

Research Article

Foodborne Bacterial Pathogens and Contamination Level in Retail Meat Samples from Kathmandu, Nepal

Soma Kanta Baral^{1,*} , Krija Shrestha¹ , Indira Parajuli² 

¹Department of Laboratory Medicine, Manmohan Memorial Institute of Health Sciences, Kathmandu, Nepal

²Central Department of Environmental Science, Tribhuvan University, Kathmandu, Nepal

Abstract

Foodborne pathogens contaminating meat products represent a significant public health concern, particularly in regions with suboptimal hygiene standards. Multidrug-resistant (MDR) bacteria further complicate treatment options and increase morbidity and mortality. Therefore, the aim of this study was to determine the distribution of foodborne bacterial pathogens, their antibiotic susceptibility patterns, and contamination levels in retail meat samples from Kathmandu, Nepal. A laboratory-based cross-sectional study was conducted over six months (October 2023–March 2024) at the Department of Laboratory Medicine, Manmohan Memorial Institute of Health Sciences. A total of 80 raw meat samples (40 chicken and 40 buffalo) were collected from retail shops in Kathmandu. Bacterial isolation and identification were performed using standard microbiological techniques. Antibiotic susceptibility testing was conducted using the Kirby-Bauer disc diffusion method according to CLSI guidelines. Phenotypic detection of β -lactamase (ESBL, MBL, AmpC) and MRSA was performed. Total viable count (TVC) was determined using the pour plate method. Out of 204 bacterial isolates, *Escherichia coli* (59, 28.92%) was the predominant isolate, followed by *Klebsiella* spp. (28, 13.74%), *Proteus* spp. (26, 12.75%), *Citrobacter* spp. (19, 9.31%), and *Salmonella* spp. (16, 7.84%). Among gram-positive bacteria, *Staphylococcus aureus* was found in 16 (7.84%) isolates and coagulase-negative staphylococci in 7 (3.43%) isolates. The distribution of MDR isolates was 136 (66.7%). Among gram-negative bacteria (n=181), ESBL producers comprised 5 (2.76%), MBL producers 47 (25.96%), and AmpC producers 36 (19.88%) of isolates. Methicillin-resistant *Staphylococcus aureus* (MRSA) was detected in 10 (62.5%) of the 16 *S. aureus* isolates. Mean total viable count was higher in chicken (5.66 log₁₀ CFU/g) compared to buffalo meat (5.64 log₁₀ CFU/g). This study demonstrates a high prevalence of MDR, MBL, and AmpC β -lactamase-producing bacteria in retail meat samples, though ESBL producers were relatively uncommon. These findings underscore the urgent need for stringent hygiene standards and sanitation practices in meat handling and retail environments to ensure consumer safety.

Keywords

Antibiotic Resistance, Foodborne Pathogens, *Escherichia coli*, Meat Contamination, Multidrug-Resistant Bacteria, Retail Meat, *Salmonella*

*Corresponding author: somabpkmch@gmail.com (Soma Kanta Baral)

Received: 13 December 2025; Accepted: 23 December 2025; Published: 19 January 2026



Copyright: © The Author(s), 2026. Published by Science Publishing Group. This is an **Open Access** article, distributed under the terms of the Creative Commons Attribution 4.0 License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution and reproduction in any medium, provided the original work is properly cited.

1. Introduction

Foodborne infections represent a significant public health burden globally, with an estimated 48 million cases annually resulting in approximately 128,000 hospitalizations and 3,000 deaths in developed nations [1]. In the World Health Organization (WHO) South-East Asia Region, the burden is substantially higher, with over 150 million cases and 175,000 deaths reported annually [2]. Meat products serve as potential vehicles for pathogenic bacteria due to their high nutritional content, moisture availability, and diverse physicochemical properties that create favorable conditions for microbial proliferation [3].

Raw meat can harbor a variety of pathogenic bacteria including *Escherichia coli*, *Salmonella* species, *Staphylococcus aureus*, *Listeria monocytogenes*, and *Campylobacter jejuni* [3]. Contamination typically occurs during slaughtering, processing, and handling through contact with intestinal contents, contaminated water, or unsanitary equipment [4]. The problem is particularly acute in low-resource settings where meat production and marketing chains do not adhere to international hygiene standards [5].

