https://fepi-jopas.federalpolyilaro.edu.ng

Molecular Identification and Antibiotic Susceptibility of Bacteria From Cow and Goat Meat In a Nigerian Market

[1]Okoh, O.A✉., [2]Osiyemi, E.O., [3]Akindele, S.T., and [4]Raufu, T.T.
[1-4]Department of Science Laboratory Technology, School of Science,
Abraham Adesanya Ijebu-Igbo, Ogun State, Nigeria.
✉ eseyi79@gmail.com

ABSTRACT
Meat is a nutrient-rich food that supports microbial growth, making it a major vehicle for foodborne infections. This study assessed the bacterial contamination and antibiotic resistance profiles of cow (beef) and goat (chevon) meat sold at Obada Market, Ijebu-Igbo, Ogun State, Nigeria. Fresh meat samples from slaughterhouses and hawkers were analyzed using standard microbiological and molecular methods. Bacterial isolates were identified by Gram staining, biochemical characterization, and 16S rRNA gene sequencing. Antibiotic susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar following CLSI (2024) guidelines. Total bacterial counts ranged from 3.09×10^2 to 5.38×10^2 CFU/mL, with hawked meat showing higher contamination. Molecular identification revealed six bacterial species: *Bacillus thuringiensis*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Enterobacter asburiae*, *Klebsiella pneumoniae*, and *Citrobacter europaeus*. Antibiotic susceptibility tests showed high resistance to amoxicillin and augmenting, while gentamicin, pefloxacin, ofloxacin, and sparfloxacin were most effective. The findings suggest that meat sold in open markets harbors antibiotic-resistant bacteria due to poor hygiene and indiscriminate antibiotic use in livestock. Improved sanitary measures, responsible antibiotic use, and regular microbial surveillance are essential to safeguard public health.

Keywords: Antibiotic resistance, Bacterial contamination, Cow meat, Food safety, Goat meat,

1.0 Introduction

Meat is one of the food items that are rich in the nutrient matrix which provides a suitable environment for the proliferation of spoilage microorganisms and common foodborne pathogens (Martín-Miguélez *et al*., 2025). The most common source of bacterial diarrheal diseases caused by meat chains are of animal origin and are connected to the environment, meat handlers/processors and the processing equipment (Chanziaras *et al*., 2014).

Meat and meat-based products are the common major reservoirs for microorganisms, among the food types investigated. Meat consists of different portions of proteins (19%), fat (2.5%), and carbohydrates (1.2%), a great fraction of water in the muscle cells (75%), and nitrogenous compounds (1.65%). Hence, it contains a good source of numerous nutrients and presents as an appropriate medium for the growth of microorganisms due to its water activity and optimum pH (Chanziaras *et al*., 2014).

Livestock such as goat and cattle are widely produced around the world, primarily for food consumption and financial gain (Milford *et al*., 2019). There is a global increase in the consumption of meat. However, its consumption shows disparities from country to country, and this is strongly linked to disposable income (Milford *et al*., 2019). The increased consumption of meat products offers an increased risk of exposure to pathogens of animal origin (Szejda *et al*., 2021).

In addition, intense production usually culminates in increases in animal wastes, huge consumption of antibiotics, overcrowding on farms, and increases in greenhouse gas emissions (climate change), causing environmental degradation as well as the release of antibiotics and antibiotic resistance genes into soil and water, which in turn promotes the development and the dispersal of pathogens resistant to antibiotics plus their resistance genes (ecological effects) (Gonzalez *et al*., 2020). As observed by Wei-wei *et al*. (2018), exposure during sales could result in contamination by a wide range of bacteria. The poor hygienic situation of markets in developing countries like Nigeria could expose meat to bacteria including *Staphylococcus* spp, *Bacillus* spp, *Vibrio* spp, *Salmonella* spp and *Listeria* spp. These organisms affect the quality of meat and are potentially harmful to humans, the consumer (Wei-wei *et al*., 2018).

In Nigeria, the agricultural sector uses up to 50% of antibiotics in farm animals for treatment and prevention of diseases and the promotion of animal health (Manyi-Loh *et al*., 2018). In many of these, however, there is neither strict regulation on antibiotic

usage nor monitoring of contamination in food derived from animals thus leading to inadequate information on the looming menace (Manyi-Loh *et al*., 2018). The continuous and indiscriminate use of antibiotics has led to the adaptation of microorganisms to antimicrobial agents (Knoppel *et al*., 2017).

