

## **Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria**

Samson O Onemu<sup>1\*</sup>, Joy E Egbokale<sup>2</sup>, Ephraim E Ibadin<sup>3</sup>, Imoleayo O Mata<sup>4</sup> and Emmanuel Ifeanyi Obeagu<sup>5</sup>

1. Samson O Onemu, Department of Medical Laboratory Science, Achievers University, Owo, Nigeria. [onemuso@achievers.edu.ng](mailto:onemuso@achievers.edu.ng)
2. Joy E Egbokale, Department of Medical Laboratory Science, Achievers University, Owo, Nigeria. [heavenlyrime@gmail.com](mailto:heavenlyrime@gmail.com)
3. Ephraim E Ibadin. Medical Microbiology Division, Medical Laboratory Services, University of Benin Teaching Hospital, Benin City, Nigeria. [ephraim.ibadin@ubth.org](mailto:ephraim.ibadin@ubth.org)
4. Imoleayo O Mata, Department of Medical Laboratory Science, Achievers University, Owo, Nigeria. [imoleayotomata@gmail.com](mailto:imoleayotomata@gmail.com)
5. Department of Medical Laboratory Science, Kampala International University, Uganda., [emmanuelobeagu@yahoo.com](mailto:emmanuelobeagu@yahoo.com)

\*Corresponding author: [onemuso@achievers.edu.ng](mailto:onemuso@achievers.edu.ng)

### **Abstract**

Beef meat is an essential source of human nourishment universally. The processing of beef often leads to the introduction of fecal bacteria from the food animal. Some of the introduced microorganisms have been traceable to food-borne illnesses and the spread of antimicrobial resistant bacterial species that are inherently more challenging and costlier to treat. The study aimed to evaluate the bacteriological quality of fresh raw beef marketed in Owo, Ondo State, Nigeria. Samples of procured fresh raw beef were examined applying standard bacteriological techniques for total aerobic count (TAC), total coliform count (TCC), variety of bacteria and susceptibility to antimicrobial agents. The TAC and TCC were much in excess of the set limits. *Klebsiella* species 118 or 35.0% of all 337 isolates was the most predominant microorganism. *Staphylococcus aureus* 33.5% was next in frequency of isolation. Other microorganisms recovered

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

were *Escherichia coli* 16.6%, *Preteus* species 10.1%, *Pseudomonas aeruginosa* 2.7%, *Enterococcus faecalis* 1.5% and *Salmonella enterica* 0.6% accounted for the least frequently isolated microorganism. The counts and variety of microorganisms that accompanied the beef samples clearly indicates a gap in hygiene ideals for handling beef that can become channels for the transmission of food-borne illnesses and source of spread of multidrug resistant bacteria to humans. This thus, necessitates the review of the processing of raw beef and monitoring enforcement of strict sanitation codes for safe beef to consumers.

## 1. Introduction

Beef meat is a major source of relevant nutriment that provides proteins, amino acids, vitamins and trace elements [1-3]. The processing of meat, transportation, storage and retail activities readily lead to the introduction of microorganisms [2,4-6]. The ability of meat to transfer pathogenic bacterial species to humans has been documented [7,8]. Meat has been shown to be an important highway from which humans can be infected with pathogenic bacteria [3,9]. The desire to keep meat free from the risk of food-borne illness has therefore, become more strident than ever [4,8]. A number of pathogenic bacteria seen in fresh raw beef across the globe include *Staphylococcus aureus* as the most dominant microorganism [10,11]. Notable food-borne diseases have been traceable to meat processed from animal carriers of *Salmonella* species and *Escherichia coli* especially serotype 0157 [12,13], as well as the most frequent causes of food-borne diseases in the United States [14]. The widespread application of antimicrobial agents in animal production is attributed to increased bacterial resistance in such food animals and the resultant existence of palpable apprehension worldwide on the impacts of these practices [7,15-19]. The emergence of pathogenic bacterial species with multiple-drug resistance, MDR genes in meat and meat products come with the attendant negative bearing on the management of such bacterial infections if transmitted to humans creates a dilemma of epic proportions [5,20-23]. Mitigating the effect of bacterial infection with the administration of antimicrobial agents has been the bedrock of modern medical care in dealing with most bacterial infections [24]. The current trend in the declining effectiveness of antimicrobial agents has dimmed the hope for their continued successful use and a key point for concern to healthcare providers across all nations [27,28]. Multidrug resistant, MDR bacteria are responsible for causing a significant number of deaths all over the world with more devastating effects in poorer countries [29]. It is projected that MDR bacterial species will be the topmost killer by the year 2050 [30]. This study intended to examine the nature and public health implications of bacterial flora accompanying fresh raw beef sold in the open market in Owo metropolis, Ondo State, Nigeria.

## 2. Materials and Methods

### 2.1. Study Design

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

The study was cross-sectional, conducted on fresh raw beef in the open market in Owo metropolis during a ten-day period between the hours of 10.00 am and 11.00 am in February 2024 to evaluate the bacteriological quality of fresh raw beef on retail.

## 2.2. Sample collection

A minimum of 100 g of fresh raw beef muscle obtained from a selected retailer into sterile polypropylene autoclavable bags and stored in a cold chamber. The samples were thereafter, transported to the laboratory for examination within two hours.

