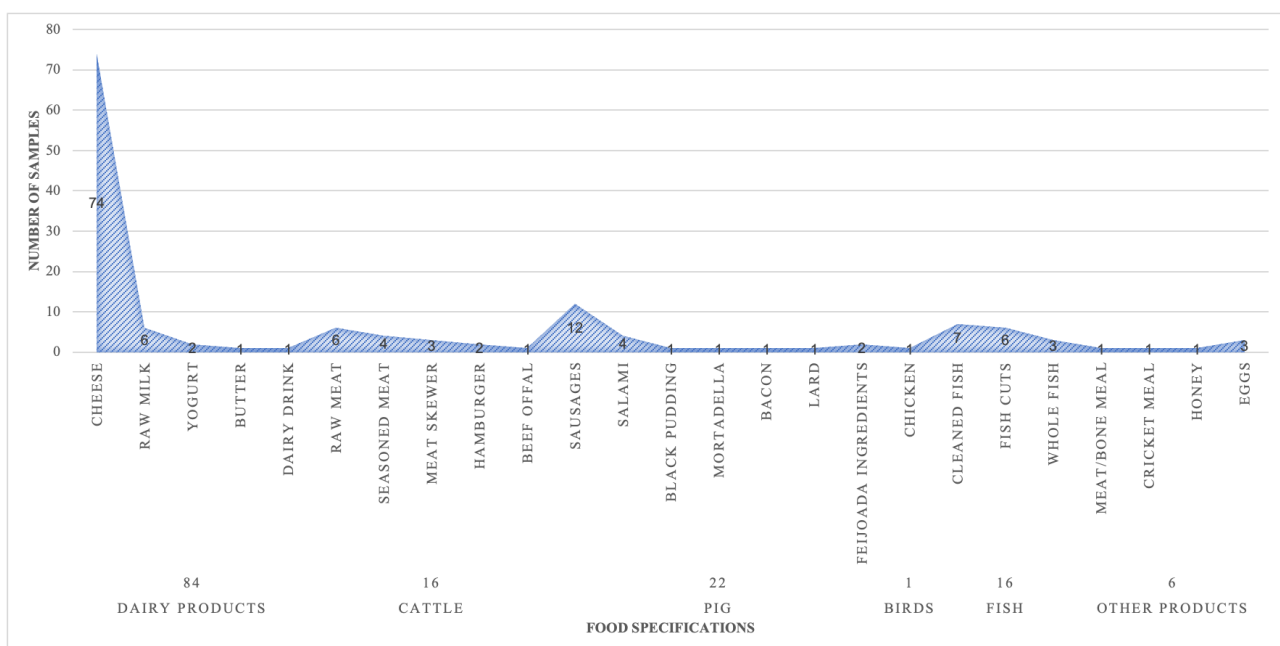
3 Results and Discussion

Between 2019 and 2024, except for 2021 due to the suspension of activities caused by the Coronavirus pandemic, 145 samples of animal-derived products were received for quality control analysis at the Laboratory of Molecular Microbiological Analysis of Foods, Faculty of Nutrition, Universidade Federal do Mato Grosso (UFMT).

When examining the number of samples and their quantitative distribution, it is evident that they were spread across groups of products derived from milk, meat, fish, and various other items such as eggs and honey. The group of foods with the highest demand for analysis consisted of dairy products, with a predominance of cheeses, which accounted for 74 out of the 84 dairy samples (Figure 1).

The other groups of animal-origin foods included products derived from beef, pork, and fish (Figure 1). The second most frequent group was pork-derived products, mainly sausages, a characteristic food widely consumed throughout the state.