This adaptation has become successful over the last decades and it has become almost impossible to treat certain bacterial infections with antibiotics. Antibiotic resistance has been attributed to several factors. These include the abuse/ misuse of antibiotics, counterfeit/fake antibiotics and the indiscriminate use of alternative medicine/herbs (Dadgostar, 2019). The above factors and the indiscriminate use of antibiotics in livestock have culminated in the antibiotic resistance pandemic (Manyi-Loh *et al*., 2018).

Furthermore, microorganisms and their resistant strains travel fast and wide around the globe, this has further complicated the issue of antibiotics resistance as the movement of people from one region to another can transfer such genes nationally and internationally (Fair & Tor, 2014). Global food distribution also plays a role in the movement of resistant bacteria (Founou *et al*., 2016).

In addition, human consumption of meat contaminated with microbes results in public health implications, causing huge illnesses or even deaths (Zerabruk *et al*., 2019). Above all, the most staggering and challenging situation is that contaminated meat can carry antimicrobial-resistant pathogens and can seriously endanger human health.

This study isolated, identified and determined the antimicrobial susceptibility of microorganisms isolated from cow meat and goat meat to conventional antibiotics.

2.0 Materials and Methods

The meat samples (beef and chevon) were purchased from the slaughter house and hawkers at Obada Market in Ijebu Igbo (6°58′19″ N, 3°59′58″ E). Freshly butchered meat sample was aseptically collected in polypropylene specimen containers and were kept in ice bag and transported to Microbiology Laboratory of Abraham Adesanya Polytechnic, Ijebu-Igbo, Ogun state, Nigeria for processing and analysis. The samples were aseptically cut into thin smaller pieces using sterile knife. The analytical portions were placed in separate sterile plastic bags to which 250 ml of buffered peptone water was added and was shaken vigorously.

Culturing and Sub-culturing

The sample reinstate was cultured on MacConkey agar, Eosin Methylene Blue (Emb) agar, Salmonella-Shigella (SS) Agar, Centrimide agar and Deoxycholate (DCA) agar and then incubated at 37ºc for 24 hours (Smith *et al*., 2023).

Identification of the isolates

The isolates were identified by Gram staining reaction, morphologies, biochemical tests (catalase, coagulase, indole, mannitol, hemolysis, centrimide, eosin methylene blue and salmonella shigella tests) as described by (Nabil *et al*., 2020).

Molecular Characterization

The genomic DNA extracted was isolated using the methodology outlined in the Quick-DNA™ miniprep plus kit (Zymo research, Biolab, USA). Briefly; 200 µl of bio fluid (yellow) was added to 1.5 ml micro tube containing 200 µl bacterial cultures. The solution was vortexed and incubated for 100°C for ten minutes. An equal volume of Genomic Binding Buffer (200 µl) was added to the digested samples and thoroughly vortex for 10-15 s. The mixtures were transferred to a Zymo-Spin™ IIC-XLR Column in collection tubes and centrifuged at ≥ 12,000 r.p.m. The collection tubes with the flow through were discarded. DNA Pre-Wash Buffer of 400 µl was added to the spin columns in a new collection tube and centrifuged at ≥ 12,000 r.p.m. Exactly 700 µl g-DNA Wash Buffer was added to the spin columns and centrifuged at ≥ 12,000 r.p.m. The collection tubes were discarded. g-DNA wash buffer of 200 µl was added to the spin columns and Centrifuge at ≥ 12,000 r.p.m. The collection tubes with the flow were discarded. The spin columns were transferred to a clean micro tube and exactly 50 µl of DNA elution buffer was added directly on the matrix. It was incubated for 5 min at room temperature, then centrifuged at maximum speed for 1 min to elude the DNA. The eluted DNA was used immediately for molecular-based applications. Prior to PCR amplification, the quality of the DNA was checked using a 1.5% agarose gel electrophoresis.

