Prevalence and antibiotic characterisation of *Escherichia coli* and *Salmonella* spp recovered from meat and its derivatives sold in retail stores: A call for public health concern

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ABSTRACT

Background: Meat and meat products are a source of bacterial contamination. Antibiotic use in animal farming has provoked the generation of antibiotic resistance, which merits public health attention.

Objectives: To examine both processed and unprocessed meat products for the occurrence of *Escherichia coli* (*E. coli*) and *Salmonella* spp., added to characterising these bacterial isolates based on their sensitivity to common antibiotics. In addition, the MAR index was calculated for each isolate to indicate whether the isolates may originate from high-risk antibiotic-use environments.

Methodology: A total of 21 meat samples were procured from six (6) retail stores across Bloemfontein. *E. coli* and *Salmonella* spp. were isolated via selective growth on microbiological media and confirmed biochemically using catalase, oxidase and sugar fermentation (TSI) tests. The Kirby Bauer disc diffusion assay was performed to evaluate antibiotic sensitivity of the isolates. MAR was calculated for each isolate using the standard formula, a/b, and the isolates were categorised based on their level of resistance as either non-MDR, MDR or XDR.

Results: Overall, 57.14% of the meat samples were contaminated with both *E. coli* and *Salmonella* spp. In addition, the specific prevalence rates stood at 42.86% for *E. coli* and 33.33% for *Salmonella* spp. However, *E. coli* and

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Salmonella spp. affected 29.41% and 17.65%, respectively, of processed meat samples. A total of 47 isolates were confirmed as oxidase negative and catalase positive but with different reactions to the fermentation of sugars. Greatest resistance was demonstrated against penicillin at100% and 89.29% by *Salmonella* spp and *E. coli*, respectively while maximum sensitivity was shown to gentamicin by *E. coli* isolates at 42.86%. A simultaneous resistance action against 15 and 14 antibiotics by *Salmonella* spp. and *E. coli,* respectively, was the greatest. A total of 45 MAR phenotypes were recovered and 91.49% of the isolates showed MAR index > 0.2, revealing they may originate from a region exposed to the routine use of antibiotics. Isolates were categorised as both MDR (42.86% for *E. coli* and 47.37% for *Salmonella* spp) and XDR (46.43% for *E. coli* and 52.63% for *Salmonella* spp).

Practical implications: The occurrence of multiple drug resistance in foodborne pathogens provides the likelihood of transfer through the food chain to humans, leading to consequences affecting human and animal health, outcomes of therapy in clinical settings, as well as aggravating the issue of antimicrobial resistance in the environment, humans and animals. The data on bacterial contamination and antibiotic resistance (MDR and XDR) can express implications for retail management

Keywords: Antimicrobial resistance; *Escherichia coli*; *Salmonella* spp; meat products; multidrug resistance (MDR); extensively drug-resistant (XDR); foodborne pathogens; food safety

1. INTRODUCTION

In South Africa, animal production is the largest agricultural sector, with poultry farming presenting as the largest agricultural industry. Tobias-Mamina et al. (2025) narrated that population growth, increased income, and urbanisation in the country has resulted in high meat consumption. South Africa is amongst the countries contributing to the increase in the total global consumption of meat. In response to the increased demand for meat products by the population, farmers drift toward intensive farming involving huge quantities of antimicrobials for growth promotion, disease control and prevention as well as for the treatment of diagnosed infections in the increased number of food-producing animals (Odey et al. 2024). This is done to increase productivity and reduce the costs of livestock production but results in greater profits or earnings (Trinchera et al. 2025). Patel and colleagues (2020) reported that the extensive use of antimicrobials on concentrated farms provoked the development of antibiotic-resistant microbes in food-producing animals. Moreover, Ndlela and Murcott (2021) argued that the processes engaged in the mass production of meat are damaging to humans and the environment. Unsafe food, including meat contaminated by microbes and associated antimicrobial resistance, poses a substantial threat to public health worldwide, and more so in Africa, because of inadequate food safety systems.

Food contamination can take place at any stage of the supply chain, and poor food handling practices by food handlers play a key role in worsening the problem (Machado-Moreira et al. 2019). Diverse microorganisms have been isolated from food that were implicated in the outbreak of foodborne infections in the different regions of the world. However, enteric bacteria are often implicated as the primary cause of foodborne infections, and they are abundantly found in both environmental and faecal matter samples (World Health Organisation 2017). Infections caused by foodborne pathogens are of great public health concern globally and have extensive economic consequences (Ronald et al. 2023).

Zoonotic bacteria, e.g., *Salmonella enterica* serovars *Enteritidis* and *Typhimurium* and the pathotypes of *E. coli* are regarded as the primary causes of foodborne diseases. *Salmonella* spp and *E. coli* are the two most important foodborne pathogens of public health concern. *E. coli* is a Gram-negative, facultative and non-spore-forming bacterium, living as a natural commensal (harmless) in the intestinal tract of humans and warm-blooded animals. Gulel et al. (2026) highlighted that meat products may become contaminated by faecal material during slaughter and processing or through environmental sources and handling practices. Hence, *E. coli* is regarded both as an indicator organism and an important food-borne pathogen associated with meat and meat-derived products (Adeyanju and Ishola 2014). Miranda and colleagues (2008) mentioned that this organism acquires antimicrobial resistance faster relative to other bacteria, and some strains have acquired virulence factors enabling them to cause diseases, projecting them as important zoonotic foodborne pathogens. Getaneh et al. (2021) remarked that *E. coli* is responsible for a great fraction of bacterial foodborne outbreaks globally. Raw or undercooked meat products, particularly minced meat, play a key role in the transmission of pathogenic *E. coli* strains to humans.

On the other hand, *Salmonella* spp are the most pathogenic microorganisms incriminated in bacterial food poisoning (Panisello et al. 2000). Globally, the bacterium remains among the most important zoonotic pathogens, associated with a huge disease burden in low- and middle-income countries (Nyanja et al. 2026). The classification of fluoroquinolone-resistant *Salmonella typhi* and fluoroquinolone-resistant non-typhoidal *Salmonella* in the high-priority tier of the WHO Bacterial Priority Pathogens List 2024 highlights the public health importance of resistant *Salmonella* infections and the growing limitations in treatment options (World Health Organisation, 2024). The clinical relevance of the organism, alongside its role in AMR surveillance within One Health framework, is the drive for continuous investigation into the bacterium. The heightened prevalence of foodborne illnesses has provoked farmers' response to the use of antimicrobials not only in treating infection but also, as growth promoters and in managing animal diseases in livestock. Other farmers do employ antibiotics for prophylaxis or metaphylaxis. O'Neill (2016) noted that bacterial pathogens, including *Salmonella spp* and *E. coli* contaminating food, have developed resistance to antibiotics that were once effective. The imprudent use of antimicrobials, which are easily accessible over the counter as promulgated by the stock remedies act of South Africa (Department of Health, 2014-2024) has worsened the development and distribution of antimicrobial resistance (AMR).

Clearly, Velazquez-Meza et al. (2022) reported that such a practice did facilitate the emergence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) *E. coli* and *Salmonella* spp. strains, complicating treatment options and heightening the risk of disease outcomes. The World Health Organisation (2022) emphasised the high and rising antimicrobial resistance of *E. coli* and *Salmonella* spp. The distribution of AMR bacteria throughout the food production chain is a significant global public health and food safety concern (Ayukekbong et al. 2017). The outcomes of increased AMR levels can include challenges in treating infections, leading to documented treatment failures, adverse side effects of drugs on patients, non-compliance with treatment and increased cost of health care (Manyi-Loh and Lues 2023).

Recently, AMR has emerged majorly as a global public health menace, threatening the effectiveness of antimicrobial agents that are employed in both the clinical and agricultural settings. Based on its widespread distribution and its ability to acquire and transfer resistance determinants through mobile genetic elements, *E. coli* is considered a key indicator organism for AMR surveillance (Nyanja et al. 2026). Apparently, hotspots for antimicrobial resistance are not only confined to clinical settings but have been extended to environmental areas influenced by human activities, including food value chains (Nelson et al. 2018). Therefore, having an in-depth understanding of the situation within the food chain in a particular region and country is imperative in addressing the threat of AMR. The reason the One

Health Approach emphasises that AMR in the environment cannot be secluded as it can possibly be transferred to other compartments, including humans, animals and food. Apparently, when bacteria develop resistance against many drugs, antibiotics lose their potency to treat and control diseases and infections (Jain et al. 2021). Therefore, the multiple antibiotic resistance (MAR) index is used to evaluate the risk of *E. coli* and *Salmonella* spp in regions with high antibiotic abuse rates (Isaiah et al. 2025). The MAR index is a practical tool that helps understand the broader impacts of antibiotic resistance spread (Woh et al. 2023). It employs a combination of measurements of antibiotic consumption and resistance of the pathogen to create a single metric that represents the level of drug resistance, thereby formulating the ratio of the number of resistant antibiotics to the total number of antibiotics that the microorganism is exposed to (Krumperman 1983).