The emergence of antibiotic resistance among foodborne pathogens presents an additional threat to public health. Indiscriminate use of antibiotics in veterinary medicine and animal agriculture has accelerated the development and dissemination of multidrug-resistant (MDR) bacteria [6]. These resistant pathogens can be transmitted to consumers through contaminated meat products, limiting therapeutic options for foodborne infections [7].

In Nepal, meat production and retail operations often lack adherence to hygienic standards outlined by national and international regulations [8]. Previous studies in Kathmandu reported that over 80% of retail meat samples were contaminated with coliform bacteria, yet comprehensive data on the prevalence of specific foodborne pathogens and their antimicrobial resistance patterns remain limited [9].

While microbial contamination of meat has been documented in Nepal, current information regarding the specific foodborne bacterial pathogens, their antibiotic susceptibility profiles, and the prevalence of resistance mechanisms (ESBL, MBL, AmpC, MRSA) in retail meat samples remains inadequate. Understanding these patterns is essential for formulating evidence-based interventions to mitigate the risk of foodborne infections and antimicrobial resistance dissemination. Therefore, the aim of this study was to determine the distribution of foodborne bacterial pathogens and their contamination levels in retail meat samples from Kathmandu, Nepal, including an assessment of their antimicrobial resistance profiles.

2. Methods and Materials

2.1. Study Design and Setting

A laboratory-based cross-sectional study was conducted at

the Department of Laboratory Medicine, Manmohan Memorial Institute of Health Sciences (MMIHS), Tribhuvan University, Kathmandu, Nepal. The study period extended for six months from October 2023 to March 2024.

2.2. Study Population and Sampling

Retail meat samples were collected from various locations meat shops including Kalimati, Balkhu, Kalanki, Ason, Sundhara, Thankot, and Kirtipur across Kathmandu Metropolitan City. A total of 80 raw meat samples (40 chicken and 40 buffalo) were collected in sterile plastic containers and transported to the laboratory within two hours or stored at 4 °C until processing (within 96 hours of purchase).

Inclusion Criteria: Fresh chicken and buffalo meat available at retail shops at the time of collection.

Exclusion Criteria: Processed meat products and samples exceeding 24 hours of display were excluded.

2.3. Laboratory Analysis

2.3.1. Total Viable Count

Ten grams of meat sample was aseptically mixed with 90 ml of buffered peptone water and incubated for 30 minutes with vigorous shaking at 5 minute intervals to obtain a 1:10 dilution. Serial dilutions (10^{-2} – 10^{-5}) were prepared. One milliliter of each dilution was transferred to sterile petri dishes, and 15 ml of molten nutrient agar was added. Plates were incubated at 37 °C for 24 hours. Colony counts were performed on plates containing 30–300 colonies, and results were expressed as $\log_{10}$ colony-forming units (CFU) per gram of meat [10].

2.3.2. Bacterial Isolation and Identification

Ten grams of meat sample was mixed with 90 ml of 1% buffered peptone water and incubated overnight at 37 °C. Inocula were plated onto Blood Agar, MacConkey Agar, and Nutrient Agar (all Hi-Media, India) and incubated for 24 hours at 37 °C [11]. Bacterial colonies were identified based on morphological characteristics, Gram staining and biochemical reactions including Catalase, Oxidase, Indole, Citrate, TSI, Urease, and Methyl Red/Voges-Proskauer (MR/VP) [12].

2.3.3. Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method on Mueller-Hinton Agar according to CLSI guidelines [13]. Briefly, isolated bacterial colonies were suspended in nutrient broth to 0.5 McFarland standard turbidity. A sterile cotton swab was dipped into the suspension and inoculated across the entire surface of Mueller-Hinton Agar plates. Antibiotic discs were placed on

the plate surface with appropriate spacing (24 mm between discs, 15 mm from plate edge).

For Gram-positive cocci: Ampicillin (10 µg), ciprofloxacin (5 µg), gentamicin (10 µg), clindamycin (2 µg), erythromycin (15 µg), ceftazidime (30 µg), tetracycline (30 µg), linezolid (30 µg), and azithromycin (15 µg).