PCR and Sequencing

The DNA was amplified by PCR with the primers ITS1 (5'- TCCGTAGGTGAACCTGCGG -3') and ITS4 (5'- TCCTCCGCTTATTGATATGC -3'). PCR cocktail contained 25 µL, containing; 12 µL Master Mix (Dongsheng Biotech, China), 1 µL template DNA, 10 µL sterilized distilled water and 1 µL of each primer. The cycling conditions were initial denaturation at 95 °C/ 5 min, followed by 30 cycles of denaturation at 94 ºC/30 s, annealing at 50 °C/ 30 s and extension at 72°C/ 30s and a final extension step at 72°C/5 min. The amplicons were resolved in 1.5%

agarose gel stained with 0.1 µg/mL ethidium bromide. The amplicons were submitted for sequencing at on a commercial basis, the amplicons were purified as well as sequenced using the Sanger sequencing technique. Standard techniques were used to perform unidirectional sequence reads, and were trimmed using the BioEdit (version 7.2.5.0) sequence tool. ABI PRISM Big Dye Terminator cycle sequencer (Macrogen, USA) was used to sequence 518F and 800R primers from PCR products obtained from the entire community and genomic DNAs. The obtained gene sequences were compared by using the National Centre for Biotech Information's Basic Local Alignment Search Tool (BLAST) search program to align the result with the sequences in Gene Bank.

Antibacterial Susceptibility Test

Antibiotic susceptibility profile of the isolates was determined by the agar disk diffusion method, also known as the Kirby-Bauer method, as described by Olawuyi *et al*. (2024) using Mueller Hinton agar. The following antibiotics (Abtek): Ciprofloxacin, Amoxicillin, Augmentin, Gentamicin, Pefloxacin, Ofloxacin, Streptomycin, Septrin, Sparfloxacin were employed. Inoculum (0.5 ml), turbidity matched that of 0.5 McFarland standard, was introduced on the surface of the agar plate with a sterile micropipette and evenly spread over using a sterile swab stick. The antibiotic disks were placed on the inoculated agar using sterile forceps. The plates were incubated at 37º C for 24 hours, readings were taken with a meter rule in millimeters. The diameter zones were recorded as sensitive, intermediate or resistant using CLSI standard interpretative chart as a guide (CLSI, 2024).

Statistical Analysis

Data generated were analyzed using descriptive statistics (using percentage values) for graph plotting on IBM SPSS and Microsoft Excel.

3.0 Results

Bacteria species isolated from the cow and goat meat samples from slaughter table shows total bacterial count of 3.48 x 10^2cfu/ml and 3.09 x 10^2cfu/ml while samples obtained from hawkers recorded total bacterial count of 5.38 x 10^2cfu/ml and 4.52 x 10^2cfu/ml respectively. The result shows that beef and chevon meat samples from the hawkers had higher bacterial count than the one from the slaughter house which could be due to prolong exposure, poor storage and more handling (Figure 1).

PCR amplification of the target gene was confirmed by agarose gel electrophoresis (Figure 2). The molecular weight marker (lane M) was included to estimate fragment sizes, with the 500 bp band serving as a reference. A distinct DNA fragment of approximately 466 bp was consistently observed in all tested isolates (lanes 1–10). The uniform presence of a single band of the expected size across all samples indicates successful and specific amplification of the target sequence. No additional nonspecific amplification products or primer-dimer formations were detected, confirming the reliability and specificity of the PCR assay.

Molecular identification of the bacterial isolates was carried out using partial sequencing of the 16S rRNA gene, followed by BLAST analysis against the NCBI GenBank database. The phylogenetic tree (Figure 3) illustrates the evolutionary relationships between the isolates and reference sequences.

Sequence alignment revealed that the isolates clustered with different genera, including *Bacillus, Pseudomonas, Enterobacter, Klebsiella,* and *Citrobacter*. The percentage sequence similarities with their closest GenBank matches ranged from 96.2% to 100%, confirming the identity of most isolates at the species level (Table 1).

The antibiotic susceptibility profile (Figure 4, Table 2) revealed variable responses of the bacterial isolates to the tested antimicrobial agents. Ciprofloxacin (CPX) demonstrated a balanced distribution, with approximately 50% of the isolates susceptible, while the remainder were intermediate or resistant. Amoxicillin (AM) exhibited no susceptibility, as all isolates were either intermediate or resistant, indicating very poor efficacy. Augmentin (AU) and streptomycin (S) showed moderate activity, with nearly half of the isolates resistant and the rest susceptible. Gentamicin (CN) and Pefloxacin (PEF) were highly effective, as more than 80% of the isolates were susceptible. Ofloxacin (OFX), cotrimoxazole (SRT), chloramphenicol (CT), and sparfloxacin (SP) also displayed strong activity, with the majority of isolates susceptible and resistance rates ranging between 20–35%.