Of great consideration is the fact that ready-to-eat (RTE) foods are gaining popularity because of their affordability and convenience for consumers; a situation occurring in sub-Saharan Africa and even in South Africa (Alimi 2016). In addition, the microbiological safety of meat and its derivatives in retail shops can be largely influenced by the slaughter process, sanitation during processing, maintaining of adequate cold chain upon storage from the processing level and to the consumer and lastly, sanitation during handling at the retail end (Borch and Arinder 2002). Investigating the microbiological quality and safety of meat and its products is of great concern to public health because foodborne pathogens are the leading cause of diseases and death in developing countries and the foodborne diseases result in significant consumption of health care resources and socio-economic losses.

Musuka and colleagues (2025) remarked that the beef sector is a vital sector for food security and livelihood in the Sub-Saharan African region, but antimicrobial resistance is a significant threat to humans, animals and public health. In South Africa, antibiotic resistance was reported in *E. coli* and *Salmonella* spp recovered from different sources, including animals (Moatshe et al. 2025). Literature is available on AMR profiles of *E. coli* and *Salmonella* spp recovered from many sources and provinces of the country, including meat samples from both formal and informal markets in the Eastern Cape (Jaja et al. 2020), raw beef and beef-based RTE products at retail outlets in Gauteng province (Onyeka et al. 2020), RTE chicken, wors, chicken gizzards, beef intestines, beef head meat at retail outlets in the North West province (Tshipamba et al. 2018), and lastly, chicken meat in the KwaZulu Natal Province (Zishiri et al. 2018). In the region (Bloemfontein), which occurs in the Mangaung Metropolitan municipality of the Free State Province, Moloi and co-authors (2021) noted the microbial contamination of meat products sold to consumers. However, the authors confirmed the presence of *Staphylococcus aureus* (*S. aureus*), *E. coli*, among others as contaminants, but the aspect of antimicrobial resistance was not a part of the study. Recently, Letuka and co-authors (2025) performed a susceptibility study on *S. aureus* recovered from RTE foods, including chicken, pork, salads, and pap (maize meal) to antibiotics, with no interest in *E. coli* and *Salmonella* spp or even RTE processed meat products. The authors revealed MDR in *S. aureus*, particularly to antibiotics such as penicillin, cefoxitin, and ciprofloxacin.

Kim et al. (2023) reported that the rapid and accurate detection of the emergence and spread of AMR in food animal production, is a key aspect of tackling AMR and requires routine AMR surveillance. Notwithstanding, surveillance of antibiotic resistance is one of the key parameters to contain antimicrobial resistance, and it is relevant from both clinical and environmental perspectives. Fourie et al. (2021) reported that *E. coli* was the most prevalent uropathogen causing community- acquired urinary tract infections in the population of the greater Bloemfontein area. Also, it is evident that the source of the bacteria (often in communities) as well as the type of bacterial strain can influence antimicrobial resistance. Therefore, a bacterial strain evolves over time, and its susceptibility pattern is most likely subjected to change (Bottery et al. 2021). Against this background, this study was conducted to assess the prevalence of *E. coli* and *Salmonella* spp belonging to the group Enterobacteriaceae as well as recovered from meat and its derivatives

procured from retail stores in the Bloemfontein region, Free State Province, South Africa, as well as to determine the antibiotic susceptibility patterns of these bacterial species to update the trend on antibiotic resistance of both bacteria in the region. Thus, informing public health strategies in terms of prescriptions and food safety practices.

2. MATERIALS AND METHODS

2.1. FOOD SAMPLE COLLECTION

A total of 21 meat samples, consisting of unprocessed (minced meat, n=4) and processed meat samples (ready-to-eat meat products such as polony, meat spreads and ham, n=17), were procured from six (6) retail stores found across the Bloemfontein area. All the stores sell directly to the consumer population. The RTE meat derivatives included a variety of polony, chopped ham roll, and liver spread, which did not require cooking or heating before eating following their purchase. The meat samples were immediately transferred into a cooler box containing ice packs to maintain the cold chain upon transporting the food samples to the laboratory at the Centre of Applied Food Sustainability and Biotechnology (CAFSaB), Central University of Technology, Bloemfontein, for microbial analysis.

A convenience sampling was employed considering the accessibility of the shops and availability of the meat products. In detail, the proximity of the stores (strategic location) to the university where laboratory bioassays were conducted added to the availability of the meat products based on consumer patronage, was greatly considered in choosing the retail stores and meat products for microbial analysis (Igbinosa et al. 2023). However, part of the limitations of our sampling method is that the findings cannot be generalisable to a greater proportion of all the retail stores and unprocessed and processed meat products circulating in Bloemfontein City. Bloemfontein city consists of several locations harbouring several retail stores. Nevertheless, the findings obtained cannot be extrapolated to include all the unprocessed and processed meat products available in this study, because the sample did not reflect the true diversity of all the retail stores as well as the meat products (both processed and unprocessed (Setia 2016).

2.2. ISOLATION AND IDENTIFICATION OF FOODBORNE BACTERIAL PATHOGENS

The meat samples were assigned codes using the letters of the alphabet (A-Z), according to Moges et al. (2024). Samples were enriched by transferring 25g of each sample into sterile McCartney bottles containing 225mL of 0.1% sterile buffered peptone water (NEOGEN, Heywood, UK). The mixture in each bottle was vortexed to ensure homogenisation at moderate speed and subsequently incubated overnight at 37 ^{o}C for growth of bacteria as per the procedure of Sodagari et al. (2015).

Following enrichment, selective growth of both *E. coli* and *Salmonella* species was performed on Harlequin *E. coli* /Coliform agar (HECA, NEOGEN, Heywood, UK) and *Salmonella Shigella* agar (SSA, Condalab, Madrid, Spain), respectively. A loopful of the overnight bacterial culture in each bottle was streaked onto solidified agar plates while observing aseptic technique. The inoculated plates were incubated at 37 ^{o}C for 18 - 24 h for the growth of *Enterobacteriaceae.* The growth of *E. coli* on HECA appeared as blue-green colonies, while smooth, opaque, colourless or black-centred colonies represented the growth of *Salmonella* spp on SSA.

2.3. BIOCHEMICAL CHARACTERISATION OF E. COLI AND SALMONELLA SPP

Further isolation involved streaking characteristic colonies onto nutrient agar to ensure purity. The presumptively identified *E. coli* and *Salmonella* spp were further confirmed by subjecting the bacterial isolates to biochemical characterisation based on the utilisation of sugars and enzyme production such as catalase test (3% v/v hydrogen peroxide, Lasec (PTY) LTD, South Africa) and oxidase test (oxidase ® test strips, SIGMA-ALDRICH, Czech Republic).

The catalase test was performed using 3% v/v hydrogen peroxide solution (hydrogen peroxide, Lasec (Pty) LTD, South Africa) to ascertain the activity of the enzyme, degrading hydrogen peroxide compound to produce water and oxygen, releasing effervescence (bubbles) (Hafezi and Khamar 2024). Briefly, a small portion of growth was picked from a distinct colony and smeared on a sterile glass slide using a sterile inoculating loop. Onto the bacterial growth culture on the glass slide, a few drops of 3% v/v hydrogen peroxide solution were added and the content mixed. A positive catalase test showed effervescence, indicating the production of oxygen bubbles on the surface of the glass slide. The degree of production of effervescence varied with the isolates. The appearance of a few bubbles within 30 seconds indicated a weak reaction, while the presence of no bubbles represented a negative test.

The ability of bacteria to produce the enzyme cytochrome oxidase was determined by performing an oxidase test while using oxidase ® test strips (SIGMA-ALDRICH, Czech Republic). Prior to testing, the bottle containing the oxidase test strips was removed from the refrigerator and kept at room temperature. The oxidase test strips were placed in a sterile petri dish. A sterile inoculating loop was used to transfer pure culture from overnight bacterial growth onto a spot on the oxidase test strip by smearing. A positive test was represented by the development of a purple colouration on the spot, 5 to 10 secs following the smearing (Manyi-Loh et al. 2023). The absence of colouration later than 60 seconds was considered a negative reaction.

Testing the bacterial isolates for the fermentation of sugars was performed using the triple sugar iron (TSI) agar test (Mast Group, Merseyside, UK) while adopting the protocol outlined by Chala et al. (2025). The TSI agar was prepared following manufacturer's instructions and dispensed in small volumes into sterile McCartney bottles and sterilised by autoclaving at 121 ^{o}C for 15 mins. Following sterilisation, the bottles were placed in a slanted position, creating a butt and a slant in each bottle. Growth from a distinct colony of each purified isolate was picked using a sterile wire loop and streaked on the slant while stabbing the butt. Inoculated bottles were accurately labelled based on the isolates and incubated at 37 ^{o}C for 18 - 24 hours. Confirmed *E. coli* isolates were presented with yellow slants and butts with hydrogen gas production, while *Salmonella* spp appeared with pink slants and yellow butts with black colouration of hydrogen sulphide gas.