## 2.3. Examination of samples

Aseptically, 10 g of beef sample removed with sterile blade and a pair of forceps, and weighed into a stomacher (Seward, United Kingdom) containing 90 mL of 1% buffered peptone water, BPW (Oxoid CM 1049) with inoculation of 0.1 mL onto dried plates of blood agar (Oxoid CM0085), MacConkey agar (Oxoid CM0007) and mannitol salt agar (Oxoid CM 271). Further ten-fold serial dilutions were done from the beef homogenate stock ( $10^{-2}$ ) to give  $10^{-3}$ ,  $10^{-4}$ ,  $10^{-5}$ ,  $10^{-6}$ ,  $10^{-7}$ ,  $10^{-8}$ , from which 0.1 mL was plated onto dried plates of nutrient agar (Oxoid CM 0003) and MacConkey agar in replicates including from the stock homogenate. The plates were thereafter, incubated at 37°C for 24-48 hours. Colonies appearing on plates showing with 3-30 colonies counted and mean from the two plates recorded as count for that dilution. The other inoculated agar plates were assessed for colonial morphology, characterization tests and identification following the scheme described by Cowan [31]. Susceptibility of isolates to antimicrobial agents was determined by Kirby-Bauer disc diffusion technique applying the guidelines of the Clinical Laboratory Standards Institute [32]. Methicillin resistance was determined with oxacillin 1.0 µg disc as marker of methicillin resistance (ORSA/MRSA) and the double disc synergy test to detect the production of extended spectrum beta-lactamases, ESBLs in enterobacterial isolate

## 3. Results

The examination of 120 beef samples yielded 337 different microorganisms with aerobic bacterial count (TAC) range of  $6.2-170.2 \times 10^4$  (mean  $\pm$  SD =  $41.13 \pm 56.51$ ) cfu/g and total coliform count, TCC of  $2.7-98.7 \times 10^4$  (mean SD =  $23.94 \pm 29.03$ ) cfu/g. The TAC in 70% samples were  $\geq 10^5$  cfu/g and 60% of TCC (Table 1). The most frequently isolated microorganism was *Klebsiella* species 118 isolates representing 35.0% of all isolates (Table 1). The next most dominant microorganism was *Staphylococcus aureus* with 113(33.3%). Other microorganisms were *Escherichia coli* 56(16.6%), *Proteus* species 34(10.1%), *Pseudomonas aeruginosa* 9(2.7%) *Enterococcus faecalis* 5(1.5%) and *Salmonella enterica* 2(0.6%) was the least dominant isolate

Table 2 represents the susceptibility of the isolated microorganisms to antimicrobial agents. All the isolates were resistant to tetracycline and 9.4% *Staphylococcus aureus* were susceptible to amoxicillin and 49.6% to amoxicillin-clavulanate. *Enterococcus faecalis* were not susceptible to amoxicillin and gentamycin, 40% inhibited by amoxicillin-clavulanate. Inhibition by other agents

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

ranged from 60-80%. Susceptibility of *Escherichia coli* and *Klebsiella* species to gentamycin varied from 39.3% to 90.0%. Susceptibility to perfloxacin, sparfloxacin and ciprofloxacin ranged from 41.6-88.2% against *Pseudomonas aeruginosa* and *Proteus* species. Cefotaxime inhibited 33.3% of *Pseudomonas aeruginosa* and 88.2% of *Staphylococcus aureus* isolates.

Methicillin resistant *Staphylococcus aureus* strains were 1.8% of the isolates. The detection of extended spectrum beta-lactamase, ESBL enzymes in the enterobacterial isolates (Table 3) showed 1.8% of *Escherichia coli*, 2.5% *Klebsiella* species, 2.9% *Proteus* species produced ESBLs.

**Table 1: Distribution of microorganisms in raw beef**

Isolate	No. of cases (%)
<i>Staphylococcus aureus</i>	113(33.5)
<i>Klebsiella</i> species	118(35.0)
<i>Escherichia coli</i>	56(16.6)
<i>Proteus</i> species 34(10.1)	
<i>Pseudomonas aeruginosa</i>	9(2.7)
<i>Enterococcus faecalis</i>	5(1.5)
<i>Salmonella enterica</i>	2(0.6)

**Table 2: Antimicrobial susceptibility pattern of isolates**

Isolate	Antimicrobial agent (%)							
	TE	A	AMC	CN	PEF	SPX	CPX	CTX
<i>Staphylococcus aureus</i>	0.0	19.4	49.6	74.5	80.5	83.1	81.4	78.8
<i>Escherichia coli</i>	0.0	0.0	0.0	39.3	62.5	64.3	62.5	55.4
<i>Klebsiella</i> species	0.0	0.0	0.0	90.0	62.5	63.3	61.7	56.7

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

<i>Proteus</i> species	0.0	0.0	2.9	85.3	88.2	85.2	79.4	67.6
<i>Pseudomonas aeruginosa</i>	0.0	0.0	0.0	50.0	41.6	41.6	58.3	33.3
<i>Enterococcus faecalis</i>	0.0	0.0	0.0	0.0	80.0	80.0	60.0	60.0
<i>Salmonella enterica</i>	0.0	50.0	100.	100.	100.0	100.0	100.0	50.0

Key:

Tetracycline (TE), Amoxicillin (A), Amoxicilin-clavulanate (AMC), Gentamycin (CN),  
Perfloxacin (PEF), Sparfloxacin (SPX), Ciprofloxacin (CPX), Cefotaxime (CTX).