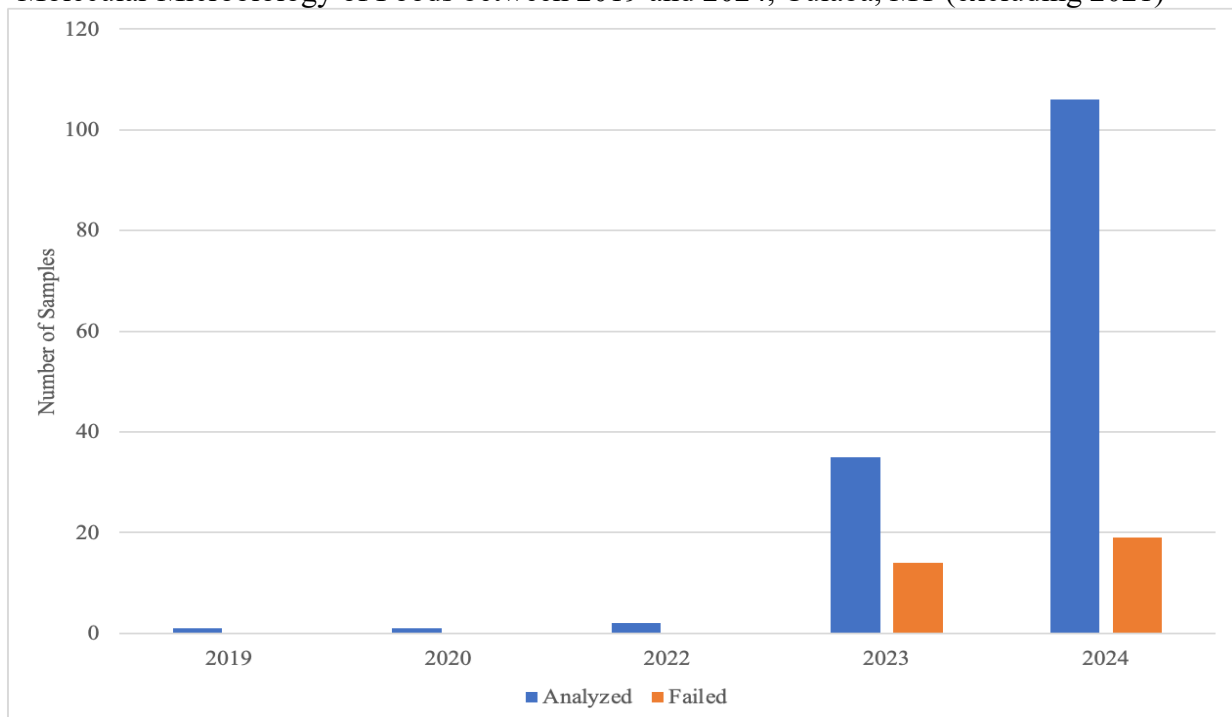
Figure 1 – Distribution of the number of animal-origin food samples, classified by food groups and by the individual designation of each product



Source : research data.

When examining the frequency of food submissions for microbiological analysis, it is observed that 2024 was the year with the highest demand, with 106 samples analyzed, of which 19 failed to meet the limits established by ANVISA (17.92%) (Figure 2). This result contrasts with the year 2023, when 14 of the 35 samples evaluated were outside the legal standards for consumption, representing approximately 40% of the samples submitted that year to LABMMA (Figure 2). No samples were submitted in 2021 due to the peak of the Covid-19 pandemic.