The confirmed oxidase negative bacterial isolates were further subcultured several times onto nutrient agar plates (NA; Condalab, Madrid, Spain) to obtain pure cultures. Growth from each pure culture was transferred into tryptone soy broth +15% glycerol medium (Basingstoke, England) contained in sterile vials and stored at -80 ^{o}C for preservation and further bioassays.

2.4. ANTIBIOTIC SUSCEPTIBILITY TESTING

The Kirby-Bauer disc diffusion protocol was adopted to examine the antibiotic susceptibility of the confirmed pathogenic bacterial isolates (Mumbo et al. 2023). Mueller Hinton agar (MHA, Condalab, Madrid, Spain) was employed in the sensitivity assessment using disc diffusion. The purified and stored isolates of both *E. coli* and *Salmonella* spp were resuscitated by subculturing on nutrient agar (NA, Condalab, Madrid, Spain) plates and incubated at 37 ^{o}C for 16 -18h. Under aseptic conditions, 3-5 distinct colonies of the overnight growth culture on nutrient agar plates were

transferred using a sterile inoculating loop into 2mL of 0.9% physiological saline (RADCHEM (PTY) LTD) contained in sterile test tubes to produce inoculum of each isolate. Each mixture or inoculum was vortexed and its turbidity adjusted to correspond to the 0.5Mc Farland standard. The inoculum was used within 15 minutes following the adjustment of its turbidity. A sterile cotton swab stick was introduced deep into each inoculum and used to inoculate the surface of MHA plates (23 mL agar in 90mm petri dish, pH 7.2) by streaking while rotating the plate to ensure its entire surface receives a uniform or even distribution of each bacterial inoculum. The plates were left for some time to allow adherence of the bacterial cells to the surface of the agar.

A sterile forceps was used to introduce the antibiotic discs onto the surface of the inoculated agar plate, making sure the discs were placed equidistance from each other. A panel of seventeen (17) antibiotic discs, belonging to 8 different antibiotic classes (Davies Diagnostics, South Africa) that are commonly employed in both human and animal health were tested in this study. Antibiotics included: ceftazidime (CAZ, 30 µg), cefoperazone (CPZ, 75 µg), cefotaxime (CTX,30 µg), ciprofloxacin (CIP, 5 µg), Aztreonam (ATM,30 µg), trimethoprim-sulfamethoxazole (TS,23.75/1.25 µg), piperacillin (100 µg), amoxicillin/clavulanate, AUG (20/10 µg), penicillin (PG (10 µg), ampicillin (AP, 10 µg), ampicillin/sulbactam, SAM (10/10 µg), imipenem (IMI,10 µg), meropenem (MEM,10µg), tetracycline (T,30 µg) gentamicin (GM,10 µg), tobramycin (TN,30 µg), amikacin (AK,30 µg). The containers harbouring the discs were preserved following the manufacturer's instructions at 4 ^{o}C in the refrigerator but were taken out and allowed at room temperature prior to their use.

The bioassay was conducted in triplicates for each bacterial isolate. The triplicates were technical repeats of the same isolate. All the plates containing the pressed discs were incubated at 37 ^{o}C for 16 -18 h for the growth of the bacterial isolates while observing their response to the antibiotics, which appeared as zones of inhibition. The diameter of the zones of inhibition around each disc was measured in millimetres (mm) and the mean of the triplicates was recorded on the respective tables. The diameter of the zones of inhibition originating from the antimicrobial susceptibility testing were interpreted as susceptible (S), or Intermediate (I) or resistant (R) according to the guidelines set by the Clinical Laboratory Standards Institute (Clinical and Laboratory Standards Institute 2022). Multidrug resistance (MDR) was defined as resistance to at least one antibiotic agent in three or more different classes of antibiotics while isolates demonstrating non-susceptibility to ≥1 agent in all but ≤2 categories were termed extensively drug-resistant (XDR) (Magiorakos et al. 2012). As a positive control, *Escherichia coli* ATCC 25922 was evaluated alongside the test bacterial isolates.

2.5. DETERMINATION OF MULTIPLE ANTIBIOTIC RESISTANCE (MAR) INDEX

The multiple antimicrobial resistance (MAR) index was determined as described previously (Krumperman 1983). This involves using the formula, a/b, where "a" equals the number of antibiotics an isolate demonstrated resistance to, while "b" represents the total number of antibiotics tested in the study. MAR >0.2 registered by an isolate suggests that the bacterial isolate originates from a region or environment described as high-risk wherein there is frequent use or indiscriminate use of antibiotics.

2.6. STATISTICAL ANALYSIS

Data or measurements were computed into a spreadsheet using Microsoft Excel (Version 365). Data analysing was performed descriptively while employing Microsoft Excel to calculate the frequencies, means, and percentages of bacterial contamination and the prevalence of antibiotic resistance in the different bacterial pathogens. The study was aimed at providing an early descriptive overview; thus, no inferential statistical tests were conducted (Wibisono et al. 2026).

3. RESULTS

3.1. PREVALENCE OF E. COLI AND SALMONELLA SPP. IN THE MEAT PRODUCTS

A total of 21 meat samples were investigated, including 4 minced meats, 4 meat spreads and 13 polony. Overall, only eight (8) processed meat products and four (4) unprocessed meat products were positive for bacterial isolates, yielding a prevalence of 57.14% (12/21). Based on the presumptive identification of *E. coli* and *Salmonella* spp by growth on selective media (HECA and SSA), the identity of the isolates was confirmed following biochemical testing (catalase, oxidase test and sugar fermentation). The positive samples represented co-contamination by both organisms and were unique for either *E. coli* or *Salmonella* spp. In relation to the meat types, unprocessed and processed meat products registered prevalent rates of bacterial contamination of 100% and 47.06%, respectively. The prevalence of *E. coli* and *Salmonella* spp varied with the meat type. Based on the uneven number of samples collected in this study, we had only 4 samples categorised as unprocessed. All the unprocessed meat samples that were tested (n=4, minced meat) showed positive for bacterial contamination by both *E. coli and Salmonella* spp representing 100% contamination. This result was based on the number of the tested unprocessed samples (n=4), which most likely had affected the result or outcome. Therefore, the finding cannot be extrapolated to include all unprocessed meat samples around this study area. Contrarily, *E. coli* showed a slightly higher prevalence of 42.86% relative to 33.33% for *Salmonella* spp. in processed meat samples (n=17).

TABLE 1: PREVALENCE OF BACTERIA IN THE DIFFERENT MEAT PRODUCTS

Food samples	Samples positive for *E. coli*	Prevalence (%)	Samples positive for *Salmonella* spp.	Prevalence (%)
Unprocessed meat (minced) (n=4)	4[b]	(4/4) 100.00	4[b]	(4/4)100.00
Processed meat products (meat spread and polony) (n=17)	5[a]	(5/17) 29.41	3[c]	(3/17) 17.65
Total (N=21)_	9	(9/21) 42.86	7	(7/21) 33.33

'b', co-contaminated samples, i.e., positive samples that contained both organisms;
'a', positive samples unique for *E. coli*; 'c', positive samples unique for *Salmonella*

A total of 47 isolates were recovered (that is 28 *E. coli* and 19 *Salmonella* sp.) from the meat products analysed in this study (Table 2). Three or four colonies of different sizes (small, moderate, large), colour intensity, and morphology were picked from the four quadrants of a plate developed on each positive sample. The isolates were treated as individual isolates because they showed varying reactions in terms of the degree of effervescence produced in the catalase test, the intensity of the purple colouration in the oxidase test and their response to the different antibiotics tested, plus their MAR index values. Based on the specific meat products,13 and 34 bacterial isolates were obtained from processed and unprocessed meat products, respectively. Overall, of the 47 isolates recovered, *E. coli* was represented by 59.57% (28/47) while *Salmonella* spp stood at a fraction of 40.43% (19/47).

TABLE 2: NUMBER OF BACTERIAL ISOLATES RECOVERED BASED ON THE TYPE OF MEAT PRODUCTS

Different meat products (n=21)	Bacterial isolates		
	E. coli	*Salmonella* spp	Total
Processed meat (polony and meat spread)	10	3	13
Unprocessed meat products (minced meat)	18	16	34
Total	**28/47 (59.57%)**	**19/47 (40.43%)**	**47**

3.2. ANTIBIOTIC SUSCEPTIBILITY TESTING

The results of the antibiotic susceptibility test conducted on the bacterial isolates are presented in Table 3. Table 3 shows the percentage susceptibility and resistance of the different groups of bacteria to the commonly used antibiotics. Overall, the isolates differed in their level or degree of sensitivity to the different antibiotics, spanning from 5.26 (ciprofloxacin) to 42.86% (gentamicin) while the resistance rate occurred in the range of 28.57 to 100%. The highest susceptibility was performed toward gentamicin by *E. coli* isolates, while the highest resistance was displayed by *Salmonella* spp against penicillin at a rate of 100%.