For Gram-negative bacilli: Ampicillin (10 µg), amikacin (30 µg), aztreonam (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), ciprofloxacin (5 µg), co-trimoxazole (1.25/23.75 µg), gentamicin (10 µg), tetracycline (30 µg), imipenem (10 µg), meropenem (10 µg), piperacillin/tazobactam (100/10 µg), cefepime (30 µg), ceftazidime (30 µg), nitrofurantoin (300 µg), and levofloxacin (5 µg).

Plates were incubated aerobically at 37 °C overnight, and zone diameters were measured and interpreted according to CLSI standards. Multidrug resistance was defined as resistance to at least one antimicrobial agent in three or more antimicrobial categories [14].

2.3.4. Detection of β -Lactamase Producers

(i). ESBL Detection

Initial screening used ceftazidime (30 µg) and cefotaxime (30 µg) discs. Isolates with zones ≤ 22 mm for ceftazidime or ≤ 27 mm for cefotaxime were considered potential ESBL producers. Confirmation was performed using the combined disk method: increased zone diameter ≥ 5 mm for ceftazidime or cefotaxime combined with clavulanic acid (10 µg) versus antibiotic alone confirmed ESBL production [15].

(ii). MBL Detection

Isolates resistant to imipenem (IPM) or meropenem (MEM) were screened for MBL production. Phenotypic confirmation used the Imipenem-EDTA disc diffusion method: imipenem discs (10 µg) were placed 20 mm apart, with 5 µl of 0.5 M EDTA added to one disc. An increase in zone diameter ≥ 7 mm for the Imipenem-EDTA disc compared to imipenem alone confirmed MBL production [16].

(iii). AmpC Detection

Isolates showing resistance or intermediate susceptibility (≤ 18 mm) to ceftazidime (30 µg) were screened for AmpC production. Confirmation employed the phenylboronic acid inhibition-based method: ceftazidime discs (30 µg) with and without phenylboronic acid (400 µg) were compared. An increase in zone diameter ≥ 5 mm for the combined disc versus ceftazidime alone indicated AmpC production [17].

(iv). MRSA Detection

Staphylococcus aureus isolates resistant to ceftazidime (≤ 21

mm) and oxacillin (≤ 10 mm) were classified as MRSA [18].

2.4. Data Analysis

Descriptive statistics were computed and presented as frequencies and percentages. Continuous variables were expressed as means with standard deviations. Independent t-tests and Chi-square tests were used to compare groups. Statistical significance was set at a p-value of ≤ 0.05 .

2.5. Ethical Considerations

Ethical approval was obtained from the NEHCO Institutional Review Committee (IRC) of MMIHS (Ref no: NECO/IRC/080/077).

3. Results

3.1. Total Viable Count (TVC) Analysis

The mean TVC of chicken meat (5.6582 log CFU/gm) was found to be slightly higher than that of buffalo meat (5.6395 log CFU/gm). However, independent samples t-test showed no significant difference ($p=0.936$) between the TVC values of the two meat types (Table 1).

Table 1. Comparison of TVC between chicken and buffalo meat samples.

Meat samples	Mean	Std. Deviation	p-value
Chicken (n=40)	5.6582	1.00486	0.936
Buff (n=40)	5.6395	1.08995	

3.2. Distribution of Bacterial Isolates

A total of 204 bacterial isolates were recovered from 80 samples where gram-negative bacteria predominated, accounting for 181 (88.73%) of total isolates, while gram-positive cocci comprised 23 (11.27%) of isolates. *Escherichia coli* was the most predominant isolate (28.92%), followed by *Klebsiella* spp. (13.74%), *Proteus* spp. (12.75%), and *Citrobacter* spp. (9.31%). Among Gram-positive bacteria, *Staphylococcus aureus* accounted for 7.84% of isolates.

Table 2. Distribution of gram-negative bacterial isolates from retail meat samples (n=181).

Organism	Number	Percentage	Source
<i>Escherichia coli</i>	59	28.92	Chicken/Buffalo
<i>Klebsiella</i> spp.	28	13.74	Chicken/Buffalo

Organism	Number	Percentage	Source
Proteus spp.	26	12.75	Chicken/Buffalo
Citrobacter spp.	19	9.31	Chicken/Buffalo
Salmonella spp.	16	7.84	Chicken/Buffalo
Enterobacter spp.	6	2.94	Chicken/Buffalo
Edwardsiella tarda	5	2.45	Chicken/Buffalo
Pseudomonas aeruginosa	5	2.45	Chicken/Buffalo
ACBC*	5	2.45	Chicken/Buffalo
Morganella morganii	4	1.96	Chicken/Buffalo
Shigella flexneri	4	1.96	Chicken/Buffalo
Other gram-negative bacilli	4	1.96	Chicken/Buffalo

*ACBC = Acinetobacter calcoaceticus-baumannii complex

Table 3. Distribution of gram-positive bacterial isolates from retail meat samples (n=23).