Overall, gentamicin, pefloxacin, ofloxacin, and sparfloxacin emerged as the most effective agents, while amoxicillin exhibited the least activity. These findings highlight the high level of resistance against commonly used β-lactam antibiotics and underscore the therapeutic importance of fluoroquinolones and aminoglycosides in managing infections caused by these isolates.

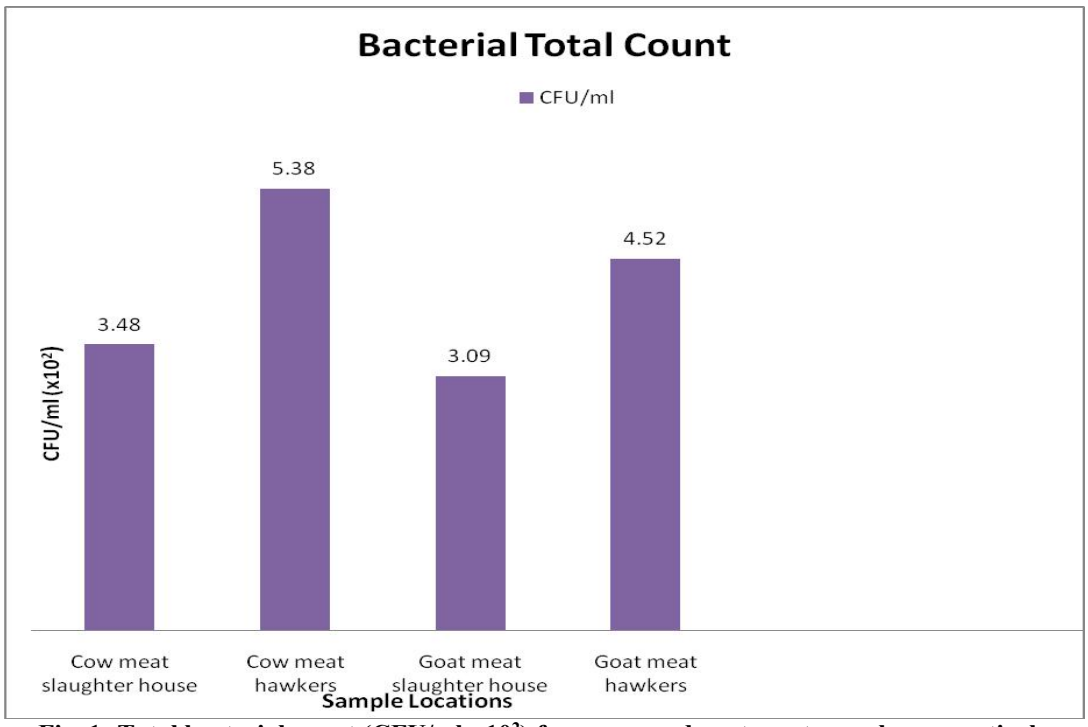


Fig. 1: Total bacterial count (CFU/ml $\times 10^2$) from cow and goat meat samples respectively