With respect to the specific bacterial group, the susceptibility profile was in the increasing order of tetracycline and meropenem (15.79%) < tobramycin and cefotaxime (26.32%) < gentamicin and trimethoprim/sulfamethoxazole (31.58%) for *Salmonella* spp. For *E. coli*, we had aztreonam and trimethoprim/sulfamethoxazole (32.14%), < tetracycline (39.29%), < gentamicin (GM) (42.86%). In terms of resistance, *Salmonella* spp demonstrated resistance in the decreasing order: penicillin (100%) > amoxicillin/clavulanate (89.47%) > ampicillin, ampicillin/sulbactam, amikacin and ceftazidime (84.21%) while the resistance rate for *E. coli* occurred at penicillin (89.29%) > cefotaxime (82.14%) > ciprofloxacin and ceftazidime (75%). Low resistance to antibiotics by` *E. coli* and *Salmonella* spp occurred against tetracycline, gentamicin (28.57%) and cefotaxime (36.84%), respectively.

TABLE 3: PREVALENCE OF BACTERIAL ISOLATES RECOVERED FROM MEAT AND ITS PRODUCTS TO CONVENTIONAL ANTIBIOTICS

Antibiotic classes	Frequency of bacterial isolates responding to antibiotic susceptibility testing (%)					
	Salmonella isolates (n=19)			*Escherichia coli* isolates (n=28)		
Penicillins	**Susceptible (S)**	**Intermediate (I)**	**Resistant (R)**	**Susceptible (S)**	**Intermediate (I)**	**Resistant (R)**
Penicillin (PG, 10µg)	(0/19) 0.00	(0/19) 0.00	(19/19)100	(2/28) 7.14	(1/28)3.57	(25/28)89.29
Ampicillin (AP,10µg)	(0/19)0.00	(3/19) 15.79	(16/19) 84.21	(3)/28)10.71	(6/28)21.42	(19/28)67.86
Piperacillin (PRL,100 µg)	(2/19) 10.50	(4/19)21.05	(13/19) 68.42	(3/28)10.71	(11/28)39.29	(14/28) 50.00
Ampicillin/Sulbactam SAM, 10/10 µg)	(0/19) 0.00	(3/19) 15.79	(16/19) 84.21	(3/28) 10.71	(6/28) 21.43	(19/28) 67.86
Amoxicillin/clavulanate (AUG 20/10 µg)	(1/19) 5.26	(1/19) 5.26	(17/19) 89.47	(4/28) 14.29	(7/28) 25.00	(17/28) 60.71
Tetracyclines						
Tetracycline (T30 µg)	(3/19)15.79	(8/19) 42.11	(8/19) 42.11	(11/28) 39.29	(9/28) 32.14	(8/28) 28.57
Monobactams						
Aztreonam (ATM, 30 µg)	(2/19) 10.53	(5/19) 26.32	(12/19) 63.16	(9/28) 32.14	(5/28) 17.86	(14/28) 50.00

Antibiotic classes	Frequency of bacterial isolates responding to antibiotic susceptibility testing (%)					
	Salmonella isolates (n=19)			*Escherichia coli* isolates (n=28)		
Sulfonamides						
Sulfamethoxazole-Trimethoprim (TS, 23.75/1.25 µg)	(6/19) 31.58	(5/19) 26.32	(8/19) 42.11	(9/28) 32.14	(6/28) 21.43	(13/28) 46.43
Carbapenems						
Meropenem (MEM,10 µg)	(3/19)15.79	(7/19) 36.84	(9/19) 47.37	(3/28) 10.71	(15/28) 53.57	(10/28) 35.71
Imipenem (IMI, 10 µg)	(1/19) 5.26	(4/19) 21.05	(14/19) 73.68	(4/28) 14.29	(8/28) 28.57	(16/28) 57.14
Quinolones						
Ciprofloxacin (CIP, 5µg)	(1/19) 5.26	(9/19) 47.37	(9/19) 47.37	(3/28) 10.71	(4/28)14.21	(21/28) 75.00
Aminoglycosides						
Gentamicin (GM,10µg)	(6/19) 31.57	(3/19) 15.79	(10/19) 52.63	(12/28) 42.86	(8/28) 28.57	(8/28) 28.57
Tobramycin (TN, 30µg)	(5/19) 26.32	(1/19) 5.26	(13/19) 68.42	(8/28) 28.57	(7/28) 25.00	(13/28) 46.43
Amikacin (AK, 30 µg)	(1/19) 5.26	(2/19) 10.53	(16/19) 84.21	(4/28) 14.29	(11/28) 39.28	(13/28) 46.43
Cephalosporins						
Cefoperazone (CPZ, 75 µg)	(1/19) 5.26	(5/19) 26.31	(13/19) 68.42	(4/28) 14.29	(11/28) 39.29	(13/28) 46.43
Ceftazidime (CAZ,30µg)	(1/19) 5.26	(2/19) 10.53	(16/19) 84.21	(2/28) 7.14	(5/28) 17.86	(21/28) 75.00
Cefotaxime (CTX, 30µg)	(5/19) 26.32	(7/19) 36.84	(7/19) 36.84	(2/28) 7.14	(3/28) 10.71	(23/28) 82.14

3.3. DETERMINATION OF THE MULTIPLE ANTIBIOTIC RESISTANCE (MAR) INDICES AND MAR PATTERNS AMONG E. COLI AND SALMONELLA SPP. ISOLATES

The MAR indices for the bacterial isolates are presented in Table 4. Overall, the prevalence of both *E. coli* and *Salmonella* isolates with MAR indices above 0.2 (MAR > 0.2) was 91.49%. Based on the pathogens, MAR indices for *E. coli* isolates occurred in the range 0.12 to 0.82. Only one (1) *E. coli* isolate presented with an MAR index value < 0.2 while three isolates showed MAR=0.2. Contrarily, all the *Salmonella* spp had an MAR index value > 0.2, occurring in the range 0.41 to 0.88.

TABLE 4: MULTIPLE ANTIBIOTIC RESISTANCE INDICES FOR BACTERIAL ISOLATES

Bacterial groups	Range of MAR indices	Total number of bacterial isolates with MAR > 0.2	Percentages (%)
Salmonella sp. (n=19)	0.41 - 0.88	19	(19/19) 100
Escherichia coli (n=28)	0.12 - 0.82	24	(24/28) 85.71
Total (N=47)		**43/47 (91.49%)**	

MAR=0.2 is not automatically termed MDR because MAR and MDR measure entirely different criteria. MAR is purely a fraction, and an isolate can yield an MAR value of 0.2 without meeting the “3 separate antibiotic category” rule.

The MAR indices represented distributions in the different resistance categories of MDR and XDR (Table 5a). Detailed isolate-level phenotypes are presented as supplementary material (Table 5b). MAR>0.2 occurred in 85.71% of *E. coli* isolates. MDR indicating resistance to at least one antibiotic agent in three different antibiotic classes was

observed in 42.86% (12/28) of the fraction of the *E. coli* isolates, while three (3) isolates, presenting 10.71% of the isolates were categorised as non-MDR. While XDR occurred at 46.43% (13/28) demonstrating resistance to ≥ 1 antimicrobial agent, except for ≤ 2 antibiotic categories. Among the *E. coli* isolates, a wide range of MDR phenotypes (total of 26 patterns) was registered, suggesting extensive heterogeneity in the resistance profiles. The most common MAR phenotype was PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP, displayed by three (3) isolates, yielding a frequency of 10.71%. The highest resistance was displayed against 14 antibiotics by 5 isolates presented by the following MAR phenotypes: PRL, AUG, SAM, MEM, CIP, IMI, TS, AK, CAZ, CPZ, ATM, PG, CTX, AP; PRL, AUG, TN, SAM, CIP, IMI, TS, CAZ, CPZ, ATM, T, PG, CTX, AP, and PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP. Lower-level patterns, for example, PG, CTX; TN, CIP, AK and TN, T, PG were less frequent unlike the complex combinations.