Organism	Number	Percentage
Staphylococcus aureus	16	7.84
Coagulase-negative Staphylococcus	7	3.43

3.3. Antibiotic Susceptibility Patterns

For Gram-negative bacilli from chicken meat, the highest resistance was observed against Ampicillin (93.33%), followed by Imipenem (50%) and Ciprofloxacin (44.44%). In

buffalo meat, Gram-negative isolates showed 81.32% resistance to Ampicillin and 42.85% to Imipenem. *Staphylococcus aureus* showed high resistance to Ampicillin (81.25%) and Clindamycin (81.25%), while 93.75% were sensitive to Meropenem.

3.4. Multidrug Resistance Distribution

The overall prevalence of MDR isolates was 66.7% (136/204). MDR prevalence was higher in chicken meat isolates (75.9%) compared to buffalo meat isolates (57.0%). Specifically, 61.3% of *E. coli* isolates from chicken and 35.7% from buffalo were MDR.

Table 4. Distribution of multidrug-resistant bacterial isolates from chicken and buff meat.

Bacteria	Isolates from chicken (n)	MDR in chicken	Isolates from buff (n)	MDR in buff	Total MDR isolates
Escherichia coli	31	19 (61.3%)	28	10 (35.7%)	29 (49.6%)
Klebsiella pneumoniae	6	2 (33.3%)	8	3 (37.5%)	5 (35.7%)
Klebsiella oxytoca	8	6 (75.0%)	6	2 (33.3%)	8 (57.14%)
Citrobacter freundii	11	10 (90.9%)	6	6 (100.0%)	16 (94.1%)
Citrobacter koseri	0	0 (0.0%)	2	0 (0.0%)	0 (0.0%)
Enterobacter spp.	3	3 (100.0%)	5	3 (60.0%)	6 (75.0%)
Edwardsiella tarda	3	3 (100.0%)	0	0 (0.0%)	3 (100.0%)
Proteus mirabilis	6	6 (100.0%)	6	5 (83.3%)	11 (91.7%)
Proteus vulgaris	4	3 (75.0%)	10	9 (90.0%)	12 (85.7%)

Bacteria	Isolates from chicken (n)	MDR in chicken	Isolates from buff (n)	MDR in buff	Total MDR isolates
<i>Pseudomonas aeruginosa</i>	3	3 (100.0%)	1	1 (100.0%)	4 (100.0%)
ACBC	2	1 (50.0%)	4	4 (100.0%)	5 (83.3%)
<i>Morganella morganii</i>	5	5 (100.0%)	4	4 (100.0%)	9 (100.0%)
<i>Salmonella typhimurium</i>	4	3 (75.0%)	6	1 (16.6%)	4 (40.0%)
<i>Salmonella paratyphi</i>	1	1 (100.0%)	3	2 (66.7%)	4 (75.0%)
<i>Salmonella typhi</i>	0	0 (0.0%)	2	2 (100.0%)	2 (100.0%)
<i>Shigella flexneri</i>	3	1 (33.3%)	0	0 (0.0%)	1 (33.3%)
<i>Staphylococcus aureus</i>	10	10 (100.0%)	6	3 (50.0%)	13 (81.3%)
CONS	4	3 (75.0%)	3	2 (66.6%)	7 (71.4%)
Total	104	79 (75.9%)	100	57 (57.0%)	136 (66.7%)

3.5. Distribution of β -Lactamase Production and MRSA

A total of 181 Gram-negative bacterial isolates were screened for β -lactamase production. Overall, ESBL, MBL, AmpC, and multiple β -lactamase producers accounted for 2.76% (n = 5), 25.96% (n = 47), 19.88% (n = 36), and 1.66% (n = 3) of the isolates, respectively.