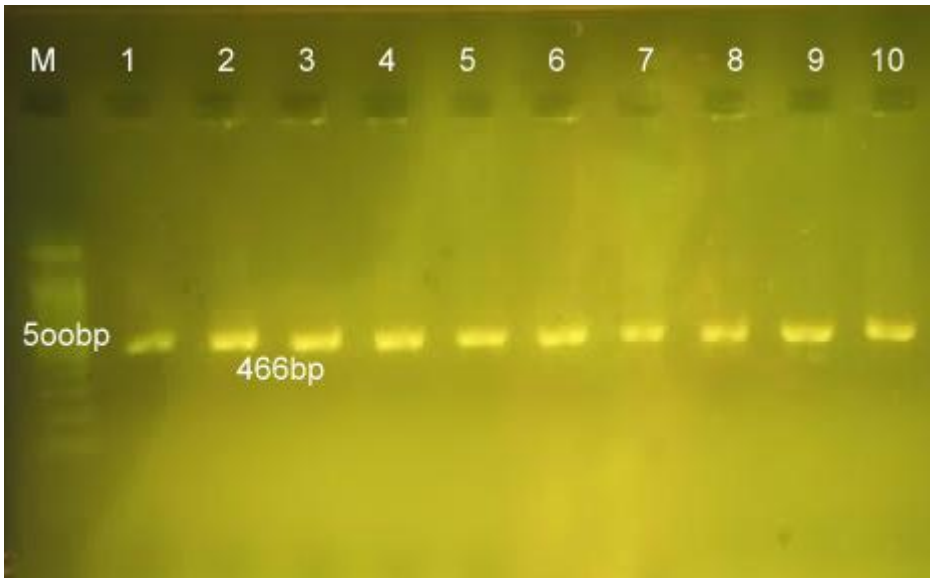


Fig. 2: Gel Electrophoresis of Isolated Bacteria

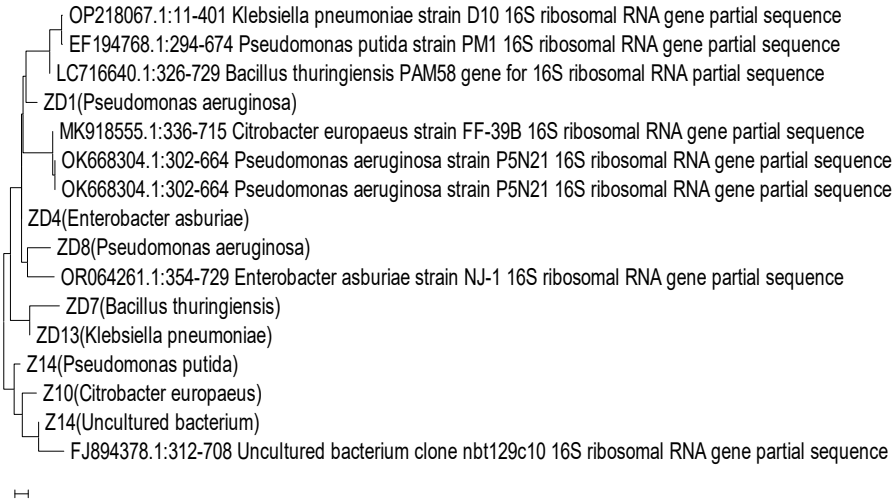


Fig. 3: Phylogenetic Tree Based on 16S rRNA Gene Sequences of Bacterial Isolates from Cow and Goat Meat Samples

Table 1: Molecular identification of bacterial isolates based on gene sequencing

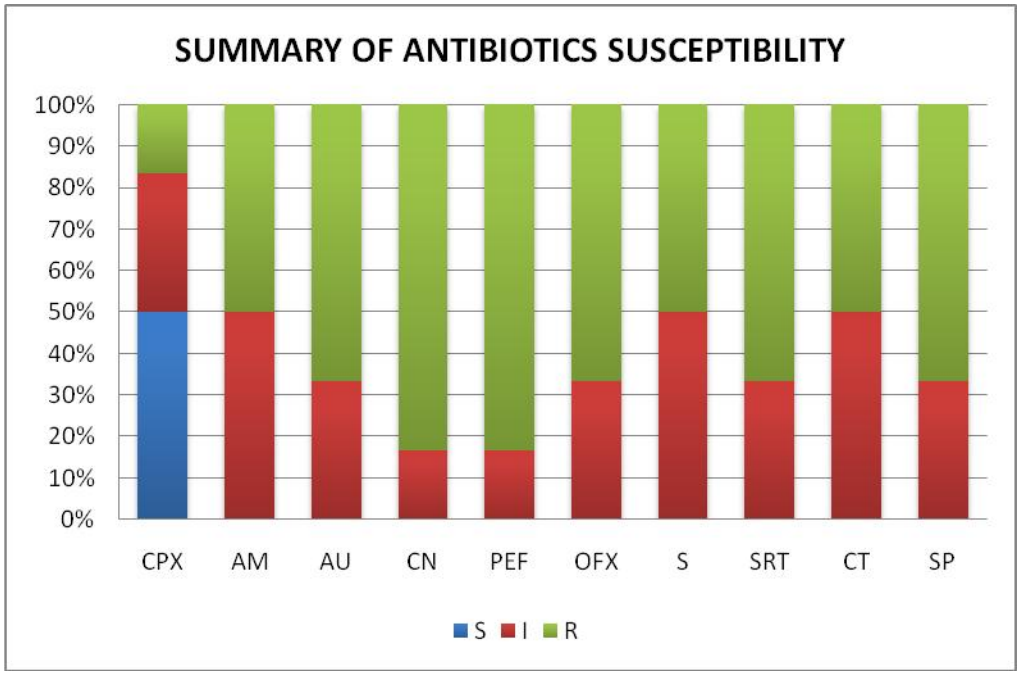
SN	Sample ID	Closest match (NCBI BLAST)	GenBank accession no.	% Similarity
1	ZD7	*Bacillus thuringiensis*	LC716640.1	99.3%
2	ZD8	*Pseudomonas aeruginosa*	OK668304.1	100%
3	ZD1	*Pseudomonas aeruginosa*	OK668304.1	100%
4	ZD4	*Enterobacter asburiae*	OR064261.1	99.7%
5	ZD13	*Klebsiella pneumoniae*	OP218067.1	99.8%
6	ZD10	*Citrobacter europaeus*	MK918555.1	99.5%
7	ZD15	*Pseudomonas putida*	EF194768.1	99.6%