All the *Salmonella* spp demonstrated resistance (100%) to multiple antibiotics. The bacterial isolates that exhibited resistance to ≥1 antimicrobial agent in ≥3 antimicrobial categories were found in 47.37% (9/19) of the fraction of the isolates while 52.63% (10/19) demonstrated resistance to ≥ 1 antimicrobial agent, except for ≤ 2 antibiotic categories. Thus, they are described as XDR. A total of 19 MAR phenotypes were recovered from *Salmonella* spp with lower-level resistance to seven (7) antibiotics presented by GM, AUG, SAM, IMI, PG, CTX, AP while a resistance displayed against 15 antibiotics as shown by CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, AK, PG, CTX, AP and CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, T, PG, CTX, AP was found in two (2) *Salmonella* spp.

TABLE 5a: CATEGORISATION OF BACTERIAL ISOLATES AS MDR AND XDR

Bacterial isolates	Number of Non MDR isolates	Number of MDR isolates	Number of XDR isolates	MAR phenotypes with highest frequency	Highest number of antibiotics involved in simultaneous resistance action
E. coli N=28	3/28 (10.71%)	12/28 (42.86%)	13/28 46.43%	3 isolates presented with PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP	14 antibiotics by 5 isolates 1.PRL, AUG, SAM, MEM, CIP, IMI, TS, AK, CAZ, CPZ, ATM, PG, CTX, AP 2. PRL, AUG, TN, SAM, CIP, IMI, TS, CAZ, CPZ, ATM, T, PG, CTX, AP 3. PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP
Salmonella spp. N=19	0 0%	9/19 47.36%	10/19 52.63%	0	antibiotics by 2 isolates 1.CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, AK, PG, CTX, AP 2. CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, T, PG, CTX, AP

4. DISCUSSION

Foodborne disease is a global menace that exerts an impact on food security and public health (Widodo et al. 2023). Foodborne pathogenic bacteria, including *Staphylococcus aureus*, *E. coli*, and *Salmonella* spp recovered from livestock and food products of animal origin have reportedly demonstrated resistance to various antibiotics. In this study, meat and its derivatives were evaluated for the occurrence of *E. coli* and *Salmonella* spp which were further examined for their resistance to commonly used antibiotics via phenotypic antibiotic characterisation. Based on the samples collected in this study, the level of bacterial contamination of the meat products (both the processed and the unprocessed) stood at 57.14%, but a 100% prevalence of bacterial contamination was associated with unprocessed (raw) meat as opposed to 47.06% for processed meat samples. Pal et al. (2018) affirmed that the level of microorganisms present in meat products can be decreased or minimised only when they are further processed (Jay et al. 2005). In addition, it can be

suggested that the disparity between the number of samples processed (n=17) and unprocessed (n=4) meat product can influence the recovery of isolates.

Although both raw and processed meat are susceptible to contamination by a wide variety of pathogenic microorganisms, including bacteria, viruses, and parasites, it is apparent that the bacterial load in raw meat could be high due to contamination of the animal's skin and gut during slaughtering (Pal et al. 2018). However, subjecting the meat to the process of grinding (minced meat), the meat mixes outer bacteria through the mixture, raising internal contamination. Contrarily, during the processing of meat to produce polony and spread among other products, the meat may receive chemical substances as preservatives and additives and may be subjected to high temperatures or heating, or boiling, smoking or curing. Thus, the high temperature and the chemical substances added, can kill some pathogenic vegetative cells found in the meat, thereby helping in the control of microorganisms in the meat products (De Silvestri et al. 2018). The findings of a higher prevalence of bacterial contamination of unprocessed meat than processed in this study is understood as Jay and colleagues (2005) affirmed that the level of microorganisms present in meat products can be reduced only when they are further processed.

A fraction of 42. 86% of the samples were contaminated by *E. coli* relative to 33.33% by *Salmonella* spp. This difference in the fraction of samples contaminated by the two pathogens could be the reason for the difference in the number of isolates recovered that belonged to each pathogenic group, 28 for *E. coli* and 19 for *Salmonella* spp represented by 59.57% and 40.43%, respectively. In addition, a prevalence of 29.41% of *E. coli* occurred in the unprocessed meat samples as opposed to 17.65% for *Salmonella* spp. The occurrence of *E. coli* may suggest faecal contamination throughout the food value chain. Contamination by *E. coli* could be attributed to the process of slaughtering of animals, unhygienic handling and unclean environmental conditions during the storage and processing of food (Effendi et al. 2018; Kendek et al. 2024). This finding is consistent with global reports, wherein *E. coli* is widely used as a sentinel indicator of hygienic failures in meat processing environments (Manyi-Loh and Lues 2023). In addition, the findings of *Salmonella* and *E. coli* in the meat samples corroborate with those of Uzeh et al. (2021) who recovered both bacterial pathogens alongside other members of the group *Enterobacteriaceae* from retail meat sold in Lagos, Nigeria. The authors affirmed that the members of the *Enterobacteriaceae* are considered useful indicators of food quality, hygiene and contamination.

Profiling of the antimicrobial susceptibility response of the bacterial isolates revealed varying levels of susceptibility and resistance to the tested antibiotics. The data are as presented in Table 3. The highest resistance was observed against penicillin by both the *Salmonella* spp and *E. coli* isolates in the magnitude of 100% and 89.29%, respectively. The findings corroborate with the high resistance to penicillins noted by Assoumy et al. (2021) in their study. Wibisono et al. (2025) affirmed that *E. coli* and *Salmonella* spp are becoming increasingly resistant to various antibiotics from year to year. Moreover, high resistance to amoxicillin/clavulanate (89.47%), ampicillin, ampicillin/sulbactam and ceftazidime (84.21%) was observed with *Salmonella* spp. while *E. coli* equally presented with high resistance to cefotaxime (82.14%), alongside ceftazidime and ciprofloxacin (75%). These findings, based on the phenotypic characterisation, suggest high resistance rates against penicillins and cephalosporins, belonging to the beta-lactam group. The high AMR rates among the *E. coli* and *Salmonella* spp reported in this study, appear worrisome because the tested antibiotics are not commonly used in animal farming or livestock production but employed as prescription in human therapy for the treatment of infections caused by enteric bacteria (Uzeh et al. 2021). Moreover, some of the antibiotics, including gentamicin, amikacin, amoxicillin/clavulanic acid, tetracyclines, ciprofloxacin, cefotaxime and trimethoprim/sulfamethoxazole are grouped as critically important antibacterials. Therefore, the observed resistance to these antibiotics in our study may pose significant emerging severe threats to public health and complicate effective

therapeutic management (Nyanja et al. 2026). The high resistance of *Salmonella* spp to ampicillin and ampicillin/sulbactam could be ascribed to the easy availability and relatively low cost, which may provoke their frequent use.

On the other hand, sensitivity of varying magnitude was equally observed among these bacterial isolates. Both groups of bacterial isolates demonstrated maximum sensitivity to common antibiotics, including gentamicin and trimethoprim/sulfamethoxazole at varying prevalence rates of 31.57% for *Salmonella* spp and 42.86% and 32.14% for *E. coli*, respectively. Clearly, the greatest sensitivity was observed with 42.86% of the *E. coli* isolates, representing the highest sensitivity to gentamicin in this study. Gentamicin, an aminoglycoside antibiotic, is a broad-spectrum drug, exhibiting its bactericidal activity by inhibiting protein synthesis in the 30S ribosomal subunit (Krause et al. 2016). In addition, 3 isolates of *E. coli* were described as non-MDR based on the definition of MDR stated by Magiorakos et al. (2012). Accordingly, 1 isolate demonstrated resistance to 2 antibiotics from two different classes, while the second isolate demonstrated resistance to 3 antibiotics that belonged to 2 different classes and the third isolate was resistant to 4 antibiotics, but these antibiotics fall under 2 different categories. Therefore, these three isolates did not satisfy the 3 separate classes rule. Even though only 1 isolate registered an MAR <0.2, this parameter measures a different criterion from MDR.

The multiple antibiotic resistance (MAR) indexing is a valuable tool that is used to evaluate the health threats associated with antimicrobial resistance in bacteria (Kathleen et al. 2016). In this study, the bacterial isolates demonstrated resistance to 2 and 15 antibiotics that were tested and resulted in MAR indices that ranged from 0.12 to 0.82 for *E. coli* isolates and 0.41 to 0.88 for *Salmonella* spp. Overall, the most frequent MAR values were 0.82 displayed by eight (8) isolates, followed by 0.71, 0.76, and 0.47 demonstrated by 7, 5, and 5 bacterial isolates, respectively. A total of 43 bacterial isolates, representing a fraction of 91.49%, showed MAR > 0.2. This may suggest that these isolates most probably originated from an environment in which antibiotics have been in frequent use or have been previously subjected to antibiotics. The MAR indices registered in this study appear contradictory to the MAR indices reported by Kasiwai and colleagues (2026) for *E. coli* and *Salmonella* spp which both occurred in the range of 0.43 to 1 in their raw beef samples obtained from abattoirs and retail shops in Nairobi, Kenya. The level of resistance in this study suggests the misuse or overuse of antibiotics in animal production. Therefore, the difference in the values could be ascribed to regional differences in antimicrobial use in terms of the type of antibiotics commonly used as well as the regulations governing the purchase and use of antimicrobials.