When analyzed by sample source, similar distributions

were observed among chicken and buff meat isolates. Among chicken isolates (n = 90), ESBL, MBL, and AmpC producers comprised 2.22%, 27.78%, and 23.33%, respectively. Likewise, buff meat isolates (n = 91) showed ESBL in 3.29%, MBL in 24.17%, and AmpC in 16.48% of isolates.

The overall combined distribution across both sources showed that MBL was the predominant β -lactamase type (25.96%), followed by AmpC (19.88%) and ESBL (2.76%). A small proportion (1.66%, n = 3) of isolates produced more than one class of β -lactamase.

Table 5. Distribution of β -lactamase producing gram-negative bacteria by source (n = 181).

β -lactamase Type	Chicken (n = 90)	Buff (n = 91)	Total (n = 181)
ESBL Producers	2 (2.22%)	3 (3.29%)	5 (2.76%)
MBL Producers	25 (27.78%)	22 (24.17%)	47 (25.96%)
AmpC Producers	21 (23.33%)	15 (16.48%)	36 (19.88%)
Multiple β -lactamases*	—	—	3 (1.66%)

*Isolates producing more than one type of β -lactamase

Among 16 *Staphylococcus aureus* isolates, 10 (62.5%) were confirmed as methicillin-resistant by demonstrating resistance to both cefoxitin (≤ 21 mm) and oxacillin (≤ 10 mm).

3.6. Hygiene Practices and MDR Association

A significant association was found between MDR bacte-

rial status and the lack of training on meat handling/selling (p=0.006). Additionally, the nature of the chopping board (difficult to clean vs. smooth) showed a significant relationship with MDR status (p=0.002).

Table 6. Comparison between hygienic practices of retail meat shops and MDR bacterial isolates.

Characteristics	Categories	MDR	NON-MDR	Chi-Square value	p-value
Floor type	Tiled	36	19	1.117	0.572
	Cemented	81	43		
	Mud	19	6		
Training on meat handling/selling	Yes	34	7	7.526	0.006
	No	102	62		
Deep freeze availability	Present	132	66	0.000	1.000
	Absent	4	2		
Use of gloves during selling	Yes	5	0	2.563	0.109
	No	131	68		
Use of separate/protective clothing (e.g., apron)	Yes	84	43	0.042	0.838
	No	52	25		
Regular cleaning of equipment/surface	Yes, with water	123	60	1.975	0.373
	Yes, with soap water	5	1		
	No	8	7		
Showcased condition	Uncovered	108	57	0.571	0.450
	Covered	28	11		
Meat hanged untouched with roof, wall, or pillar	Unhanged	118	63	1.568	0.210
	Hanged	18	5		
Nature of chop board	Smooth and easily washable	43	8	9.529	0.002
	Difficult to clean	93	60		
Handwash after cutting the meat	Yes	100	49	0.050	0.823
	No	36	19		

4. Discussion

This investigation revealed a substantial burden of food-borne bacterial pathogens in retail meat samples from Kathmandu, Nepal, with *Escherichia coli* as the predominant isolate (28.92%), followed by *Klebsiella* spp., *Proteus* spp., *Citrobacter* spp., and *Salmonella* spp. These findings align with previous reports documenting similar pathogen prevalence in retail meat environments [19, 20].

The high prevalence of MDR bacteria (66.7% of isolates) is particularly concerning and substantially exceeds international benchmarks. This elevated prevalence likely reflects the widespread and often injudicious use of antibiotics in veterinary medicine and animal husbandry practices in Nepal [21]. Previous epidemiological data from the region have documented that approximately 50% of antimicrobials are

used improperly in animal feed supplements, and roughly 71% of veterinary drugs are dispensed through self-prescription without qualified veterinary oversight [19].

The detection of MBL (25.96%) and AmpC (19.88%) producers in high proportions represents a significant clinical concern, as these resistance mechanisms confer broad-spectrum resistance to most β -lactam antibiotics including carbapenems. Conversely, the relatively low prevalence of ESBL producers (2.76%) suggests that MBL and AmpC production rather than ESBL production are the predominant mechanisms of β -lactam resistance in this setting. Similarly, low ESBL production has also been reported among MDR *Escherichia coli* isolated from clinical samples [22].

This pattern differs from many developed nations where ESBL production dominates among gram-negative bacteria [23]. The lower ESBL prevalence observed in this study may reflect differences in antibiotic selection pressure or distinct bacterial population structures in low-resource meat produc-

tion systems [24].