Table 3: Detection of ESBLs in isolates

Isolate	Positive cases (%)
<i>Escherichia coli</i> (n=55)	1 (1.8)
<i>Klebsiella</i> species (n=118)	3 (2.5)
<i>Proteus</i> species (n=314)	1 (2.9)
<i>Pseudomonas aeruginosa</i> (n=9)	0 (0)
<i>Salmonella enterica</i> (n=2)	0 (0)

4. Discussion

Fresh raw beef marketed in the open market in Owo metropolis contained aerobic and coliform counts in excess of the level  $10^4$  cfu/g recommended as upper limits [33-35]. The total aerobic count, TAC and total coliform counts, TCC were also respectively higher than the suggested baseline limits. This mirrors the poor microbiological quality of the beef samples and a reflection of non-adherence to strict cleanliness ideals required for handling fresh raw meat and meat products. This represents a direct signal for conceivable harm from such meat sources [36], since meat from muscles of healthy animals do not contain microorganisms. Even though, the number of microorganisms in fresh beef does not directly reflect the risk of harm to health [21,37],

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

microbial count of  $10^6$  cfu/g or higher was recorded in 70% of the samples which is the threshold that regularly signify meat spoilage [33]. Bacterial counts of  $10^7$ - $10^8$  cfu/g are linked constantly with the onset of alteration in organoleptic properties such as appearance, odour and flavour [21]. Lower numbers of microorganisms in meat and meat products are advantageous in maximizing the shelf life and diminishing the possibility for food-borne illnesses [9]. The beef samples revealed a variety of bacterial species that are relevant not only in their potential to initiate diseases in humans through food as a major source of attention worldwide but also in zoonotic infections [8,9,38]. The most predominant microorganism isolated was *Klebsiella* species (36.0%), as a member of the enterobacteria, they are always present in waste materials, natural bodies of water and abattoirs. Their detection in beef is critical for risk assessment of the source and cleanliness of beef [39]. Members the genus especially *Klebsiella pneumoniae* is habitually associated with a high degree of notoriety for antimicrobial resistance in a wide range of human infections as well as a major microorganism in hospital acquired infections, HAIs [40]. The interaction between humans and animals predictably leads to exchange of microorganisms and when this involves multidrug resistant bacteria, the outcome can have confounding impact on the health of humans [41]. *Staphylococcus aureus* (33.5%) was the next in frequency as a colonizer of a wide variety of domestic and wild animals that is commonly found in meat products [11,42], with the potential for transmission into humans [43-45]. *Staphylococcus aureus* is of exceptional importance in man as a commensal in some humans and a key pathogen that can initiate an extensive range of infections in humans, some of which could lead to high rate of mortality [46-48]. *Escherichia coli* (16.6%) was the third most frequent bacterium. Studies have shown that this microorganism gains access into beef from cattle feces during evisceration and handling [8,49]. *Escherichia coli* contaminating beef may thus become transmissible to humans. A large number of *Escherichia coli* serotypes are capable of producing verotoxin involved in food-borne illnesses that range from mild to intense bloody diarrhea [8,50]. *Proteus* species were 10.1% of all the isolates. This microorganism inhabits the intestinal tract of many animals and man with a wide array of species. *Proteus* species are opportunistic pathogens with the ability to cause several types of human infections when transmitted to the appropriate body site [51]. The detection of *Proteus* species in beef is a sign that they originate from the feces of the animal or introduction during handling and therefore, a signal of potential health risk [52]. A low proportion of *Pseudomonas aeruginosa* (2.7%) encountered in the study is consistent with observation from other studies [53]. In spite of the low prevalence rate of *Pseudomonas aeruginosa* and being a psychrotrophic bacterium that can thrive between 0-4°C and a key microorganism in the putrefaction and spoilage of meat and meat products kept at low temperatures [54]. The organism is of great significance in causing HAIs and multidrug resistance of the organism in most clinical settings prompted the World Health Organization, WHO to classify it as an organism of critical priority for concerted effort to curtail or eradicate the infection caused by the organism [55,56]. *Enterococcus* species typically get into meat from feces as a classical intestinal bacterium. The detection in meat is an indicator of very low bacteriological purity and unsanitary handling techniques [21]. The regular detection of *Enterococcus* species in beef is disconcerting due to its ability to initiate infections with highly multidrug resistant strains, highlights the important need for beef to be available to consumers from secured sources [57-59]. The contamination of meat and meat products with antimicrobial resistant, AMR bacteria derived