Table 2: Zones of inhibition of the standard antibiotics against the isolates

Isolates	CLSI (mm) S= ≥21 I= 16–20 R= ≤15	CPX (mm)	AM (mm)	AU (mm)	CN (mm)	PEF (mm)	OFX (mm)	S (mm)	SRT (mm)	CT (mm)	SP (mm)
ZD4		22	10	10	18	10	10	10	10	10	18
ZD7		23	19	16	13	14	15	20	20	16	16
ZD8		18	18	16	15	20	14	16	18	19	14
ZD10		15	18	10	10	10	17	13	10	10	10
ZD13		20	10	10	10	10	10	10	10	10	10
ZD15		23	19	15	10	11	17	17	15	16	15

ZD4- *Enterobacter asburiae,* **ZD7**- *Bacillus thuringiensis*, **ZD8-** *Pseudomonas aeruginosa*, **ZD10-** *Citrobacter europaeus*, **ZD13-** *Klebsiella pneumonia*, **ZD15-** *Pseudomonas putida*, **CPX-** Ciprofloxacin, AM= Amoxicillin, AU= Augmentin, **CN-** Gentamicin, **PEF-** Pefloxacin, **OFX-** Ofloxacin, **S-** Streptomycin, **SRT-** Septrin, **SP-** Sparfloxacin, **CT-** Clotrimoxazole **CLSI**- Clinical and Laboratory Standards Institute, **S**- Sensitive, **I**-Intermediate, **R**- Resistant.

.



Keys: S- Sensitive, I- Intermediate, R- Resistant, CPX- Ciprofloxacin, AM- Amoxicillin, AU- Augumentin, CN- Gentamycin, PEF- Perfloxacin, OFX- Ofloxacin, S- Streptomycin, SRT- Septrin, CT- Clotrimoxazole, SP- Sparfloxacin.

Fig. 4: Summary of Antibiotics Susceptibility

4.0 Discussion

From the study, both cow (beef) and goat (chevon) meat samples harbored diverse bacterial species, including *Bacillus thuringiensis*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Enterobacter asburiae*, *Klebsiella pneumoniae*, and *Citrobacter europaeus*. These findings indicate that meat sold at both slaughterhouses and by hawkers can serve as potential reservoirs of pathogenic and spoilage microorganisms. The higher bacterial counts obtained from hawked meat compared to those from the slaughterhouse suggest post-slaughter contamination due to poor handling, exposure to dust and flies, and lack of refrigeration, conditions commonly reported in open markets in Nigeria and other developing countries (Wei-wei *et al*., 2018; Zerabruk *et al*., 2019).