The widespread development of multidrug resistance is a growing concern among Gram-negative bacteria (Higgins 2007). Multi-drug resistance (MDR) was equally demonstrated by the bacterial pathogens. Ayukekbong et al. (2017) explained that the extensive occurrence of MDR in the environment is a direct aftermath of the random use and abuse of antimicrobials because these antimicrobials are easily bought over the counters without prescriptions from physicians or veterinarians. MDR indicating resistance to at least one antibiotic agent in three different antibiotic classes was observed with 42.86% *E. coli* and 47.37% *Salmonella* spp, suggesting that therapeutic options could be limited in the treatment of enteric infections caused by *E. coli* and *Salmonella* spp (Ahmed et al. 2024) Therefore, they are now of critical public health significance. The phenomenon, multidrug resistance, is prominent in *E. coli*, posing a significant threat to the population on a global level. In terms of antibiotic classes, as shown in Table 5b, the isolates exhibited forty-five (45) different resistance patterns (MAR phenotypes, i.e., 26 resistance patterns by *E. coli* and 19 resistance patterns by *Salmonella* spp). This showed a wide range of MAR phenotypes reflecting extensive heterogeneity in the resistance profiles. However, the highest resistance pattern was observed against eight (8) antibiotic classes shown by two (2) *Salmonella* isolates.

More elaborately, *E. coli* isolates demonstrated resistance to three (7.14%), to five (28.57%) and to seven (14.29%) antibiotic classes, although five (5) isolates demonstrated antibiotic resistance to fourteen (14) antibiotics of the seventeen tested, yielding three different MAR phenotypes, including PRL, AUG, SAM, MEM, CIP, IMI, TS, AK, CAZ, CPZ, ATM, PG, CTX, AP, PRL, AUG, TN, SAM, CIP, IMI, TS, CAZ, CPZ, ATM, T, PG, CTX, AP and PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP. The MAR phenotypes suggest a concurrent resistance to 14 antibiotics. On the other hand, *Salmonella* spp exhibited resistance to three (10.52%), to five (31.57%) and seven (21.05%) antibiotic classes, but 2 isolates exhibited resistance against fifteen (15) of the seventeen tested antibiotics, resulting in two (2) different MAR phenotypes such as CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, T, PG, CTX, AP and CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, AK, PG, CTX, AP. A simultaneous resistance action against 15 antibiotics calls for concern because of the likelihood of the dissemination of antibiotic resistance.

The predominance of complex resistance combinations, especially involving beta-lactams (cephalosporins and penicillins), aminoglycosides, tetracyclines, trimethoprim-sulfamethoxazole (Table 5b) may suggest sustained antimicrobial selection pressure within the meat continuum. Overall, the most common MAR phenotype was observed with three (3) *E. coli* isolates: PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP, spanning multiple major antibiotic classes that are commonly employed in livestock production systems. Moreover, some bacterial isolates (Table 5b) presented with resistance to nearly all the tested antibiotics, including carbapenems. In the present study, resistance to carbapenems occurred at 5.26% and 15.79% for *Salmonella* spp and 57.14% and 35.71% for *E. coli* against imipenem and meropenem, respectively. The carbapenems have been used to treat numerous *Enterobacteriaceae* infections. Thus, this might have facilitated a rapid growth in their resistance to the same. The rapid distribution of carbapenem resistant *Enterobacteriaceae* (CRE) in the community is a national epidemiologic concern, because *Enterobacteriaceae* are common causes of nosocomial and community infections (Mukuna et al. 2021).

TABLE 5b: MAR PHENOTYPES OF THE DIFFERENT BACTERIAL ISOLATES AND THE RESISTANCE CATEGORIES OF THE ISOLATES

Frequency of isolates (%)	MAR phenotypes	Antibiotic classes involved	Number of antimicrobials the isolates was resistant to	Number of antibiotics Classes the isolates were resistant to	Character of resistant strains
		***Salmonella* species (n=19)**			
1 (5.26)	GM, AUG, SAM, IMI, PG, CTX, AP	Aminoglycosides, penicillins, cephalosporins, carbapenems	7	4	MDR
1(5.26)	CAZ, GM, AUG, TN, SAM, AK, PG, CTX	Cephalosporins,aminoglycosides, penicillins	8	3	MDR
1(5.26)	ATM, CPZ, TN, IMI, CIP, T, PG, AP	Monobactams, cephalosporins, aminoglycosides, carbapenems, quinolones, tetracyclines, penicillins	8	7	XDR
1(5.26)	GM, AUG, SAM, IMI, TS, T, AK, PG, AP	Aminoglycosides, penicillins, carbapenems, sulphonamides, tetracyclines	9	5	MDR
1(5.26)	CAZ, GM, PRL, AUG, TN, SAM, AK, PG, AP	Cephalosporins, aminoglycosides, penicillins	9	3	MDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, SAM, IMI, TS, AK, PG	Cephalosporins, monobactams, penicillins, carbapenems, sulphonamides, aminoglycosides	10	6	XDR

Frequency of isolates (%)	MAR phenotypes	Antibiotic classes involved	Number of antimicrobials the isolates was resistant to	Number of antibiotics Classes the isolates were resistant to	Character of resistant strains
1(5.26)	CAZ, PRL, AUG, TN, MEM, IMI, CIP, AK, PG, CTX	Cephalosporins, penicillins, carbapenems, aminoglycosides, quinolones	10	5	MDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, MEM, IMI, AK, PG, AP	Cephalosporins, monobactams, penicillins, carbapenems, aminoglycosides	10	5	MDR
1(5.26)	CAZ, GM, PRL, TN, SAM, CIP, TS, T, AK, PG, AP	Cephalosporins, aminoglycosides, penicillins, quinolones, tetracyclines, sulphonamides	11	6	XDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, SAM, MEM, IMI, TS, AK, PG, AP	Cephalosporins, monobactams, penicillins, carbapenems, aminoglycosides, sulphonamides	12	6	XDR
1(5.26)	CAZ, ATM, GM, CPZ, AUG, TN, SAM, MEM, IMI, AK, PG, AP	Cephalosporins, aminoglycosides, penicillins, carbapenems, monobactams	12	5	MDR
1(5.26)	CAZ, GM, CPZ, AUG, TN, SAM, MEM, IMI, CIP, AK, PG, AP	Cephalosporins, aminoglycosides, penicillins, carbapenems, quinolones	12	5	MDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, SAM, MEM, IMI, CIP, T, AK, PG, AP	Cephalosporins, penicillins, monobactams, carbapenems, quinolones, tetracyclines, aminoglycosides	13	7	XDR
1(5.26)	CAZ, ATM, GM, CPZ, PRL, AUG, TN, SAM, IMI, AK, PG, CTX, AP	Cephalosporins, monobactams, aminoglycosides, penicillins, carbapenems	13	5	MDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, CIP, TS, T, AK, PG, AP	Cephalosporins, monobactams, penicillins, quinolones, sulphonamides, tetracyclines, Aminoglycosides, carbapenems	14	8	XDR
1(5.26)	CAZ, ATM, GM, CPZ, PRL, AUG, TN, SAM, IMI, CIP, T, AK, PG, AP	Cephalosporins, monobactams, aminoglycosides, penicillins, carbapenems, quinolones, tetracyclines	14	7	XDR
1(5.26)	CAZ, ATM, GM, CPZ, PRL, AUG, TN, SAM, TS, T, AK, PG, CTX, AP	Cephalosporins, monobactams, aminoglycosides, penicillins, sulphonamides, tetracyclines	14	6	XDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, AK, PG, CTX, AP	Cephalosporins, monobactams, penicillins, carbapenems, quinolones, sulphonamides, aminoglycosides	15	7	XDR
1(5.26)	CAZ, ATM, CPZ, PRL, AUG, TN, SAM, MEM, IMI, CIP, TS, T, PG, CTX, AP	Cephalosporins, Monobactams, penicillins, carbapenems, quinolones, aminoglycosides, sulphonamides, tetracyclines	15	8	XDR

***Escherichia coli* (n=28)**

Frequency of bacterial isolates (%)	MAR phenotypes	Antibiotic classes involved	Number of antimicrobials isolates were resistant to	Number of antibiotic classes	Character of the resistant strain
1(3.57)	PG, CTX	Penicillins, cephalosporins	2	2	Not MDR
1(3.57)	TN, CIP, AK	Aminoglycosides, quinolones	3	2	Not MDR
1(3.57)	TN, T, PG	Aminoglycosides, tetracyclines, penicillins	3	3	MDR
1(3.57)	PRL, CAZ, PG, CTX	Penicillins, cephalosporins	4	2	Not MDR
1(3.57)	SAM, CIP, TS, PG, AP	Penicillins, quinolones, sulphonamides	5	3	MDR
1(3.57)	PRL, MEM, CIP, CAZ, CPZ, ATM, CTX	Penicillins, carbapenems, quinolones, cephalosporins, monobactams	7	5	MDR