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54



from the intestinal tract of animals has elicited sharp criticisms on the use of antimicrobial agents in livestock [60]. This encourages the emergence of resistant strains through selective pressure and the propensity to cause severe nosocomial infections [61,62]. The recovery of *Salmonella enterica* - a non-typhoid salmonella, NTS from 0.6% of the samples and a key causative agent of food-related illnesses [12,63,64] with a significant number of infections in the United States of America [65]. There is no doubt, therefore, that *Salmonella enterica* infection may be common in Nigeria due to poorer asepsis levels and ineffective monitoring of beef processing and handling practices. *Salmonella enterica*'s infection rate of 4.2% reported in abattoir workers in Nigeria [66] does not account for the level of infection traceable to meat products in the consuming public. Resistance of the isolates to tetracycline implies that infection with any of the isolates are untreatable with this agent. The regular use of tetracycline at sub-therapeutic doses in animals feedlots is suggested a major contributory factor in the high rate of resistance seen with tetracycline and source of peril to humans and animals alike and the environment as well [67-69]. One strain (50%) of *Salmonella enterica* was susceptible to each of amoxicillin and cefotaxime, and susceptibility to other agents was 100%. Susceptibility of the isolates to other agents ranged from 41.6-100% with perfloracin sparfloracin, ciprofloracin and lower against cefotaxime with susceptibility ranging from 33.3-78.8% for *Staphylococcus aureus*. Only isolates of *Staphylococcus aureus* (49.6%) were susceptible to amoxicillin-clavulanate, 2.9% of *Proteus* species and 100% *Salmonella enterica* were also respectively susceptible. Each of which points to the variability of antimicrobial agents needed for managing infections with these microorganisms. Two (1.8%) *Staphylococcus aureus* were methicillin resistant, MRSA strains. This should generate intense interest, as MRSA infections are some of the most difficult to treat bacterial infections [70]. Studies have reported that MRSA strains have a lower prevalence in livestock than in humans as this study has revealed [46,47,71,72]. Reports indicate that these strains derive their source from the livestock rather than from humans [73], which firmly places the focus on food asepticism [74]. The detection of MRSA in beef calls for process review from the slaughterhouse to the retail outlets [75,76]. Extended spectrum beta-lactamase, ESBLs detection for MDR organisms amongst the Gram-negative isolates ranged from 1.8% of *Escherichia coli* strains to 2.9% of *Proteus* species. These microorganisms are a cause of variety of human infections and multidrug resistant strains implicated in infections of opportunities [77]. The lower rate of ESBL observed in this study may echo the source of beef obtained mainly from the traditionally bred stock where the animals roam-free and substantially free from the administration of antimicrobial agents. The presence of ESBLs producing bacteria in animal-sourced food emphasizes the pressing need for new and innovative strategies to combat bacterial resistance [78].

## 5. Conclusion

The presence of very high bacterial loads in fresh raw beef meat marketed in Owo metropolis is a source of serious unease as this may serve as a veritable vehicle for the transmission of food-borne ailments that are associated with MDR organisms with heightened prospects for longer duration of illness, higher healthcare costs and elevated mortality rates. There is therefore, the need for a complete overhaul of the steps adopted in fresh raw beef processing and handling to the retail outlets in Nigeria.

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

## References

1. Kassem II, Nasser NA, Salibi J. Prevalence and loads of faecal pollution indicators and the antibiotics resistance phenotypes of *Escherichia coli* in raw minced beef in Lebanon. Food, 2020; 9(11): 1543. Doi.org/10.3390/foods911543.
2. Osemwowo E, Omoruyi IM, Kurittu P, Heikinheimo A, Friedriksson-Ahomata M. Bacterial quality and safety of raw beef: A comparison between Finland and Nigeria. Food Microbiol, 2021; 100: 103860, doi.org/10.1016/j.fm.2021.103860.
3. Warmate D, Onarinde B. Food safety incidents in the red meat industry: A review of food-borne disease outbreaks linked to the consumption of red meat and its products 1991-2021. Int. J. Food Microbiol, 2022; 398(2): 110240. doi.org/10.1016/j.ijfoodmicro.2023.110240.
4. Bhandari N, Nepali DB, Paudyal S. Assessment of bacterial load in broiler chicken meat from the retail meat shops in Chitwan, Nepal. Int. J. Microbiol, 2013; 2(3): 99-104. doi.org/10.3126/ijim.v2i3.8671.
5. Petternal C, Galler H, Zarfel G, Luxner J, Haas D, Grisold AJ, et al. Isolation of and characterization of multidrug resistant bacteria from meat in Austria. Food Microbiol, 2014; 44: 41-46.
6. Ronald C, Matofari JW, Nduka JM. Antibiotic resistance of *E. coli* strains in ready-to-eat meat products in Nakuru County, Kenya. Microbe, 2023; 1(2023), doi.org/10.1016/j.microb.2023.1000022.
7. Omer AS, Saiwa E, Sanaa OY, Elzubeir IE. Antibiotic susceptibility and production of extended beta-lactamase (ESBL) of *Escherichia coli* strains isolated from meat. Afr J Microbiol Res. 2021; 15(7): 370-376.
8. Ali S, Alsayegh AF. Review of major meat-borne zoonotic bacterial pathogens. Front. Public Heal. 2022 10: 1045599. doi.103389/fpubh.2022.1045599.
9. Rani ZT, Mhlongo LC, Hugo A. (2023). Microbial profiles of meat at different stages of distribution chain from the abattoir to retail outlets. Int. J. Environ. Res. Public Health, 2023; 20(3): 1986. doi.10.3390/ijerph.20031986.
10. Tsehayneh B, Yageh T, Agmas B. Evaluation of bacteria load and antibiotic resistance pattern of *Staphylococcus aureus* from ready to eat beef in Bahir Dar City, Ethiopia. Int. J. Microbiol, 2022; 2022: doi.org/10.1155/5560596.