The isolation of *Pseudomonas*, *Enterobacter*, *Klebsiella*, and *Citrobacter* species agrees with earlier reports that these organisms are commonly associated with meat spoilage and foodborne infections (Szejda *et al.,* 2021; Founou *et al.,* 2016). *Pseudomonas* spp., in particular, are known psychrotrophic bacteria capable of growing at low temperatures and contributing to meat spoilage even under refrigeration (Martín-Miguélez *et al.,* 2025). Similarly, *Enterobacter* and *Klebsiella* species are coliforms indicative of fecal contamination, which may originate from animal intestines, water, or equipment used during processing (Chanziaras *et al.,* 2014). The presence of *Bacillus thuringiensis*, though primarily considered non-pathogenic, could also point to environmental contamination since members of this genus are spore-formers that persist in soil and dust.

The molecular identification results further confirmed the reliability of conventional techniques in characterizing bacterial isolates from meat samples. The sequence similarities (96.2–100%) and clear clustering on the phylogenetic tree shows the diversity of bacterial flora in the sampled meat and their evolutionary relationships with known pathogenic strains in the GenBank database.

The antibiotic susceptibility profile of the isolates revealed alarming resistance to several β-lactam antibiotics, particularly amoxicillin and augmentin, with all isolates showing either resistance or intermediate response. This finding is consistent with previous studies of (Manyi-Loh *et al.,* 2018; Dadgostar, 2019) who reported extensive β-lactam resistance among foodborne bacteria due to the uncontrolled use of antibiotics in livestock production. The high resistance to amoxicillin and augmentin suggests possible production of β-lactamase enzymes capable of inactivating these drugs (Knoppel *et al.,* 2017).

However, gentamicin, pefloxacin, ofloxacin, and sparfloxacin exhibited high activity against most isolates, with over 80% susceptibility observed. These antibiotics belong to the aminoglycoside and fluoroquinolone classes, which are known for their broad-spectrum efficacy and lower rates of resistance in environmental and foodborne bacteria (Fair and Tor, 2014). The intermediate resistance observed in some isolates to ciprofloxacin and streptomycin is noteworthy, as it signals the gradual emergence of multidrug-resistant (MDR) strains that could limit therapeutic options. The occurrence of such resistant isolates in food sources poses significant public health risks since these bacteria or their resistance genes can be transmitted to humans through consumption or handling of contaminated meat (Gonzalez *et al.,* 2020; Founou *et al.,* 2016).

The findings from this study have shown the role of meat as a potential vector in the dissemination of antimicrobial-resistant bacteria. The results align with reports that livestock farming and meat production systems are major contributors to the global spread of resistance determinants due to the overuse of antibiotics in animal husbandry (Manyi-Loh *et al*., 2018). This situation is a serious concern in developing nations where regulatory frameworks governing antibiotic use are weak or absent, and monitoring of residues or resistant organisms in food is rarely enforced.

The detection of resistant *Enterobacteriaceae* such as *Klebsiella* and *Enterobacter* in meat is particularly worrisome, as these bacteria are frequently implicated in hospital and community acquired infections. Their presence in food implies a possible route for transfer of resistance genes from environmental or animal sources to human pathogens via horizontal gene transfer mechanisms (Fair & Tor, 2014).

Overall, the study provides evidence that both cow and goat meats sold in local markets may harbour multidrug-resistant bacteria. Improving hygienic practices during slaughtering, handling, and marketing, coupled with strict regulation of antibiotic use in livestock production, is crucial to mitigating this threat. Regular microbial surveillance and antimicrobial resistance profiling of foodborne bacteria are also recommended to guide policy formulation and ensure food safety.

5.0 Conclusion

Results from the study has demonstrated that both cow and goat meats sold in the study area, are contaminated with various bacterial species, including *Pseudomonas*, *Enterobacter*, *Klebsiella*, *Citrobacter*, and *Bacillus*. The high bacterial load, particularly in meat obtained from hawkers, has revealed the role of poor handling, exposure to unhygienic environments, and lack of proper storage in microbial contamination. The molecular results confirmed the identity of these isolates, while the antibiotic susceptibility profile revealed widespread resistance to β-lactam antibiotics such as amoxicillin and augmentin, and relatively high susceptibility to gentamicin, pefloxacin, ofloxacin, and sparfloxacin.