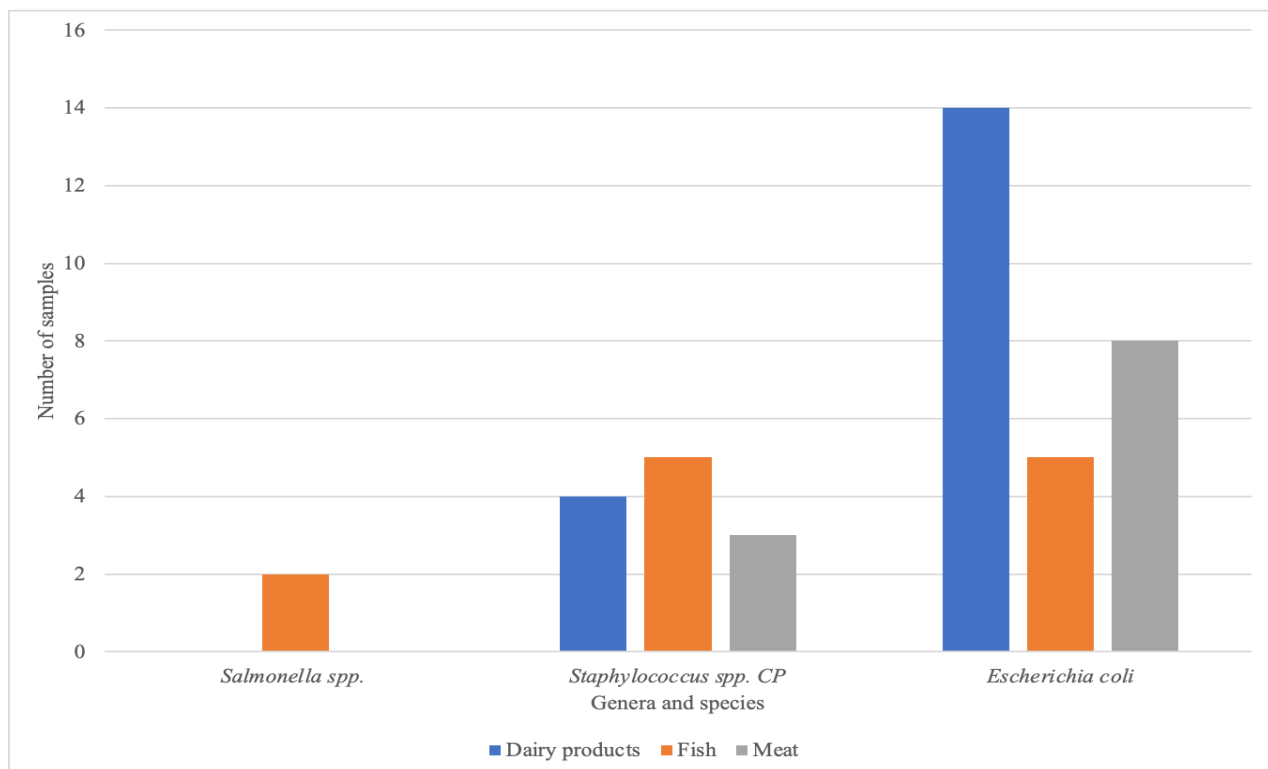
Figure 2 – Distribution of the frequency of food samples submitted to the Laboratory of Molecular Microbiology of Foods between 2019 and 2024, Cuiabá, MT (excluding 2021)



Source : research data.

Among the 33 food samples that failed to meet the standards, those belonging to the dairy, fish, and meat groups were included. Notably, we highlight the samples from the fish group, which showed contamination by *Salmonella* spp., coagulase-positive *Staphylococcus* spp., and *Escherichia coli* (Figure 3), indicating issues related to raw material handling. Additionally, we emphasize the dairy products, mainly due to the alarming levels of *Escherichia coli* detected (Figure 3).

Figure 3 – Frequency and number of samples testing positive for *Salmonella* spp., coagulase-positive *Staphylococcus* spp., and *Escherichia coli* in dairy, fish, and meat products analyzed at LABMMA, Cuiabá, MT, between 2019 and 2024



Source: resrarch data.

Therefore, the foods received by the Laboratory of Molecular Microbiological Analysis of Foods at UFMT belonged to the groups of dairy, meat, fish, and other miscellaneous products, such as eggs and honey, during the period from 2019 to 2024 (excluding 2021). However, among the foods submitted, dairy products predominated, with cheeses representing the majority of the items evaluated. Among the dairy products assessed in this study, cheese showed the highest number of non-compliant samples due to the presence of *Escherichia coli* and coagulase-positive *Staphylococcus*.

In addition, the occurrence of thermotolerant coliforms at 45°C, Enterobacteriaceae, *Escherichia coli*, and Shiga toxin-producing *Escherichia coli* (STEC) has been reported in cheeses in the South, North, Northeast, and Central-West regions of Brazil (Fox; Jiang; Gobius, 2018; Kamimura *et al.*, 2019; Bordini *et al.*, 2020; Paim; Baratto, 2021). *Staphylococcus* spp. and coagulase-positive *Staphylococcus* spp. have also been identified in cheeses from these same regions (Kamimura *et al.*, 2019; Bordini *et al.*, 2020), in addition to *Salmonella* spp. (Fox; Jiang; Gobius, 2018), although *Salmonella* spp. was not found in cheeses and dairy products in the present study.