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54



11. Sanlibaba P. Prevalence of antibiotic resistance and enterotoxin production of *Staphylococcus aureus* isolated from retail raw beef, sheep and lamb meat in Turkey. Int. J. Food Microbiol, 2022; 361, doi.org/10.1016/j.foodmicrob.2021.1094.
12. Gutema F, Abdi ED, Agga GE, Firew S, Rasschaert G, Mattheus, et al. Assessment of beef carcass contamination with *Salmonella* and *E. coli* 0157 in slaughter houses in Bishofu, Ethiopia. Int J Food Contamination, 2020; 8(3), doi.org/10.1186/s40550-021-00082-1.
13. Asfaw T, Genetu D, Shenkute TT, Amare YE, Yitayew B. High levels of multi-drug resistant and beta-lactamase producing bacteria in meat and meat contact surfaces, Debre-Berhan, Ethiopia. Int. J. Drug Resistance, 2023; 16: 1965-1977.
14. Laufer AS, Grass J, Holt K, Whicharh JM, Griffin P. M. Gould LH. (2011). Outbreaks of *Salmonella* infections attributed to beef - United States 1973-2011. Epidemiol Infect, 2011; 143(9): 2003-2013, doi.1017/s0950268814003112.
15. Cameron A, McAllister TA. Antimicrobial usage and resistance in beef production. J Animal Sci Biotechnol, 2016; 7(68): doi.org/10.1186/s40104-016-02127-3.
16. Saud B, Pandeh G, Khichaju S, Dhungana G, Aswathi MS, Shrestha V. (2019). Multidrug resistant bacteria from raw meat of buffalo and chicken. Nepal Vet Med Int, 2019; 2019: doi.org/10.1155/2019/9760268.
17. Baah DA, Koley RJ, Dayie NT, Dayie NT, Cojie FS. Multidrug resistant gram-negative bacteria contaminating meat sold in Accra, Ghana. Pathogens. 2022; 11(12): 1517 doi.org/10.3390/pathogens1121517.
18. Mukuna W, Aniume T, Pokhareb B, Khwatenge C, Kilonzo-Nthenge A. Antimicrobial susceptibility profiles of pathogenic and commensal bacteria recovered from cattle and goat farms. Antibiotics (Basel), 2023; 12(2), doi.org/10.3390/antibiotics.12020420.
19. Innes GK, Patton AN, Nachman KE, Casey JA, Stapleton GS, Graham AG, et al. Distance and destination of retail meat in the United States food system. Sci. Rep, 2023; 13: 21024. doi.org/10.1038/s41598-023-48197-2.
20. Burnham C, Leeds J, Nordmann P, O'Grady J, Jean P. (2017). Diagnosing antimicrobial resistance. Nat Rev Microbiol, 2017; 15: 697-703.
21. Gonzalez-Gutierrez M., Fernandez C, Alonso-Calleja C, Capita R. Microbial load and antibiotic resistance in raw beef preparations from North-West Spain. Food Sci Nutr. 2019; 8(2): doi.org/10.1002/fsn3.1319.
22. Rahman MM, Husna A, El-Shalwany HA, Alaim J, Runa NY, Badmuzzaman AT, et al. Isolation and molecular characterization of multidrug resistant *Escherichia coli* from chicken meat. Sci Rep, 2020; 10: 2199. doi.org/10.1038/s41598-020-78367-2.

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. Elite Journal of Public Health, 2024; 2 (6): 40-54