Frequency of isolates (%)	MAR phenotypes	Antibiotic classes involved	Number of antimicrobials the isolates was resistant to	Number of antibiotics Classes the isolates were resistant to	Character of resistant strains
1(3.57)	MEM, CIP, IMI, GM, CAZ, CPZ, CTX	Carbapenems, quinolones, aminoglycosides, cephalosporins	7	4	MDR
1(3.57)	TN,, TS, GM, AK, T, PG, CTX	Aminoglycosides, sulphonamides, tetracyclines, penicillins, cephalosporins	7	5	MDR
1(3.57)	SAM, CIP, IMI, AK, CAZ, ATM, PG, CTX	Penicillins, quinolones, carbapenems, aminoglycosides, cephalosporins, monobactams	8	6	XDR
1(3.57)	AUG, SAM, CIP, GM, AK, CAZ, PG, AP	Penicillins, quinolones, aminoglycosides, cephalosporins	8	4	MDR
1(3.57)	AUG, SAM, IMI, AK, CAZ, PG, CTX, AP	Penicillins, carbapenems, aminoglycosides, cephalosporins	8	4	MDR
1(3.57)	PRL, MEM, CIP, IMI, AK, CAZ, T, PG, CTX	Penicillins, carbapenems, quinolones, aminoglycosides cephalosporins, tetracyclines	9	6	XDR
1(3.57)	AUG, SAM, MEM, CIP, IMI, CAZ, PG, CTX, AP	Penicillins, carbapenems, quinolones, cephalosporins	9	4	MDR
1(3.57)	PRL, TN, SAM, IMI, TS, GM, AK, T, PG, AP	Penicillins, aminoglycosides, carbapenems, sulphonamides, tetracyclines	10	5	MDR
1(3.57)	AUG, TN, SAM, CIP, AK, CAZ, ATM, PG, CTX, AP	Penicillins, aminoglycosides, quinolones, cephalosporins	10	4	MDR
1(3.57)	AUG, TN, CIP, IMI, GM, AK, ATM, T, PG, CTX, AP	Penicillins, aminoglycosides, quinolones, carbapenems, aztreonam	11	5	XDR
1(3.57)	AUG, SAM, MEM, CIP, TS, CAZ, CPZ, ATM, PG, CTX, AP	Penicillins, carbapenems, quinolones, sulphonamides, cephalosporins, monobactams	11	6	XDR
1(3.57)	PRL, AUG, TN, SAM, CIP, TS, CAZ, CPZ, ATM, PG, CTX, AP	Penicillins, aminoglycosides, quinolones, sulphonamides, cephalosporins, monobactams	12	6	XDR
1(3.57)	PRL, AUG, TN, SAM, CIP, IMI, GM, AK, CAZ, PG, CTX, AP	Penicillins, aminoglycosides, quinolones, carbapenems, cephalosporins	12	5	MDR
1(3.57)	PRL, AUG, SAM, CIP, IMI, GM, AK, CAZ, CPZ, PG, CTX, AP	Penicillins, quinolones, carbapenems, aminoglycosides, cephalosporins	12	5	MDR
1(3.57)	PRL, AUG, SAM, MEM, IMI, TS, CAZ, CPZ, ATM, T, PG, CTX, AP	Penicillins, carbapenems, sulphonamides, monobactams, tetracyclines	13	5	XDR
1(3.57)	PRL, AUG, TN, SAM, CIP, TS, CAZ, CPZ, ATM, T, PG, CTX, AP	Penicillins, quinolones, sulphonamides, cephalosporins, monobactams, tetracyclines	13	5	XDR
1(3.57)	AUG, SAM, CIP, IMI, TS, GM, AK, CAZ, CPZ, ATM, PG, CTX, AP	Penicillins, quinolones, carbapenems, sulphonamides, aminoglycosides, cephalosporins, monobactams	13	7	XDR
1(3.57)	PRL, AUG, SAM, MEM, CIP, IMI, TS, AK, CAZ, CPZ, ATM, PG, CTX, AP	Penicillins, carbapenems, quinolones, sulphonamides, aminoglycosides, cephalosporins, monobactams	14	7	XDR
1(3.57)	PRL, AUG, TN, SAM, CIP, IMI, TS, CAZ, CPZ, ATM, T, PG, CTX, AP	Penicillins, quinolones, carbapenems, sulphonamides, aminoglycosides, cephalosporins, monobactams	14	7	XDR
3 (10.71)	PRL, AUG, TN, SAM, MEM, CIP, IMI, TS, CAZ, CPZ, ATM, PG, CTX, AP	Penicillins, aminoglycosides, carbapenems, quinolones, sulphonamides, cephalosporins, monobactams	14	7	XDR

PG, Penicillin; Ap, ampicillin; SAM, ampicillin/sulbactam; PRL, piperacillin; CTX, cefotaxime; AUG, amoxicillin/clavulanate; T, tetracycline; ATM, aztreonam; TS, sulfamethoxazole/trimethoprim; MEM, meropenem; IMI, imipenem, CIP, ciprofloxacin; GM, gentamicin; AK, amikacin; CAZ, ceftazidime; CPZ, cefoperazone; CTX, cefotaxime

The presence of multidrug-resistant bacterial isolates in the food chain in this region is a call for concern because of the likelihood of transmission of the antibiotic-resistant bacteria. Also, MDR (42.86% for *E. coli* and 47.39% for *Salmonella* spp) and XDR (46.43% for *E. coli* and 52.63% for *Salmonella* spp) bacterial isolates were detected in our samples. However, Wibisono et al. (2025) noted a level of MDR of 42% and 43% for *E. coli* and *Salmonella* spp, respectively, isolated from chicken meat sold in traditional markets in Gresik District, East Java, Indonesia. This disparity between these findings could be associated with differences in sampling, laboratory methods employed and the degree of uncertainty. The occurrence of such drug-resistant bacterial isolates in meat samples emphasises an urgent need to reinforce antimicrobial stewardship in food animal production, conduct routine resistance surveillance, implement hygiene interventions at slaughter and retail, as well as suggest the responsible use of antibiotics to hinder the transfer of resistant bacteria to humans.

4.1 FOOD SAFETY IMPLICATIONS AND ONE HEALTH APPROACH

Antimicrobial resistance has huge implications for human and animal medicines and in the food industry. The presence of antibiotic-resistant bacteria in food is worrisome because there is a great likelihood of transmission to humans throughout the food chain (Manyi-Loh and Lues 2023). One Health Approach recognises the interconnectedness of human, animal, and environmental health. This concept highlights pathways for the circulation of resistant pathogens between the three domains. As observed in this study, our findings registered antibiotic resistance in magnitude of 84.21- 100% for *Salmonella* spp and 82.14 - 89-29% for *E. coli*, indicating the potential for the public to become exposed to bacterial pathogens alongside antibiotic resistance via retail outlets (Stapleton et al. 2024). Numerous possible effects of AMR explained by several authors include: the use of much more expensive drugs, more invasive or critical route of drug administration, and the use of antibiotics with lower intrinsic activity (Cella et al. 2023; Ajose et al. 2024). These factors could lead to the following, namely heightened level of deaths, increased complications, extended hospital stay, additional toxicity, extra expenses, treatment failure, the need for intravenous therapy as opposed to oral therapy, and the lack of antibiotics active against the disease-causing agents in the future (Bitew et al. 2025). More worrisome or concerning is the development of MDR, defined as those resistant to three or more antibiotic classes and XDR. The severity of the outcomes or effects of AMR tends to increase, moving from MDR to XDR with resistance demonstrated against increasing antimicrobial classes or categories (Innes et al. 2023). Therefore, the findings of MDR and XDR *E. coli* (42.86%, 46.43%) and *Salmonella* spp., (47.36%, 52.63%), respectively, in this study, intensify concerns regarding food safety and public health and the resultant infections caused by these bacterial isolates will be more difficult to treat (De et al. 2025). The hygienic quality of meat products is a crucial determining factor of their microbiological safety, as improper food handling further increases the possibility of contamination.

