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Evaluation of Microbial Contamination and Diversity in Raw Goat Meat from Selected Abattoirs in Awka, Nigeria

Ugochukwu Chukwuma Okafor*, Ikechukwu Martins Nwobu, Chidiebele Lawrence Ozuah

Department of Applied Microbiology and Brewing, Faculty of Biosciences, Nnamdi Azikiwe University, Awka, Nigeria

*Correspondence: uc.okafor@unizik.edu.ng

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ABSTRACT: The present investigation aimed to quantify and characterize the microbial diversity and contamination load in raw goat meat procured from abattoirs within the Awka Metropolis, with a focus on hygiene indicator microorganisms and pathogenic entities. Raw meat samples were systematically collected from five predefined anatomical regions—liver, muscle, top site, belly, and genitals—on five randomly selected carcasses from multiple abattoirs. The samples were cultured using an array of selective media, leading to the identification and enumeration of thirteen fungal isolates and sixteen bacterial isolates. The isolates were subsequently purified and identified to the species level through comprehensive macroscopic, microscopic, and biochemical analyses. The microbial contamination load was then compared against local and international regulatory benchmarks. All measured contamination levels were found to be within permissible thresholds, with most microbial loads reflecting the prevailing sanitary and environmental conditions within the Awka Metropolis. The study revealed the presence of pathogenic bacterial species with the following frequencies: *Escherichia coli* (100%), *Klebsiella* spp. (60%), *Salmonella* spp. (60%), and *Staphylococcus aureus* (100%). Among fungal contaminants, *Candida albicans* (80%), *Aspergillus niger* (80%), and *Fusarium* spp. (60%) were predominant. The microorganisms identified were primarily opportunistic pathogens but posed significant risks to public health, particularly to individuals with pre-existing conditions or compromised immune systems. These findings underscore the urgent need for enhanced sanitary protocols not only within abattoirs but also in the management of water sources and overall hygiene infrastructure throughout Awka, in order to mitigate microbial transmission risks and safeguard public health.

KEYWORDS: Microbial contamination**;** pathogenic bacteria; raw goat meat; fungal isolates; sanitary protocols

1. Introduction

The consumption of raw or undercooked meat has been a longstanding practice across many cultures, often serving as a key source of protein and vital nutrients. However, this dietary

practice carries the risk of exposure to foodborne pathogenic microorganisms. Goat meat, also known as caprine meat, is considered a popular delicacy due to its unique flavor profile, relatively low fat content, and rich nutrient composition. The widespread consumption of goat meat in developing countries raises notable concerns, particularly in local abattoirs where meat is handled in less controlled environments. Inadequate implementation of sanitary measures during slaughtering and meat processing often leads to substantial microbial contamination, with serious public health implications [1, 2].

Abattoirs represent critical points for microbial contamination as they serve as central nodes in the meat production chain and provide a highly favorable environment for various microorganisms, including both normal flora and opportunistic pathogens. The nature and prevalence of these microorganisms are directly linked to slaughtering processes, environmental conditions, and hygienic practices [3]. Poor carcass handling techniques, improper cleaning of slaughter equipment, and suboptimal storage conditions are among the numerous factors that contribute to the microbial contamination of meat [4, 5]. Adequate sanitation practices in abattoirs are therefore essential, as inadequate sanitation can lead to the introduction and proliferation of pathogenic microorganisms such as Escherichia coli, Salmonella spp., Staphylococcus aureus, and various fungal species that pose significant health risks to consumers [6, 7].

Escherichia coli is widely recognized as an indicator organism in meat, commonly used to signify fecal contamination, which often results from poor handling during slaughter or improper storage [8, 9]. Salmonella species are known to be a leading cause of gastrointestinal illnesses, while Staphylococcus aureus, which may lead to foodborne toxicosis, is frequently detected in contaminated meat samples [10, 11, 12]. Fungal pathogens such as *Candida albicans*, *Aspergillus niger*, and *Fusarium spp.* also pose a serious threat, primarily due to their potential to produce mycotoxins, which are hazardous to public health, particularly among immunocompromised individuals [13, 14, 15].