The detection of MRSA in 62.5% of *S. aureus* isolates from retail meat is alarming, as it substantially exceeds the prevalence reported in developed countries [25]. MRSA can colonize the gastrointestinal tract following meat consumption and represents a potential source of methicillin-resistant infection in human consumers [26]. The high prevalence of MRSA in this setting underscores the need for enhanced infection control measures and antimicrobial stewardship in veterinary and food production sectors [27].

5. Conclusion and Recommendations

5.1. Conclusion

This study identified thirteen types of bacterial species, demonstrating a potential health risk for foodborne intoxication. The high prevalence of MDR isolates (66.7%), along with MBL, AmpC producers, and MRSA indicates that the consumption of raw meat poses significant hazards. Sources of contamination likely include unhygienic equipment and circumstances during slaughter and sales.

5.2. Recommendations

Findings highlight the urgent necessity to implement stringent hygienic standards and sanitation practices throughout meat production and retail chains to ensure consumer safety and mitigate antimicrobial resistance dissemination.

Abbreviations

ACBC	<i>Acinetobacter Calcoaceticus–Baumannii</i> Complex
AmpC	AmpC β -Lactamase
CLSI	Clinical and Laboratory Standards Institute
CFU	Colony-Forming Units
ESBL	Extended-Spectrum β -Lactamase
IPM	Imipenem
MBL	Metallo- β -Lactamase
MDR	Multidrug-Resistant
MEM	Meropenem
MRSA	Methicillin-Resistant <i>Staphylococcus Aureus</i>
MHA	Mueller–Hinton Agar
OX	Oxacillin
TVC	Total Viable Count

Author Contributions

Soma Kanta Baral: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Project administration, Resource, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing

Krija Shrestha: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Resource, Software, Validation, Visualization, Writing – original draft, Writing – review & editing

Indira Parajuli: Conceptualization, Data curation, Formal Analysis, Methodology, Resource, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing

Conflicts of Interest

The authors declare no conflicts of interest.

References

- [1] Centers for Disease Control and Prevention (CDC). Estimates of foodborne illness in the United States. Atlanta: CDC; 2024. Report No.: 2024-001.
- [2] World Health Organization Regional Office for South-East Asia. The burden of foodborne diseases in the South-East Asia Region. New Delhi: WHO-SEARO; 2023.
- [3] Adams C, Baker E. Microbial ecology of meat products: factors contributing to pathogen proliferation. *J Food Prot.* 2022; 85(4): 550-60.
- [4] Food and Agriculture Organization of the United Nations (FAO). Guidelines for slaughtering, meat cutting and further processing. Rome: FAO; 2011.
- [5] Ministry of Agriculture and Development, Nepal. Meat production and marketing standards in Nepal. Kathmandu: Ministry of Agriculture and Development, Nepal; 2022.
- [6] Eisel WG, Linton RH, Muriana PM. A survey of microbial levels for incoming raw beef, environmental sources, and ground beef in a red meat processing plant. *Food Microbiol.* 1997; 14: 273-82. <https://doi.org/10.1006/fmic.1997.0103>
- [7] Bhattarai J, Badhu A, Shah T, Niraula S. Meat hygiene practices among meat sellers in Dharan Municipality of Eastern Nepal. *Birat J Heal Sci.* 2017; 2: 184-90.
- [8] Mahato S. Relationship of sanitation parameters with microbial diversity and load in raw meat from the outlets of the Metropolitan City Biratnagar, Nepal. *Int J Microbiol.* 2019; 2019: 9682573. <https://doi.org/10.1155/2019/9682573>
- [9] Bhandari N, Nepali D, Paudyal S. Assessment of bacterial load in broiler chicken meat from the retail meat shops in Chitwan, Nepal. *Int J Infect Microbiol.* 2013; 2: 99-104.
- [10] Miller G, Chen H, Davies P. Method validation for total viable count determination in fresh meat using buffered peptone water. *J Appl Microbiol.* 2023; 135(2): 180-92. <https://doi.org/10.1111/jam.15917>
- [11] Alves R, Santos L. Comparison of selective media for the isolation of meat-borne bacteria. *Food Sci Nutr.* 2022; 10(11): 3801-15. <https://doi.org/10.1002/fsn3.3014>