The occurrence of these microorganisms in cheeses and other dairy products may be linked to

the use of raw milk in their preparation, which is strongly influenced by the microbial ecosystem of raw milk combined with the environmental conditions (personnel and facilities) where production and handling occur (Bonilla-Luque *et al.*, 2023). Additional contamination sources include the cheese production environment, such as equipment, water, coagulants, and cross-contamination between raw materials and finished products (Martínez-Vasallo *et al.*, 2019). A notable concern is the growing niche market of consumers seeking raw milk and raw milk cheeses, motivated by sensory quality and artisanal characteristics largely shaped by the microbial ecosystem of raw milk (Bonilla-Luque *et al.*, 2023). Current legislation allows the production of raw milk cheeses only when they undergo fermentation for at least 60 days before consumption (Kamimura *et al.*, 2019).

For improved sanitary control in dairy production, special attention must also be given to production management systems focused on environmental hygienic–sanitary conditions (Lacorte *et al.*, 2022). In the food production chain, effective implementation of Food Safety Management Systems (FSMS) is essential for producing safe and high-quality foods (Lacorte *et al.*, 2022). Most modern FSMS rely on Good Manufacturing Practices (GMPs) and Standard Sanitation Operating Procedures (SSOPs) as prerequisite programs for the development and implementation of effective HACCP plans and Self-Control Programs recommended by the Brazilian Ministry of Agriculture (Lacorte *et al.*, 2022).

Escherichia coli and coagulase-positive *Staphylococcus* spp. and *Salmonella* spp. were detected in fish samples analyzed at LABMMA, consistent with findings reported by Kyule *et al.* (2022). *Staphylococcus* spp. and *Salmonella* spp. were also observed in yellow hake (*Cynoscion acoupa*) (Machado *et al.*, 2025); *Salmonella* spp. in sururu mussels (*Mytella strigata*) (Silva *et al.*, 2025); and *Salmonella* spp. in fish and fish products in several countries (Sheng; Wang, 2021). As a major public health pathogen, the presence of *Salmonella* spp. is frequently reported in microbiological investigations in aquaculture, even though this bacterial genus is not part of the natural microbiota of fish, and evidence remains insufficient to determine whether fish develop clinical symptoms indicative of infection (Porto *et al.*, 2023). *Escherichia coli* has also been found in fish sold in Menofila, Egypt (Hassanien; El-Gazzar; Abou, 2020).

Staphylococcus aureus found in fish typically originates from the handler's microbiota, and its presence in fish samples can be attributed to contamination from personnel, the environment, or cross-contamination through utensils (Olagbemide; Akharaiyi, 2021). The presence of *E. coli* may also be related to improper evisceration practices during cleaning and processing.

According to Reis *et al.* (2025), several factors contribute to the persistence of *Salmonella* spp.

on fish surfaces after processing. The receiving stage is one of the critical control points in industrial processing, since fish frequently arrive at the facility already externally contaminated—on their scales, and with organic matter such as mud, soil, and mucus. Moreover, proper storage, sanitary quality of ice, and conservation/holding conditions influence the occurrence of spoilage and pathogenic bacteria in fish (Mendes *et al.*, 2024). A recent study reported that extending fish exposure time to NaClO (specifically to 30 minutes) may be a promising strategy for controlling this pathogen in the final product (Nunes *et al.*, 2024).

Red and white meats from mammals, birds, amphibians, aquatic animals, and reptiles have been consumed by humans since ancient times (Ali *et al.*, 2022). In this study, red and white meats showed contamination by *Escherichia coli* and coagulase-positive *Staphylococcus* spp. Similarly, ground beef samples in Minas Gerais showed contamination by thermotolerant coliforms at 45 °C, *Escherichia coli*, and *Salmonella* spp.

