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Prevalence of Bacterial Pathogens and Their Antibiogram Profile in Raw Buffalo Meat from Maharashtra State, India

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Abstract Foods of animal origin are an extremely important source of protein to the public in developing countries. However, the safety and quality of meat can be severely compromised by microbial contamination. Moreover, the presence of antibiotic residues in meat poses a significant public health concern due to its effects on human health through direct or indirect consumption. This study investigates the prevalence of pathogenic microbes in raw buffalo meat and evaluates their antibiogram profiles to ensure meat safety. A total of 250 raw buffalo meat samples were collected from the slaughterhouses in Mumbai region. The samples were subjected to microbiological analysis for detection of common foodborne pathogens, including *Bacillus* spp., *Salmonella* spp., *Escherichia coli*, *Listeria monocytogenes*, *Staphylococcus aureus* and *Pseudomonas* spp. The most prevalent pathogen in buffalo meat was found to be *Staphylococcus aureus* (26.00 %), followed by *Salmonella* spp. (18.40 %), *E. coli* (11.2 %) and *Bacillus cereus* (16.40 %), while *Pseudomonas* spp. and *Listeria monocytogenes* were absent in the samples. The bacterial isolates were further subjected to antibiotic susceptibility testing using disc diffusion method and the antibiogram revealed varying resistance profiles (MAR index > 0.2) with significant resistance observed against conventionally used antibiotics such as chloramphenicol, amikacin, cefotaxim, co-trimaxole and gentamicin. The current study emphasizes on the need for implementation of stringent hygiene practices and effective collaboration to implement antimicrobial stewardship in meat production and processing industry. The study concluded that the importance of regular monitoring and implementation of corrective measures to enhance food safety and safeguard consumer health.

Keywords: *Antibiogram, Buffalo meat, Food safety, MAR index, Pathogens, Public Health*

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1. Introduction

Foodborne illnesses hold significant public health significance, particularly in developing and underdeveloped countries. They severely hamper the productivity, besides having an impact on the economy of the nation [1]. Improper cooking, cross contamination of meat and unhygienic slaughter practices are a few among the reasons contributing to the occurrence of foodborne diseases, indirectly leading to yield reduction and associated economic losses. Thus, antimicrobials are used for the treatment of clinical diseases in animals. Due to increased demand of the livestock sector, feeding antimicrobials (antibiotics) as growth promoter at sub-therapeutic doses to swine, cattle and poultry has become an integral part of the farm animal production [2,3]. Antibiotic residues are metabolites that are found in trace amounts in any edible portion of the animal product, after the administration of the antibiotics. The consumption of such food may contribute to the development of antibiotic resistance in animals or humans [4]. Animals excrete a considerable portion of antibiotics through faeces and urine, creating a substantial risk of active metabolite accumulation in the environment due to their persistent nature. Antibiotic growth promoters are known to suppress the gut bacteria leaving more nutrients for chicken to be absorbed for greater growth [5]. The residues are further passed on via the food chain. Food of animal origin harboring pathogenic and non-pathogenic bacteria serves as a platform for evolution of new drug-resistant and multidrug-resistant (MDR) bacteria via horizontal exchange of drug-resistant genes [6]. the

consumption of food containing antimicrobial residues directly or indirectly affects human health. Direct effects include the development of antibiotic-resistant bacteria and the accumulation of residues in various target organs, while indirect effects arise from exposure to resistant organisms to different components of the ecosystem, such as water and soil [7].

The consumption of animal-derived food containing residues can lead to the transfer of antibiotic-resistant bacteria to humans, immunopathological effects, autoimmunity, carcinogenicity mutagenicity-nephropathy, hepatotoxicity, reproductive disorders etc.

The widespread use of antimicrobials has led to the development of antimicrobial resistance (AMR) among bacteria which has aggravated due to the inappropriate use of antibiotics in the medical and veterinary sectors [8]. Misuse and overuse of antibiotics may culminate into development of drug-resistant pathogens resulting in poor response to treatment. The use of antibiotics in animals has raised concerns due to its potential threat to public health, due to transmission to humans, leading to the failure of medical treatments [9]. The resistant bacteria may also be released into the environment and then transferred into new hosts in the environment [10,11].