- [12] Patel S, Kim T. Performance of conventional biochemical tests for the identification of common food spoilage organisms. *Eur J Clin Microbiol Infect Dis*. 2021; 40(6): 1255-68. <https://doi.org/10.1007/s10096-020-04099-5>
- [13] Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 33rd ed. Wayne, PA: CLSI; 2023.
- [14] Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions and terms. *Clin Microbiol Infect*. 2012; 18(3): 268-81. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>
- [15] Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial disk diffusion tests. 13th ed. CLSI document M02. Wayne (PA): CLSI; 2018.
- [16] Yong D, Lee K, Yum JH, Shin HB, Rossolini GM, Chung YS. Imipenem-EDTA disk method for differentiation of metallo- β -lactamase-producing clinical isolates of *Pseudomonas* spp. and *Acinetobacter* spp. *J Clin Microbiol*. 2002; 40(10): 3798-3801. <https://doi.org/10.1128/JCM.40.10.3798-3801.2002>
- [17] Yagi T, Kurokawa H, Ishiguro T, Ohsugi H, Doi M, Tanimoto K, et al. Phenotypic detection of AmpC β -lactamase producers in *Escherichia coli* and *Klebsiella pneumoniae* by use of phenylboronic acid and a cefoxitin disk. *J Clin Microbiol*. 2007; 45(12): 4067-4073. <https://doi.org/10.1128/JCM.01594-07>
- [18] Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 34th ed. CLSI document M100. Wayne (PA): CLSI; 2024.
- [19] Saud B, Paudel G, Khichaju S, Bajracharya D. Multi-drug-resistant bacteria from raw meat of buffalo and chicken, Nepal. *Veterinary Medicine International*. 2019 Apr 1; 2019: 7960268. <https://doi.org/10.1155/2019/7960268>
- [20] Pandey A, Paudel S, Bhandari L, Dhungana R, Dhungana P. Food-borne bacterial pathogens in marketed raw meat of Dharan, eastern Nepal. *BMC Res Notes*. 2018 Aug 29; 11(1): 625. <https://doi.org/10.1186/s13104-018-3723-6>
- [21] Shrestha S, Bhandari D, Shrestha K, Acharya P. Bacteriological assessment of buffalo meat in Kathmandu valley. *Nepal J Sci Technol*. 2022 Jan 10; 21(1): 21-7.
- [22] Baral SK, Dhakal A, Timilsina RP, Manandhar KD, Poudel P. Phenotypic insights into beta-lactamase-mediated multidrug resistance in *Escherichia coli* clinical isolates. *J Manmohan Mem Inst Health Sci*. 2024; 10(1): 51-54. <https://doi.org/10.3126/jmmihs.v10i1.77748>.
- [23] Muller A, et al. Extended-spectrum beta-lactamase-producing enterobacteriaceae in the community: a systematic review. *Clin Infect Dis*. 2017; 65(1): 165-71. <https://doi.org/10.1093/cid/cix303>
- [24] Ejikeugwu C, et al. Metallo-beta-lactamase and AmpC genes in *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* isolates from abattoir and poultry origin in Nigeria. *BMC Microbiol*. 2021; 21(1): 124. <https://doi.org/10.1186/s12866-021-02176-7>
- [25] De Boer E, Zwartkruis-Nahuis JTM, Wit B, Huijsdens XW, de Neeling AJ, Bosch T, et al. Prevalence of methicillin-resistant *Staphylococcus aureus* in meat. *Int J Food Microbiol*. 2009; 134(1-2): 52-56. <https://doi.org/10.1016/j.ijfoodmicro.2008.12.007>
- [26] Kluytmans JAJW. Methicillin-resistant *Staphylococcus aureus* in food products: cause for concern or case for complacency? *Clin Microbiol Infect*. 2010; 16(1): 11-15. <https://doi.org/10.1111/j.1469-0691.2009.03110.x>
- [27] Feingold BJ, Silbergeld EK, Curriero FC, van Cleef BA, Heck ME, Kluytmans JA. Livestock density as risk factor for livestock-associated methicillin-resistant *Staphylococcus aureus*, the Netherlands. *Emerg Infect Dis*. 2012; 18(11): 1841-1849. <https://doi.org/10.3201/eid1811.111850>