Meat is a highly perishable product and must be stored under refrigeration to control microbial growth and spoilage (Mathew; Jaganathan, 2017; Mateus *et al.*, 2018). Meat allows colonization by a wide range of microorganisms, which may originate from post-slaughter contamination from air, water, soil, handlers, and processing equipment (Stellato *et al.*, 2016). From farm to table, meat microbiota is strongly influenced by poor hygiene practices among handlers, who serve as vectors for the dissemination of microorganisms through their hands, wounds, lips, skin, and hair (Siluma *et al.*, 2023).

Food handlers' hands may act as vectors for foodborne pathogens such as *Salmonella* spp., *Campylobacter jejuni*, *Staphylococcus aureus*, and *Escherichia coli*, particularly when proper hand hygiene is not maintained (Oliveira, 2024). *Staphylococcus* spp., *E. coli*, and *Salmonella* spp. have been detected on the hands of butchers in Arba Minch, Ethiopia, increasing the risk of meat contamination (Kanko; Seid; Alemu, 2023).

In the boxplot illustrating microbial counts, coagulase-positive *Staphylococcus* spp. showed a median of 10⁴ CFU/g or mL among dairy foods; however, among fish samples, the median was approximately 10⁵ CFU/g (Figure 4). For *Escherichia coli*, the boxplot shows median counts of 10² CFU/g or mL in meat and dairy samples. In contrast, fish samples exhibited a median of 10⁴ CFU/g for *E. coli* (Figure 4), which is considered undesirable for food.

Figure 4 – Boxplot of colony-forming unit (CFU) counts of *Escherichia coli* and coagulase-positive *Staphylococcus* spp. detected in meat, dairy, and fish products analyzed by LABMMA, Cuiabá, MT



Source: resrarch data.

This survey showed the frequency and percentage of foods whose microbiological analysis results exceeded the maximum acceptable population limits established by the current regulation — Normative Instruction No. 161 of 2022 — for the different food groups (Brazil, 2022). For raw pork and beef, the acceptable limits of *Escherichia coli* are 10^2 and 10^4 CFU/g, respectively; for seasoned pork and beef, the limit is 10^2 CFU/g for *E. coli*, as well as 10^4 CFU/g for *Staphylococcus* spp. coagulase-positive counts as the maximum acceptable population (Brazil, 2022). In sausages, *E. coli* counts ranged from 10 to 10^2 CFU/g for beef and pork sausages, respectively, and the acceptable limit for *Staphylococcus* spp. coagulase-positive is 10^2 CFU/g (Brazil, 2022). In dairy samples, cheeses showed *E. coli* counts ranging from 10 to 10^2 CFU/g, while *Staphylococcus* spp. coagulase-positive was detected at 10^2 CFU/g. In raw fish intended to be cooked before consumption, *E. coli* was allowed up to 50 CFU/g, and *Staphylococcus* spp. coagulase-positive up to 10^2 CFU/g (Brazil, 2022). For all food groups, the regulation establishes the absence of *Salmonella* spp. in 25 grams or milliliters of food (Brazil, 2022).

Thus, the elevated counts detected in the samples are concerning, as the microorganisms observed in this study are also reported in epidemiological studies that describe the main etiological agents of foodborne outbreaks in Brazil. Data from the Ministry of Health at the national level indicate

the ten most frequently detected microorganisms, of which *Salmonella spp.*, *Escherichia coli*, and *Staphylococcus aureus* stand out, based on surveys covering 11 years (2007–2017) (Daeger *et al.*, 2019), 19 years (2000–2018) (Finger *et al.*, 2019), and 7 years (2015–2021) (Oliveira Junior *et al.*, 2023). Reports show an alternation in the main agents responsible for outbreaks in Brazil: from 2000 to 2010, *Salmonella spp.* and *Staphylococcus spp.* were among the leading causes of foodborne outbreaks. From 2011 to 2021, *Escherichia coli* and *Salmonella spp.* were most prominent (Bones *et al.*, 2025; Silva *et al.*, 2025).