These findings emphasize the need for strict hygiene measures during meat processing and marketing, as well as rational use of antibiotics in livestock production. Regular monitoring of antimicrobial resistance in foodborne bacteria should be implemented as part of national food safety and public health surveillance programs. Consumer awareness on the risks associated with the consumption of improperly handled meat is also essential. Ultimately, enforcing regulatory control over antibiotic use in animal farming will be a key strategy in mitigating the spread of antimicrobial-resistant pathogens through the food chain.

Acknowledgment

We wish to express our gratitude to God Almighty for seeing us through this study, and also appreciate the management and staff of Abraham Adesanya Polytechnic for providing a conducive environment for learning.

Conflict of Interest

There was no conflict of interest among the authors

References

Chanziaras, G., Miszczycha, S., & Bonnet, R. (2014). Microbiological contamination pathways in meat production and processing environments. *Food Control*, 35(1), 141–150. https://doi.org/10.1016/j.foodcont.2013.06.025

Clinical and Laboratory Standards Institute (CLSI). (2024). *Performance standards for antimicrobial susceptibility testing: 34th informational supplement (M100-S34)*. CLSI.

Dadgostar, P. (2019). Antimicrobial resistance: Implications and costs. *Infection and Drug Resistance*, 12, 3903–3910. https://doi.org/10.2147/IDR.S234610

Fair, R. J., & Tor, Y. (2014). Antibiotics and bacterial resistance in the 21st century. *Perspectives in Medicinal Chemistry*, 6, 25–64. https://doi.org/10.4137/PMC.S14459

Founou, L. L., Founou, R. C., & Essack, S. Y. (2016). Antibiotic resistance in the food chain: A developing country-perspective. *Frontiers in Microbiology*, 7, 1881. https://doi.org/10.3389/fmicb.2016.01881

Gonzalez, R. M., López, C. G., & Fernández, M. (2020). Environmental dissemination of antibiotic resistance genes from livestock farming: A review. *Science of the Total Environment*, 727, 138106. https://doi.org/10.1016/j.scitotenv.2020.138106

Knoppel, A., Nasvall, J., & Andersson, D. I. (2017). Evolution of antibiotic resistance without antibiotic exposure. *Antimicrobial Agents and Chemotherapy*, 61(11), e01495-17. https://doi.org/10.1128/AAC.01495-17

Manyi-Loh, C., Mamphweli, S., Meyer, E., & Okoh, A. (2018). Antibiotic use in agriculture and its consequential resistance in environmental sources: Potential public health implications. *Molecules*, 23(4), 795. https://doi.org/10.3390/molecules23040795

Martín-Miguélez, J., García-López, I., & Carballo, J. (2025). Microbial spoilage and safety concerns in meat and meat products: An updated review. *Meat Science*, 211, 109025. https://doi.org/10.1016/j.meatsci.2025.109025

Milford, A. B., Henchion, M., & Sørheim, O. (2019). Meat consumption: Trends and environmental impact. *Meat Science*, 154, 44–52. https://doi.org/10.1016/j.meatsci.2019.04.011

Nabil, M. M., El-Shafey, A. A., & Abd-El-Gawad, M. (2020). Bacteriological examination and identification of microorganisms isolated from meat and meat products. *Egyptian Journal of Microbiology*, 55(2), 165–176.

Olawuyi, S. T., Adebayo, O. O., & Olayinka, A. T. (2024). Antibiotic susceptibility pattern of bacterial isolates from ready-to-eat foods in Southwest Nigeria. *African Journal of Clinical Microbiology*, 23(1), 58–67.

Szejda, K., Hall, J., & Gouveia, J. (2021). Global patterns in meat consumption and associated foodborne disease burden. *Frontiers in Nutrition*, 8, 681745. https://doi.org/10.3389/fnut.2021.681745

Wei-wei, Z., Hong-mei, L., & Jian, W. (2018). Microbial contamination of meat in developing markets: Risk factors and control measures. *Journal of Food Protection*, 81(9), 1500–1508. https://doi.org/10.4315/0362-028X.JFP-18-050

Zerabruk, K., Retta, N., Muleta, D., & Tefera, G. (2019). Bacteriological quality and safety of raw meat from abattoirs and retail outlets in Ethiopia. *International Journal of Food Microbiology*, 290, 76–82. https://doi.org/10.1016/j.ijfoodmicro.2018.09.012