Awka Metropolis, located in the capital city of Anambra State in southeastern Nigeria, presents a valuable case study for evaluating microbial contamination in raw goat meat. This region exhibits a wide variation in agricultural practices and food safety standards across different abattoirs. Due to cultural and dietary preferences, the demand for goat meat in the region is considerably high. However, the sanitary conditions of local abattoirs in Awka have not been extensively studied, resulting in limited information about the extent and severity of microbial contamination in goat meat consumed locally. In light of this knowledge gap, there are growing concerns that the actual public health risks associated with raw goat meat in this area may be underestimated.

This study aimed to examine the microbial diversity, hygiene indicator microorganisms, and pathogens present in raw goat meat sourced from multiple abattoirs within Awka Metropolis. Specifically, it sought to identify bacterial and fungal contaminants across five distinct anatomical parts of randomly selected carcasses and to evaluate the contamination levels against both local and international food safety standards. The study also considered the sanitary and environmental factors influencing contamination levels, focusing on hygienic practices, water sources, slaughtering techniques, and operating conditions in the abattoirs. The findings provide further insight into the microbial dynamics within this environment and support the development of optimal strategies to enhance the safety of raw goat meat and protect public health in Awka Metropolis.

Given the increasing global incidence of foodborne diseases, it is becoming imperative to prioritize the safety of meat and related products, particularly those sourced from slaughterhouses in developing nations. Doing so helps protect consumers and reduce the risk of zoonotic disease transmission [16, 17]. Amid the growing discourse on food safety in Africa and in Nigeria in particular, this study aims to provide valuable data to inform policy decisions related to abattoir sanitation, meat inspection protocols, and initiatives to reduce foodborne illnesses. The data, methodologies, and findings presented here contribute to the expanding body of literature on raw goat meat contamination in Africa and highlight the urgent need for comprehensive intervention strategies to improve meat safety in Awka and similar urban centers across the country and the continent.

2. Materials and Methods

2.1.Study area.

The study was conducted in Awka, the capital city of Anambra State, southeastern Nigeria, located at geographic coordinates 6.2220°N and 7.0821°E. The research involved two distinct abattoirs within the Awka metropolis. These sites were selected based on their representation of local slaughter practices and their commonly used methods for processing goat meat. The study primarily aimed to analyze microbial contamination and community composition at these sites in relation to prevailing sanitary conditions. Notably, abattoir workers were observed discharging goat excreta into the surrounding environment, and in many cases, engaging in open defecation within the premises.

2.2.Sample collection.

Five anatomical regions of goat carcasses were selected for sampling. Goat meat samples were obtained from two abattoirs in Awka and labeled as follows: A – Liver; B – Muscles; C – Top leg (loin); D – Belly; and E – Genitals. These sites were chosen to provide a broad representation of microbial contamination across various tissue types. The anatomical parts were carefully shredded to expose internal tissue and enable thorough assessment of contamination. Raw meat samples were collected in sterile bags, which were immediately labeled for accurate identification. The samples were then transported to the laboratory for microbiological and biochemical analyses.

Figure1. Sampled abbattoirs in Awka Metropolis.

2.3.Isolation, characterization, and identification of bacterial and fungal isolates.

Microbial assessment was carried out using methods described by [18]. These standard protocols facilitated the isolation of bacterial and fungal pathogens, enabling a robust analysis

of the microbial contamination profile. Enumeration and characterization of heterotrophic bacteria, coliforms, and potential fungal pathogens were conducted. Total heterotrophic and coliform bacteria were enumerated following the method described by [19]. To determine the bacteriological count, a 10^{-1} dilution containing 1 g of each meat sample was prepared in 9 mL of sterile saline solution, followed by inoculation on Nutrient Agar. The plates were incubated for 24–48 hours at 37°C. After incubation, bacterial colonies were classified and quantified based on morphological characteristics.

2.4.Biochemical identification of the isolates.

A series of biochemical tests, as described by [18] and [20], were used to identify and classify the bacterial and fungal isolates.

2.4.1. Gram staining technique.

Gram staining, used to determine the Gram reaction of bacterial isolates, was conducted according to the procedure outlined by [21]. Smears were air-dried and heat-fixed on slides, then stained with crystal violet for 30 seconds and rinsed with distilled water. Iodine solution was applied for 30 seconds, followed by another rinse. Decolorization was performed briefly using acetone-alcohol, and smears were counterstained with safranin for 60 seconds. After air drying, the slides were examined under an oil immersion microscope. Gram reaction, cell morphology, and colony arrangement were recorded.