23. Zhou IC, Shual X, Lin Z, Yu, X, Ba X, Holmes MA, et al. Association between particulate matter (PM)<sub>2.5</sub> air pollution and clinical antibiotic resistance: A global analysis, *Lancet*, 2023; 7(5): E649-E659.
24. Conceicao S, Queiroga MC, Larago M' Antimicrobial resistance in bacteria from meat and meat products: a one-health perspective. *Microorganisms*, 2023; 11(10): 2581, doi.org/microorganisms11102581.
25. Zowawi HM, Harris, PN, Roberts MJ, Tambyal PA, Schambi MA, Pezzani MD, et al. The emerging threats of multidrug resistant gram-negative bacteria in Urology. *Nat Rev Urol*, 2015; 12: 570-584.
26. Bassetti M, Peghin M. How to manage KPC infections. *Ther Adv Infect Dis*, 2020; 7: doi.10.1177/2049936-1620912049.
27. Mestrovic T, Robles A, Swetschinski LR, Ikuta KS, Gray AP, Weaver ND, et al. The burden of bacteria antimicrobial resistance in the WHO European Region in 2019: A cross-country systematic analysis. *Lancet*, 2022; 7(11): E897-E913.
28. Mitiku A, Aklilu A, Tsalla T, Woldemariam M, Manilal A, Biru, M. Magnitude and antimicrobial susceptibility profiles of gram-negative bacterial isolates among patients suspected of urinary tract infections in Arba Minch General Hospital, Southern Ethiopia. *PloS ONE*, 2022 17(12): e0279887.
29. Murray CJ, Skunji K, Ikuta KS, Sharara R, Swetschinski L, Aguila GR, et al. Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *Lancet*, 2022; 399(10825): 629-655.
30. Stanton IC, Bethel A, Frances A, Leonard C, Gazew H, Garside R. Existing evidence on antibiotic resistance, exposure and transmission to humans from the environment: A systematic map. *Environ. Evidence*, 2022; 11(8): doi.org/10.1186/s13750-022-22262-2.
31. Cowan ST. Cowan and Steels' Identification of Medical Bacteria, Cambridge, 1974, p 1-174.
32. Clinical Laboratory Standards Institute. *Performance standards for antimicrobial susceptibility testing* (30th edition), M100. CLSI, 2020; Wayne, PA, USA. p 1-332
33. FAO. General hygiene principles for handling meat, FAO, 2012; fao.org/1810-0708/FAO.
34. Kumar P, Haribabu Y, Manjunath. Microbiological quality of meat collected from municipal slaughterhouses and retail meat shops from Hyderabad Karnataka Region. India. *APCBEE Procedia*, 2014; 8: 364-369.

35. Adjei VY, Mensah GI, Kanadu AP, Tano-Debrah. K, Ayi I, Addo KK. Microbial safety of beef along the along beef value chains in the Ashaiman Municipality of Ghana. *Fron. Vet Sci*, 2022; 9: doi.org/10.3389/fvets.2022.813422.
36. Madoroba E, Magwedere K, Chaora NS, Mattle I. Muchadeyi F, Mathole MA, et al. Microbial communities of meat and meat products: an exploratory analysis of the product quality and safety at selected enterprises in South Africa. *Microorganisms*, 2021; 9(3):507, doi.10.3390/microorganisms9030.507.
37. Kanko T, Seid M. and Alemu M. Evaluation of bacteriological profile of meat contact surfaces, handling practices of raw meat and its associated factors in butcher shops of Arba Minch town Southern Ethiopia – A facility base across sectional study. *Food Safety and Risk*, 2023; 10(1): doi.org/10.1186/s40550.
38. Prasad, M.P.braham, R., O'dea, M., Sahibzada, S. and Abraham, R. (2022). Phenotypic and genotypic assessment of antimicrobial resistance in *Escherichia coli* from Australian cattle populations at slaughter. *J Food Prod*, 2022; 85(4): 563-570, doi.10.4315/JFP-21-430..
39. Tesfaye H, Alemayehu H, Desta AF, Eguale T. Antimicrobial susceptibility profile of selected enterobactriaceae of waste-water samples from health facilities, abattoir, downstream rivers and a WWTP in Addis Ababa, Ethiopia. *Antimicrobial Resist Infect Contr*, 2019; 8: 134, doi.org/10.1186/s13756-019-0588-1.
40. Kurekci C. Unaldi O, Sahin S, Garcia-Meniao I, Hammerl JA. Impact and diversity of ESBL-producing *Klebsiella pneumoniae* recovered from raw chicken meat samples in Turkiye. *Antibiotics*, 2023; 13(1): 14;doi.10.3390/antibiotics13010014.
41. Zhang S, Yang G, Ye Q, Wu Q, Zhang J, Huang Y. Phenotypic and genotypic characterization of *Klebsiella pneumonia* isolated from retail food in China. *Front Microbiol*. 2018; 9: doi.org/3389/ficb.2018.00289.
42. Tsehayneh B, Yayeh T, Agmas B. Evaluation of bacterialload and antibiotic resistance pattern of *Staphylococcus aureus* from ready-to-eat raw beef in Buhir Dar City, Ethiopia. *Int. J. Microbiol*, 2021; e5560596; doi.org/10.1155/5560596.
43. Adugna F, Pal M, Girmay G. Prevalence and antibiogram assessment of *Staphylococcus aureus* in beef at municipal abattoir and butcher shops in Addis-Ababa, Ethiopia. *Biomedical Res Int*, 2018: 5017685, doi.10.1155/2018/5017685.
44. Abdalrahman LS, Wells H, Fakhr M. *Staphylococcus aureus* is more prevalent in retail beef livers than other beef cuts. *Pathogens*, 2015; 4(2): 182-198.
45. Odetokun IA, Adetona MA, Ade-Yusuf RO, Adewole AO, Ahmed AN, Ghali-Mohammed, et al. *Staphylococcus aureus* contamination of animal-derived foods in Nigeria: a

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. *Elite Journal of Public Health*, 2024; 2 (6): 40-54