4.2 IMPLICATIONS FOR RETAIL MANAGEMENT

4.2.1 Retailer food-safety responsibilities and consumers' trust

Contamination may originate from unsanitary abattoirs, contaminated equipment, handlers' poor hygiene, or environmental sources (air and water). Before the meat products are delivered to the consumers, the livestock moves from producers to processors and to retailers, a route described as the farm to fork pathway. Processor facilities hold an intermediary role between farm and fork, and the meat products might become contaminated with bacteria at specific steps during processing or from the processor environment itself (Stapleton et al. 2024). Following the packaging of the meat products, they are distributed to retail outlets for retail consumers. Retailers with food businesses are responsible for the food they transport, store and sell. The practice of food safety procedures (including temperature control, cross-contamination prevention, sanitation and cleaning, employee hygiene and training, pest control,

regulatory compliance, traceability and withdrawals, stock management and rotation) is pivotal in the food supply chain, spanning from farm to fork. Retailers perform numerous activities, interact with both the producers and the consumers and are the centre where products meet the consumers; hence, they have a lead role in overseeing food safety, having a direct effect on the community interacting. Retailers are mandated to ensure good food safety carried out through good retail practices, including neat storage of foods, adjusting temperature to suit the products on display and storage, regularly cleaning the room and storage area, developing a regular schedule for store cleaning and lastly, build protocols for withdrawing expired products and arranging for product rotation or movement (Widhajati and Rahmawati, 2025). In our study, a prevalence of 57.14% of bacterial contamination in the tested products was observed, which could be attributed to the reduced application of food safety principles. Food safety is an issue of great consideration in society, especially for retailers to ensure that safe food is made available to consumers to prevent the emergence of foodborne diseases. Considering the issue associated with food poisoning, there is need for public awareness in increasing attention to awareness of healthy and hygienic food for consumption (Widhajati and Rahmawati, 2025). When consumers become aware that a certain business prioritises food safety, they tend to trust the retailer, positively improving sales. However, a contrary finding about the business might result in a loss of trust in the retailer by the consumer. Such findings as recovered from this study can increase reputational risk for the retailer.

In addition, retailers have the responsibility to tackle antimicrobial resistance. Bacterial pathogens and MDR bacteria have penetrated all parts of the farm-to-fork pathway. AMR is a highly complex and multifaceted issue requiring multiple responses that engage actors across a range of disciplines. In this light, the responsibility for antibiotic resistance is manifold and extends across authorities, food producers, consumers, retailers, and civil society. Food consumption is one of the key factors contributing to AMR (Ancillotti et al. 2022). The use of antimicrobials in food-producing animals can lead to the development of AMR in bacteria from food-producing animals, which ultimately can enter the food chain, thus reaching humans. Consumers are viewed as a driving force in the market owing to their vital role demonstrated in that they influence how foods are produced through their choices (World Health Organisation 2017). One way to help deal with AMR is to promote behavioural change, including consumer behaviour. Therefore, public knowledge regarding the harms of AMR and its implications should be improved through effective communication, education and training (Ancillotti et al. 2022). Redding and colleagues (2021) remarked that consumers often believed that the issue with food is that antibiotic residues remain in foods that have been produced with antibiotics. However, antibiotic resistance is disseminated through environments where antibiotics are being used (antibiotic pollution) and via the food chain through direct or indirect exposure to resistant bacteria. The producers, the retailers and their families constitute the public as well as the consumers; therefore, they need awareness and understanding relating to food safety and AMR. Through their food choices, consumers can exert an impact on decision-makers because, on an individual and collective basis, they have the responsibility to choose, within the boundaries of their political, economic, and socio-cultural contexts, i.e., it is the consumers who decide what they do and do not purchase (Ancillotti et al. 2022). The findings about microbial contamination and antibiotic resistance of both processed and unprocessed meat products have the potential to affect consumers' trust. Since consumers are often mindful of the quality of the food that they eat, public campaigns and sensitisation on food hygiene, sanitation and AMR-related problems are obvious. The effect of engagement with the population should not be underestimated. Accordingly, Roser-Renouf et al. (2016) remarked that a bottom-up movement which shed light on AMR-related problems would benefit the antibiotic resistance issue by increasing people's commitment to change. This strategy raises consumers' awareness of the AMR problem and of their function as consumers can decide where and what to buy. This eventually will have an effect on reducing the use of antibiotics in food systems.

4.2.2 Cold-chain, in-store handling practices

Contamination often begins at the slaughtering stage and continues during handling, storage and retail. Meat and its derived products are a good medium for microbial growth. In this light, the way and the conditions under which meat products are kept or stored are very paramount. Refrigeration of meat products is one of the preferred methods to control microbial growth, thereby preventing contamination (Rovira et al. 2023). Therefore, maintaining the cold chain during transportation and storage of the meat products is very essential. Our findings revealed bacterial contamination of tested products, highlighting the growth of microbes. This suggests that the cold-chain during storage could have been compromised.

4.2.3 Quality-control procedures

Quality management can be expressed in terms of quality assurance and quality control, which helps to ensure the products always meet the established food quality standards and comply with regulatory requirements. The quality of food has a great influence on consumer safety, regulatory compliance, and brand reputation. Testing of the products of each batch production for inconsistencies helps to maintain the quality of the products and identify any contamination. In reducing contamination in meat and microbial growth, good manufacturing practices, hazard analysis and critical control points are the two very prominent quality control programmes in meat production (Sabyrbekova and Ilgekbayeva 2024). Even though the level of bacterial contamination in terms of number of counts was not evaluated, the recovery of *E. coli* and *Salmonella* isolates and their resistance counterparts poses questions relating to quality control management.

4.2.4 Staff training

Ecological analysis revealed that food contact surfaces (e.g., porous wood boards) and processing machinery (e.g., mincers) could serve as resilient reservoirs or hotspots of untreatable pathogens due to biofilm build-up, that can resist the actions of antimicrobial disinfectants and other food-safety sanitation protocols (Shakoor et al. 2026). Biofilms are complex microbial colonies commonly found in meat retail shops, attached to surfaces of knives, cutting boards and mincing machines and forming an extracellular matrix that confers resistance to cleaning solutions and antibiotics (Donlan and Costerton 2002). Biofilm-forming bacteria contaminating meat-processing surfaces and machinery enhance bacterial persistence, promote increased tolerance to disinfectants and antimicrobial agents, thus posing a substantial threat to food safety and public health (Shakoor et al. 2026). The significance of food safety culture should not be minimised in the food industry. Improving awareness and understanding of food safety culture and AMR through effective communication, education and training is obvious due to the findings recovered in this study. Food handlers play a great role in the contamination of food in the food business. It is a legal obligation that all food handlers are supervised, instructed, and/or trained in food hygiene or food safety matters corresponding with their work activities (Julve and Dael 2025). Food safety training (focusing on personal hygiene, contamination, storage and temperature mishandling, and working while sick) is central to the survival of any food business, and it is one of the ways to improve food safety in a workplace. However, it is not a single event, but a regular and good quality, ongoing training event that contributes to a holistic understanding and competence in overall health and safety requirements when handling food (Tappes et al. 2019).

5. CONCLUSION

This study revealed the microbial contamination (*E. coli* and *Salmonella* spp) of more than half of the fraction (prevalence of 57.14%) of meat and its derivatives obtained from the selected retail stores. *E. coli* was the most

frequently isolated organism, with many isolates showing resistance to commonly used antibiotics, namely, penicillin and ceftazidime. Overall, 91.46% of the bacterial isolates showed MAR > 0.2, suggesting that most bacterial isolates emerged from an environment where there has been routine use of antibiotics. Varying proportions of MDR and XDR isolates of *E. coli* and *Salmonella* spp were observed in this study, with few bacterial isolates showing resistance to fourteen (14) and fifteen (15) antibiotics, respectively. Such findings suggest that the retail sector dealing with meat and its products could be a potential hotspot for the emergence and spread of antibiotic resistance. Therefore, presenting a huge negative effect on food safety alongside public health. To alleviate these risks, urgent and coordinated efforts are needed: policy-level enforcement of hygiene regulations, structured food safety training programmes for meat handlers, and regular monitoring of antibiotic resistance trends in foodborne pathogens. However, limitations such as the unbalanced sample size for both processed and unprocessed meat products and the absence of molecular analysis of resistance genes reveal the need for further research to better understand AMR mechanisms in retail settings.

6. LIMITATIONS OF THE STUDY

The findings in this study is limited by the unbalanced sample (the processed samples were far more than the unprocessed samples), local sampling (samples were procured just from around Bloemfontein even though the Mangaung municipality consists of three major towns; Botshabelo, Thaba Nchu and Bloemfontein), presumptive identification (molecular methods were not used to confirm the identity of isolates and strains), clustering of isolates, and phenotypic-only resistance testing (molecular identification of resistance genes will authenticate the data on AST).

Further studies involving molecular analysis will help confirm the identity of the bacterial isolates and reveal the types of genes expressing antibiotic resistance, in addition to identifying virulence factors/genes, which will reveal the pathogenic potential of the bacterial isolates. Evaluating the biofilm-forming potential of the bacterial strains will reveal further huge implications in terms of pathogenicity and antibiotic resistance among the confirmed isolates.

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