2.4.2. Catalase test.

The catalase test was performed as described by [22] to detect the presence of the catalase enzyme. A small inoculum of the bacterial isolate was placed on a clean slide, followed by the addition of a drop of 3% hydrogen peroxide. Bubbling, due to the breakdown of hydrogen peroxide into water and oxygen, indicated a positive result.

2.4.3. Oxidase test.

The oxidase test was carried out following the method of [23]. A colony of the bacterial isolate was placed on filter paper impregnated with oxidase reagent using a sterilized bent glass rod. The development of a dark purple color within 10 seconds indicated a positive result due to the presence of cytochrome c oxidase.

2.4.4. Test for motility.

Motility was assessed by inoculating bacterial isolates into semi-solid motility medium using a sterile straight wire and incubating at 37°C for up to 72 hours. Motile organisms were identified by the diffusion of growth away from the stab line, while non-motile bacteria showed growth restricted to the inoculation site [24].

2.4.5. Saccharide fermentation assay.

Sugar fermentation tests were performed by inoculating isolates into sugar-containing media and incubating at 37°C. Media were monitored daily for up to seven days. A color change to pink indicated acid production, while gas formation was identified by bubbles in a Durham tube.

2.4.6. Indole test.

The indole test was conducted by inoculating isolates into peptone water and incubating at 37°C for 48 hours. After incubation, 2–3 drops of Kovac's reagent were added. The appearance of a crimson or pink layer at the interface signified a positive result.

2.4.7. Voges-Proskauer (VP) test.

The VP test identified acetyl methyl-carbinol production. Isolates were cultured in glucose phosphate broth at 37°C for 48 hours. After incubation, 0.6 mL of alpha-naphthol and 0.2 mL of 40% potassium hydroxide were added. A red color indicated a positive result.

2.4.8. Urease test.

Bacterial isolates were inoculated onto urea agar slopes and incubated at 37°C for five days. A color change from yellow to red or pink indicated a positive result, suggesting urease activity and the hydrolysis of urea into ammonia.

2.4.9. Citrate utilization test.

Citrate utilization was evaluated using Simmons' citrate agar. Following inoculation, the tubes were incubated at 37°C for up to seven days. A positive result was indicated by a blue color in the medium.

2.4.10. Coagulase test.

The coagulase test was used to detect *Staphylococcus aureus*. A 1:10 dilution of plasma was mixed with the isolate in saline and incubated at 37°C for 4 hours. Clot formation within the incubation period confirmed a positive result.

2.4.11. Lactophenol cotton blue stain test.

Fungal identification was performed using lactophenol cotton blue staining. A drop of stain was placed on a clean slide, and a fungal isolate was teased onto the slide using sterile wires. A coverslip was gently applied, and the slide was examined under a microscope for structural features.

2.5. Statistical analyses.

Statistical analyses were conducted using one-way ANOVA and Chi-square tests to assess the distribution of bacterial and fungal isolates across samples. Statistical significance was determined at the 5% level. Data were analyzed using SPSS version 21.0 and GraphPad Prism 6® (trial version) software (GraphPad Software, CA, USA).

3. Results and Discussion

Table 1 presents the total colony counts of bacterial isolates obtained from raw goat meat samples collected from five anatomical regions. The colony counts ranged from 65 CFU/g in the liver (Sample A) to 155 CFU/g in the genitals (Sample E). All samples met the local microbiological standards for fresh meat, as indicated by the "Pass" status. The highest bacterial load was observed in the genital sample, while the liver showed the lowest count.

Overall, the total colony plate counts ranged between 10^4 and 10^5 CFU/g, which falls within the acceptable limits established by Nigerian regulatory guidelines for fresh meat products.

Table 1. Total colony count of bacterial isolates from raw meat sample.

Sample	Colonies Per Plate (in duplicates)		Conformity With Standard Locality
A	65	68	Pass
B	77	70	Pass
C	100	98	Pass
D	113	120	Pass
E	155	156	Pass

Key: A = Liver Sample; B = Muscle Sample; C = Top site Sample; D = Stomach Sample; E = Genital Sample
SON/NAFDAC Acceptable limit: ≤ 10^6 CFU/g threshold for Total Viable Count.