- systematic review 2007-2022. *Food Safety Risk*, 2022; 10(6): doi.org/10.1180/s40550-023-00106-y
46. Velasco U, Quezadu-Aguilez M, Bello-Toledo H. *Staphylococcus aureus* in the meat supplychain: detection methods, antimicrobial resistance and virulence factors. In: *Staphylococcus and Streptococcus* (Sahra Kirmusaoglu edition), eBook, 2019: doi.10.5772/interchopen.85620.
  47. Dorjgochoo A, Batbayar A, Tsend-Ayush A, Erdenebayar O, Byambadorj B, Sarantuya J *et al.* Detection of virulence factors of *Staphylococcus aureus* isolated from retail sale in the markets of Ulaanbantar City, Mongolia. *BMC Microbiol*, 2023; 372: doi.org/10.1186/s12866-023-03122-2.
  48. Onemu SO, Onemu-Metitiri MO, Obeagu EI. Prevalence of coagulase-negative *Staphylococcus aureus* strains in clinical specimens at the University of Benin Teaching Hoospital, Benin City, Nigeria. *Asian J Res Infect Dis*, 2023; 14(4): 49-53.
  49. Aslam M, Nattress F, Greer G, Yost C, Gill C, McMullen. Origin of contamination and genetic diversity of *Escherichia coli* in beef cattle. *Appl Environ Microbiol*, 2003; 69(5): 2794-2799.
  50. Chique C, Hynds P, Burke LP, Morris D. Contamination of domestic ground water systems by verotoxigenic *Escherichia coli* (VTEC), 2003-2019: a global scoping review. *Water Research*, 2021; 188: doi.org/10.1016/j.water.2020.116496.
  51. Sanches MS, Da-Silva CR, Silva LC, Montini VH, Barboza MG, Guidone GH, *et al.* *Proteus mirabilis* from community-acquired urinary tract infection (UTI-CA) shares genetic similarity and virulence factors with isolates from beef and pork meat. *Microb Pathog*, 2021; 158:105098; doi.10.1016/j.micpath.2021.105098.
  52. Li Z, Pen C, Zhang G, Shen Y, Zhang Y, Liu C, *et al.* Prevalence and characteristics of multidrug resistant *Proteus mirabilis* from broiler farms in Shandong Province, China. *Poult Sci*, 2022 101(4): doi.1016/j.psj.2022.101710.
  53. Stellato G, Utter D, Voorhis A, De-Angelis M, Eren AM, Ercolini D. A few *Pseudomonas* oligotypes dominate in the meat and dairy processing environment. *Front Microbiol*, 2017; 8: 264, doi.10.3389/fmicb.2017.00264.
  54. Elbehiry A, Marzouk E, Aldubaib M, Moussa I, Abalkhail A, Ibrahim M *et al.* *Pseudomonas* species prevalence, protein analysis and antibiotic resistance: an evolving health challenge. *AMB Express*, 2022; 12(53): doi.10.1186/s13568-022-01390-1.
  55. Barlow RS, McMillan KE, Duffy LL, Fegan N, Jordan D, Mellor, G.E.(2017) Antimicrobial resistance status of *Enterococcus* from Australian cattle populations at slaughter. *PLoS ONE*, 2017; 12(5): e0177728, doi.10.1371/journal.pone.0177728.

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. *Elite Journal of Public Health*, 2024; 2 (6): 40-54

56. Reig, S., Le-Gouvellec A, Bleves S. What is new in the anti-*Pseudomonas aeruginosa* clinical development pipeline since the 2017-WHO alert? *Front Cell Infect Microbiol*, 2022; 12: doi.org/10.3389/fmicb.2022.930.9731.
57. Zaidi SZ, Zaheer R, Barbieri R, Cook SL, Hannon SJ, Booker CW et al. Genomic characterization of *Enterococcus hirae* from beef cattle feedlots and associated environmental continuum. *Front Cell Microbiol*, 2022; 13:859990, doi.10.3389/fcimb.2022.85990.
58. Mattle I, Atanda AC, Pieneef R, Magwedere K, Mefuna T. Resitance and phylogenomics of *Enterococcus faecalis* isolated from raw muscle foods of beef origin in Guteng, South Africa. *Genomics*, 2023; 115(6): 110742, doi.org/j.ygen.2023.110742.
59. Barlow R, McMillan KE, Duffy LL, Fegan N, Jordan D, Mellor GE. Antimicrobial resistance status of *Enterococcus* from Australian cattle populations at slaughter, *PLoS ONE*, 2017; 12(5): e0177728, doi.10.1371/journal.pone.0177728.
60. Van TT, Yidana Z, Smooker PM, Coloe PJ. Antibiotic use in food animals worldwide, with a focus on Africa: pluses and minuses. *J Global Antimicrob Resistance*, 2020; 20: 170-177.
61. Beukers AG, Zaheer R, Goji N, Amoako KK, Chaves AV, Ward MP, McAllister TA. Comparative genomics of *Enterococcus* species from bovine feces. *BMC Microbiol*, 2017; 19(52): doi.org/10.1186/s12866-017-0962-1.
62. Agga E, Galloway HO, Notisinghe AM. Effects of age and Pasteur type on the concentration of tetracycline and macrolides resistant *Enterococcus* species in cow calf pr0duction system. *Frot Antibiot*, 2022; 1(2021): doi.org/10.3389/fabi.2022.1052316.
63. Eng SK, Pssparajah P, Ab-Mutalib NS, Ser H, Ghan, KG. Lee LH. (2015). *Salmonella*: a review on pathogenesis and antibiotic resistance. *Front Life Sci*, 2015; 8(3): 284-293, doi.org/10.1080/21553769.2015.1051243.
64. Canning M, Birhane MG, Dewey-Mattia D, Lawinger H, Cote A, Gieraltowski L *et al.* *Salmonella* outbreaks linked to beef, United States 2012-2019. *J Food Protection*, 2023; 86(5): doi.org/j.jfp.2023.10007,
65. Levent G, Schlochtermeir A, Ives SE, Norman KN, Lawhhon SD, Loneragan GH *et al.* Population dynamics of *Salmonella enterica* within beef cattle cohorts followed from single dose metaphylactic antibiotic treatment until slaughter. *Appl Environ Microbiol*, 2024; 85(23): e01386-19, doi.10.1128/AEM.01386-9.
66. Aworh MK, Nilssen P, Egyir B, Owusu FA, Hendriksen RS. A rare reservoir of non-typhoid *Salmonella enterica* isolated from humans, beef cattle and abattoir environments in Nigeria. *PLoS ONE*, 2024; 19(1): e0296971.