There are also studies describing regional situations of Waterborne and Foodborne Disease Outbreaks in Brazil, which report *Staphylococcus spp.* or *S. aureus*, *Salmonella spp.*, and *Escherichia coli* as being implicated in outbreaks in Paraná (Perlin; Perlin; Martins, 2016), Pernambuco, Rio Grande do Norte, Sergipe, Piauí, and Paraíba (Oliveira *et al.*, 2021), São Paulo (Nunes *et al.*, 2017; Faustino *et al.*, 2007), the Federal District (Nunes; Mota; Caldas, 2013), and Rio Grande do Sul (Welker *et al.*, 2010).

Aiming at a global overview, a review of publications on foodborne outbreaks from 2017 to 2021 indexed in the Web of Science concluded that the causative agents most frequently reported were *Salmonella spp.*, *Escherichia coli*, and *Staphylococcus spp.* These were the most frequent pathogens reported in 12 studies conducted in countries such as Germany, Brazil, Canada, China, South Korea, Denmark, and the United States (Prado *et al.*, 2021). This pattern was also observed in the official laboratory report from the city of Santander, Calabria, Spain, which revealed contamination by *Escherichia coli*, *Staphylococcus spp.* coagulase-positive, and *Salmonella spp.* in dairy and meat products (Blanco-Rios; Casadiego-Ardila; Pacheco, 2009).

In the present study, *Escherichia coli* and *Staphylococcus spp.* coagulase-positive were the most frequently detected microorganisms in dairy and meat products. However, in fish, in addition to these microorganisms, *Salmonella spp.* was also detected — the only group in which its presence was observed. Studies investigating foodborne outbreaks have reported positive samples for *Escherichia coli* and *Staphylococcus spp.* coagulase-positive in meat products (Bones *et al.*, 2025; Marques *et al.*, 2022; Prado *et al.*, 2021; Finger *et al.*, 2019; Daeger *et al.*, 2019; Feltes; Ariseto-Bragotto; Block, 2017), dairy products (Bones *et al.*, 2025; Marques *et al.*, 2022; Prado *et al.*, 2021; Feltes; Ariseto-Bragotto; Block, 2017), as well as fish and fish products (Marques *et al.*, 2022; Finger *et al.*, 2019; Feltes; Ariseto-Bragotto; Block, 2017).

This study revealed an alarming prevalence of pathogenic microorganisms in artisanal animal-derived products in the state of Mato Grosso, indicating a real risk to public health. The identification of elevated counts of *Escherichia coli* and *Staphylococcus spp.* coagulase-positive, along with the presence of *Salmonella spp.* in fish samples, underscores the urgent need for interventions in this production chain. It is imperative to implement stricter sanitary control measures and promote

educational actions for producers, in order to reduce contamination and ensure food safety, thus protecting the health of the local population.

Data from the Notifiable Diseases Information System (SINAN) show that bacterial agents are the main causative agents of Waterborne and Foodborne Diseases (DTHA) (Silva *et al.*, 2025). Therefore, monitoring and controlling bacterial contamination is a major challenge for food safety (Alves *et al.*, 2021). In this context, Brandão *et al.* (2022) state: “In the field of food microbiology, research in sanitary surveillance plays an important role in generating data and other technical-scientific outputs essential for risk analyses, which may support the creation and/or modification of regulations in the field or lead to more immediate and effective control and inspection actions.”

When making food choices, consumers are influenced by several factors, including health, taste, and price, and these decisions may reflect congruent or incongruent behaviors depending on the individual (Manfroi, 2024). Therefore, this socioeconomic behavior requires the implementation of actions and regulations aimed at ensuring food safety for the population and protecting public health by preventing foodborne diseases, as well as ensuring the quality of foods reaching the final consumer (Xavier *et al.*, 2025).

4 Conclusion

It is concluded that the main pathogenic contaminants found in artisanal meat, dairy, and fish products in the state of Mato Grosso are *Escherichia coli*, coagulase-positive *Staphylococcus spp.*, and *Salmonella spp.*

The results clearly indicate the need for improved hygiene and sanitary practices to mitigate the presence of these pathogens, which would lead to essential sanitary advances across the different stages of processing.

These findings may contribute to the development of local public policies aimed at strengthening the artisanal animal-based food production chain.

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