Table 2 presents the total counts of bacterial and fungal isolates obtained from raw goat meat samples collected from five anatomical regions. Sample A (liver) contained three bacterial and two fungal isolates, while Sample E (genitals) recorded the highest microbial presence with four bacterial and three fungal isolates. In total, 16 bacterial and 13 fungal isolates were identified across all samples. The muscle (Sample B), top leg/loin (Sample C), and stomach (Sample D) each exhibited three bacterial isolates and two to three fungal isolates. These results indicate widespread bacterial contamination across all tissue types, with fungal contamination particularly elevated in the genital sample.

Table 2. Total bacterial and fungal isolates of raw meat samples.

Sample	Bacterial isolate	Fungal isolate
A	3	2
B	3	3
C	3	3
D	3	2
E	4	3
5	**16**	**13**

Key: A = Liver Sample; B = Muscle Sample; C = Top site Sample; D = Stomach Sample; E = Genital Sample.

The microbial assessment of raw goat meat samples from five anatomical sites—liver, muscle, top leg, stomach, and genitals—revealed statistically significant differences in total bacterial colony counts. One-way ANOVA analysis yielded an F-value of 230.08 with a p-value of 7.48×10^{-6}, confirming that the observed variations in colony counts among the different sites were not due to random chance. The genital sample (Sample E) exhibited the highest bacterial load, while the liver sample (Sample A) had the lowest, highlighting a clear disparity in microbial contamination levels based on anatomical location. Conversely, a Chi-square test assessing the distribution of bacterial and fungal isolates across the samples produced a χ^2 value of 0.235 with a p-value of 0.9936, indicating no statistically significant association between anatomical site and microbial type distribution. This suggests that, although total bacterial contamination varies by location, the relative proportions of bacterial to fungal isolates remain consistent across the different tissue sites.

Figure 2 illustrates the distribution of bacterial and fungal isolates across different anatomical sites. The genital samples exhibited the highest number of bacterial isolates (four) and also had the highest fungal count (three). This was followed by the liver and stomach samples, both of which recorded the lowest fungal counts (two). Bacterial isolate counts were uniform across all anatomical sites, three isolates each, except for the genital site, which had four bacterial isolates.

Table 3 presents a summary of the morphological characteristics of bacterial isolates obtained from raw goat meat samples. Each sample (A–E) contained isolates with distinct features such as elevation, margin, color, shape, and size, which aid in species identification.

Sample A, for example, included *Staphylococcus aureus* (yellow, spherical, large), *Klebsiella* spp. (greyish-white, circular, large), and *Escherichia coli* (creamy, circular, small). Similar morphological patterns were observed in the other samples, with *Staphylococcus aureus*, *Klebsiella* spp., *Salmonella* spp., and *Escherichia coli* identified as predominant species. These morphological characteristics are crucial for distinguishing bacterial species and assessing the potential public health risks associated with raw meat consumption.

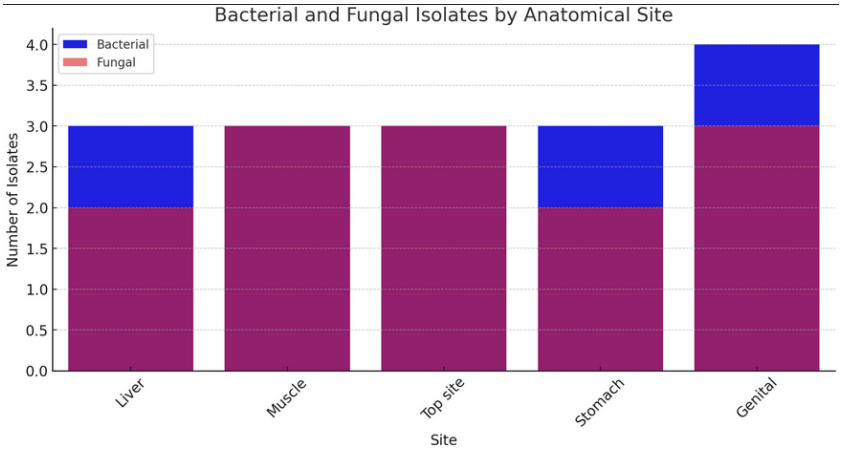

Figure 2. Bacterial and fungal isolate distribution by anatomical sites.