**Citation:** Onemu SO, Egbokale JE, Ibadin EE, Mata IO, Obeagu EI. Bacteriological Examination of Fresh Raw Beef on Retail in the Open Market in Owo Metropolis, Ondo State, Nigeria. *Elite Journal of Public Health*, 2024; 2 (6): 40-54

67. Granados-Chinchilla F, Rodriguez C. Tetracycline in feedstuffs: from regulation to analytical methods: bacterial resistance and conventional health implications. *Anal Methods Chem*, 2017;1315497, doi.10.1158/2017/1315497.
68. Manyi-Loh C, Mamphweli S, Meyer E, Okoh A. Antibiotics use in agriculture and its consequential resistance in environmental sources: potential public health implication. *Molecules*, 2018; 23(4): 795, doi.10.3390/molecules23000795.
69. Kimera Z, Mshana SE, Rweyemamu MM, Mboera LE, MateeMI. (2020). Antimicrobial use and resistance in food-producing animals and the environment: an African perspective. *Antimicrob Resist Infect Control*, 2020; 9(37): doi.10.1186/s13756-020-0697-x.
70. Jackson CR, Davis JA, Barrat JB. Prevalence and characterization of methicillin *Staphylococcus aureus* isolates from retail meat and humans in Georgia. *J Clin Microbiol*, 2013; 51(4): 1199-1207.
71. Haskell KJ, Schriever SR, Fonoimoama KD, Haw B, Hair BB, Wienclaw TM et al. Antibiotic resistance is lower in *Staphylococcus aureus* isolated from antibiotic-free raw beef as compared to conventional raw beef. *PLoS ONE*, 2018; 13(12): e0206712, doi.10.1371/journal.pone.020.6712.
72. Gelbicova T, Brodikova K, Karpiskova R. Livestock associated methicillin resistant *Staphylococcus aureus* in Czech retail ready-to-eat meat products. *Int J Food Microbiol*, 2022; 374: 109727, doi.org/10.1016/j.ijfoodmicro.2022.109727.
73. Liang T, Liang Z, Wu S, Ding Y, Wu G, Gu B. Global prevalence of *Staphylococcus aureus* in food products and its relationship with the occurrence and development of diabetes mellitus. *Medicine Advances*, 2023; 1(1): 53-78.
74. Martinez-Vazquez AV, Mandujano A, Gruz-Gonzalez E, Guerrero A, Vazquez J, Cruz-Pulido WL et al. Evaluation of retail meat as a source of ESBL *Escherichia coli* in Tamaulipas, Mexico. *Antibiotics (Basel)*, 2022; 11(12): 1715, doi.10.3390/antibiotics1112795.
75. Sadiq A, Samad M, Saddam, Basharat N, Ali S, Roohullah et al. Methicillin resistant *Staphylococcus aureus* (MRSA) in slaughterhouses and meat shops in capital territory of Pakistan 2018-2019. *Front Microbiol*, 2020; 11: doi.org/10.3389/fmicb.2020.577707.
76. Ribeiro J, Silva V, Monteriro A, Vieira-Pinto M, Igrejas G, Reis FS et al. Antibiotic resistance among gastrointestinal bacteria in broilers: a review focused on *Enterococcus* spp. and *Escherichia coli*. *Animals*, 2023; 13(8):1362; doi.org/ani13081362.
77. Ma, CQ, Han YY, Zhou, L., Peng, WQ, Mao, LY, Yang X, Wang Q, et al. Contamination of *Proteus mirabilis* harbouring antimicrobial resistance genes in retail meat and aquatic



products from markets in China. Front Microbiol. 2022; 13:  
doi.org/10.3389/fmicb.2022.1086800

78. Ribeiro LF, Nespolo NM, Rossi, GA Fairbrother JM. Exploring extended-spectrum beta-lactamase (ESBL) producing Escherichia coli in food-producing animals and animal derived foods. Pathogens, 2024; 13(4): 346, doi.org/10.3390/pathogens13040346.