Table 3. Morphological properties of bacterial isolates from caprine meat sample in Awka Abattoirs.

Sample	Elevation	Margin	Colour	Shape	Size	Probable organism
A_1	Flat	Entire	Yellow	Spherical	Big	*Staphylococcus aureus*
A_2	Dome shaped	Entire	Greyish white	Circular	Large	*Klebsiella spp*
A_3	Dome shape	Entire	Creamy	Circular	Small	*Escherichia coli*
B_1	Flat	Entire	Yellow	Spherical	Big	*Staphylococcus aureus*
B_2	Dome shaped	Entire	Greyish white	Circular	Large	*Klebsiella spp*
B_3	Dome shaped	Entire	Creamy	Circular	Small	*Escherichia coli*
C_1	Flat	Entire	Yellow	Spherical	Big	*Staphylococcus aureus*
C_2	Convex	Entire	Greyish white	Circular	Large	*Salmonella spp*
C_3	Dome shaped	Entire	Creamy	Circular	Small	*Escherichia coli*
D_1	Flat	Entire	Yellow	Spherical	Big	*Staphylococcus aureus*
D_2	Convex	Entire	Greyish white	Circular	Large	*Salmonella spp*
D_3	Dome shaped	Entire	Creamy	Circular	Small	*Escherichia coli*
E_1	Flat	Entire	Yellow	Spherical	Big	*Staphylococcus aureus*
E_2	Convex	Entire	Greyish white	Circular	Large	*Klebsiella spp*
E_3	Dome shaped	Entire	Greyish white	Circular	Large	*Salmonella spp*
E_4	Dome shaped	Entire	Creamy	Circular	Small	*Escherichia coli*

The bacterial isolates identified in this study exhibited intact margins. The isolated bacteria comprise *Staphylococcus aureus, Escherichia coli, Salmonella* spp., *and Klebsiella* spp. The diversity of bacterial genera and the presence of coliform microorganisms in the samples suggest potential fecal contamination and health implications, aligning with the findings of [25, 26], which identified pathogenic bacteria from abattoirs. The *Klebsiella* spp. reported in this study were not reported by studies aforementioned, and this may suggest that *Klebsiella spp.*, may be endemic to Awka Metropolis and localized to raw meats in Awka Metropolis. This conjecture may largely be supported by [27] who reported *Salmonella spp. and Staphylococcus spp.* from raw beef sold in Accra, the Capital city of Ghana, and Birim North District in the Eastern Region of Ghana, respectively. Interestingly, bacteria such as *Enterococcus* spp., *Diplococcus* spp., and *Micrococcus* spp. were not isolated from raw meat in Cape Coast, a finding which may equally suggest that these bacterial species may be endemic

to those geographical locations from which the meat samples were obtained and assessed for microbial contamination.

Table 4 presents the biochemical characteristics of bacterial isolates from raw goat meat samples. The table includes various tests such as Gram staining, indole, motility, methyl red, Voges-Proskauer, catalase, citrate, urease, and sugar fermentation (glucose and fructose). The results show that *Staphylococcus* spp. (A1, B1, C1, D1, E1) is Gram-positive, cocci in clusters, and produces acid gas in glucose and fructose fermentation. *Klebsiella* spp. (A2, B2, E2) is Gram-negative, short rods in chains, and also ferments glucose but not fructose. *Escherichia coli* (A3, B3, C3, D3, E4) is Gram-negative, rod-shaped, and exhibits positive results for indole and motility tests. *Salmonella* spp. (C2, D2, E3) is Gram-negative, rod-shaped in chains, and negative for indole and motility, with specific fermentation patterns. Table 5 further displayed the occurrence of individual bacterial species in the different samples. *Staphylococcus aureus* and *Escherichia coli* were found dominant in all five meat samples while the occurrence of other bacterial species varied in the different samples.

Table 4. Biochemical characteristics of bacterial isolates.

Isolates	Gram Staining	Form	Indole	Motility	Methyl Red	Voges–Proskauer	Catalase	Citrate	Urease	Glucose	Fructose	Probable Organism
A1	+	Cocci Clusters	-	-	+	+	+	+	-	AG	A	*Staphylococcus* spp.
A2	-	Short rod in chains	-	-	+	-	-	+	-	AG	G	*Klebsiella* spp.
A3	-	Rod in chains	+	+	+	-	+	-	-	AG	A	*Escherichia coli*
B1	+	Cocci Clusters	-	-	+	+	+	+	-	AG	A	*Staphylococcus* spp.
B2	-	Short rod in chains	-	-	+	-	-	+	-	AG	G	*Klebsiella* spp.
B3	-	Rod in chains	+	+	+	-	+	-	-	AG	A	*Escherichia coli*
C1	+	Cocci Clusters	-	-	+	+	+	+	-	AG	A	*Staphylococcus* spp.
C2	-	Rod in chains	-	-	+	-	-	+	-	AG	-	*Salmonella* spp.
C3	-	Rod in chains	+	+	+	-	+	-	-	AG	A	*Escherichia coli*
D1	+	Cocci Clusters	-	-	+	+	+	+	-	AG	A	*Staphylococcus* spp.
D2	-	Rod in chains	-	-	+	-	-	+	-	AG	-	*Salmonella* spp.
D3	-	Rod in chains	+	+	+	-	+	-	-	AG	A	*Escherichia coli*
E1	+	Cocci Clusters	-	-	+	+	+	+	-	AG	A	*Staphylococcus* spp.
E2	-	Short rod in chains	-	-	+	-	-	+	+	AG	G	*Klebsiella* spp.
E3	-	Rod in chains	-	-	+	-	-	+	-	AG	-	*Salmonella* spp.
E4	-	Rod in chains	+	+	+	-	+	-	-	AG	G	*Escherichia coli*

Key: AG – Acid Gas production.

Table 5. Occurrence of bacterial species in raw meat sample.

Sample	Bacterial isolate
A	*Staphylococcus aureus, Klebsiella spp., Escherichia coli*
B	*Staphylococcus aureus, Klebsiella spp., Escherichia coli*
C	*Staphylococcus aureus, Salmonella spp., Escherichia coli*
D	*Staphylococcus aureus, Salmonella spp., Escherichia coli*
E	*Staphylococcus aureus, Klebsiella spp., Salmonella spp., Escherichia coli*

Key: A = Liver Sample; B = Muscle Sample; C =Top site Sample; D = Stomach Sample; E = Genital Sample

In the findings of this study, high bacterial counts had contaminated raw meat, which conforms to previous research [28], which referenced the presence of varying toxigenic bacteria. Fungi isolated were grouped based on their macroscopic identification as shown in Table 6.

Table 6. Macroscopic characteristics of fungal isolates.

Sample	Growth	Texture	Front view	Back view	Probable organism
A1	Rapid	Creamy	Greyish white	Greyish white	*Candida albicans*
A2	Rapid	Powdery	Dark black	Greyish white	*Aspergillus niger*
B1	Rapid	Powdery	Dark black	Greyish white	*Aspergillus niger*
B2	Abundant	Cotton and wooly	Brownish red	Greyish red	*Fusarium spp.*
B3	Rapid	Creamy	Greyish white	Greyish white	*Candida albicans*
C1	Abundant	Cotton and wooly	Brownish red	Greyish red	*Fusarium spp.*
C2	Rapid	Creamy	Greyish white	Greyish white	*Candida albicans*
C3	Moderate	Velvety	Bluish-green	Yellowish white	*Penicillium spp.*
D1	Abundant	Cotton and wooly	Brownish red	Greyish red	*Fusarium spp.*
D2	Rapid	Powdery	Dark black	Greyish white	*Aspergillus niger*
E1	Abundant	Cotton and wooly	Brownish red	Greyish red	*Fusarium spp.*
E2	Rapid	Creamy	Greyish white	Greyish white	*Candida albicans*
E3	Rapid	Powdery	Dark black	Greyish white	*Aspergillus niger*

A diversity of fungal genera isolated in this study aligns with previous findings by [29] and [30], who reported the presence of *Penicillium* spp., *Aspergillus* spp., and *Candida* spp. in various raw meat samples. The detection of *Candida albicans* is particularly concerning, as this opportunistic pathogen can cause infections in immunocompromised individuals. Additionally, *Aspergillus niger* and *Penicillium* spp. are known producers of ochratoxins, mycotoxins associated with nephrotoxicity and carcinogenicity. *Fusarium* spp., another genus identified in this study, is capable of producing trichothecenes and fumonisins, compounds that may suppress the immune system and induce gastrointestinal disturbances. In total, eight genera of microorganisms were isolated in this study. The probable organisms identified include: *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella* spp., *Salmonella* spp., *Candida* spp., *Aspergillus* spp., *Penicillium* spp., and *Fusarium* spp., with *E. coli* and *S. aureus* showing the highest frequency across the samples.

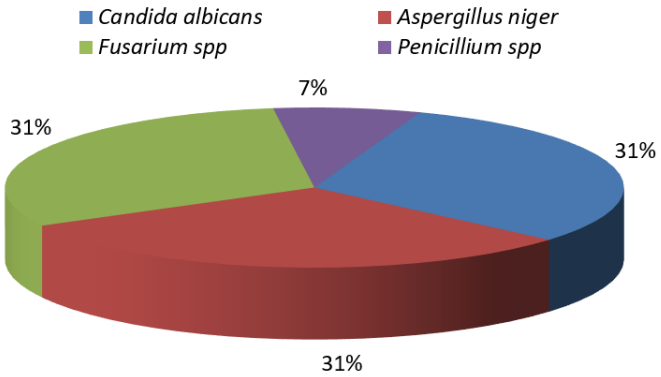

Figure 3. Frequency of occurrence of all fungal isolates.

Figure 3 illustrates a comparative assessment of fungal isolate percentages from different abattoirs, with prevalence ranging from 7% to 31%. *Aspergillus niger*, *Fusarium* spp., and *Candida albicans* each exhibited an occurrence rate of 31%, while *Penicillium* spp. accounted for the lowest frequency at 7%. These results are consistent with the findings of [30] and [31],

who previously isolated similar fungal genera from cow dung and meat samples from the Awka Central Abattoir.

4. Conclusion/Recommendation

At the conclusion of this study, the presence of microorganisms in raw caprine meat sourced from selected abattoirs in Awka was confirmed. Both the current findings and previous studies conducted within the same region consistently demonstrate that raw goat meat in Awka harbors a distinct microbial profile influenced by factors such as inadequate slaughterhouse hygiene, poor water quality, improper waste disposal practices, and local handling procedures. *Escherichia coli* and *Staphylococcus aureus* emerged as the predominant isolates from goat meat samples collected at the selected abattoirs in Awka metropolis. The presence of these organisms, alongside specific biochemical characteristics observed, strongly indicates fecal contamination of the caprine meat samples examined. This contamination suggests the possible presence of harmful microorganisms in the raw goat meat, likely facilitated by the meat's abundant supply of essential and secondary nutrients that promote bacterial growth. The isolated organisms pose a risk of opportunistic infections, particularly for immunocompromised individuals or those with underlying health conditions. Consequently, there is an urgent need to improve sanitary conditions in water reservoir tanks and sources in the region. It is recommended that regulatory authorities enforce stricter meat inspection protocols and provide hygiene training for meat handlers, alongside ensuring adequate refrigeration throughout the meat supply chain. Additionally, public awareness campaigns and the updating of microbial standards are essential to enhance food safety. This study has some limitations, including the sample size, potential seasonal variation, the lack of molecular confirmation of isolates, and the possibility of laboratory contamination, all of which may have influenced result interpretation. Future research should consider comparing freshly slaughtered goat meat with meat that has been stored for some time. Investigations into the impact of transportation on microbial contamination and load are also crucial, given that most slaughtered animals in abattoirs are transported to markets before sale.

Author contributions

UCO co-supervised the work, took part in the experiment, did part of the design and arranged the final manuscript, CLO co-designed and co-supervised the work, and IMN carried out the experiment. All the authors read and approved the final manuscript.

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Competing Interests

The authors hereby declare that competing interests do not exist regarding the publication of this research.

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