The absence of consensus on standardized policies at both international and national levels in veterinary practices, coupled with limited research, uncharacterized risk impacts, and conflicting stakeholder interests, has led to prolonged neglect of this issue. Considering all the above facts, the present investigation aimed to determine the antimicrobial residue and resistance pattern of isolates/ pathogens recovered from foods of animal origin.

2. Material and Methods

Sample collection and storage:

A total of 250 freshly slaughtered raw buffalo meat samples were collected from the Deonar slaughterhouse, Mumbai, India wherein animals are brought in from all over Maharashtra and neighbouring states. The samples were labelled, packed and brought in insulated container on ice, to the laboratory, Department of Veterinary Public Health, Mumbai Veterinary College, Parel, Mumbai and stored at 4°C for not beyond 24 hours until cultured on standard bacteriological media.

Isolation of bacteria and microbial analysis:

All the buffalo meat samples were trimmed with sterile knife. Samples (25 g) were transferred to 225 mL of Buffered Peptone Water (BPW) and homogenized with stomacher for 10 min. Serial dilution was performed up to 10^{-6} prior to culturing of samples on plates containing culture media. Isolation of bacterial agents from meat samples using selective media was performed using CLSI guidelines (2019) [12].

Isolation of *E. coli*:

One mL of serially diluted sample was spread on the surface of Eosin Methylene Blue (EMB Agar) and incubated further at 37°C for 24 to 48 hours. Presence of metallic green sheen appearance confirmed the presence of *E. coli*. [13].

Isolation of Staphylococcus aureus:

Pre-incubated samples (1.0 mL) in BPW were spread on the surface of Baird-Parker Agar medium (Himedia, India) enriched with Egg Yolk Tellurite Emulsion and incubated further for 37°C for 24 to 48 hours. Black colonies surrounded by opaque halo on Baird- Parker agar is considered presumptive *S. aureus* [14].

Isolation of *Bacillus cereus*:

Pre-incubated samples (1.0 mL) in BPW were spread on the surface of Bacillus Cereus Agar. Greenish colonies are indicative of presence of *Bacillus cereus* [15].

Isolation of *Salmonella* spp.:

From each pre-enriched culture in BPW, 1 mL was inoculated into 10 mL of Rappaport Vassilliadis enrichment broth, followed by incubation at 37°C for 24 h. A loopful from each enriched broth was streaked onto xylose-lysine-desoxycholate (XLD) agar and incubated at 37°C for 24 h. Pink colonies with black centre on XLD agar is presumptive of *Salmonella* spp. [16].

Isolation of *Listeria* spp.:

Pre- enrichment of the sample performed with Half Fraser medium, followed by incubation at 30°C for 24 h. Secondary enrichment was performed by transferring 1 mL incubated Half Fraser medium to 10 mL Fraser Broth. Incubate at 35-37°C for 48±2 hours. Further, inoculation performed on PALCAM Agar to confirm the presence of colonies. The presence of grey green colonies with black centre and black halo is suggestive of *Listeria* spp. [17].

Isolation of *Pseudomonas* spp.:

Pre-incubated samples (1.0 mL) in BPW were spread on the surface of Pseudomonas Selective Agar (CFC) agar. The presence of blue/green or brown pigmentation or fluorescence is indicative of presumptive *Pseudomonas* spp. [18]. Discrete colonies were sub cultured into fresh agar plates aseptically to obtain pure cultures of the isolates. Pure isolates of resulting growth were then stored at 4°C and used for further confirmation of bacteria. Colonies identified as discrete on nutrient agar were carefully examined macroscopically for cultural characteristics such as shape, color, size and consistency. Gram staining as well as appropriate biochemical tests were carried out according to standard procedures. The isolates were identified by comparing their morphological and biochemical characteristics with standard reference organisms with those of known taxa, as described in Bergey's Manual for Determinative Bacteriology (1994) [19].

Antimicrobial Susceptibility Test:

Antimicrobial resistance profiling of the recovered microbial isolates was tested using the disk diffusion method. The guidelines of Clinical Laboratory Standards Institute (Clinical and Laboratory Standards Institute, 2019) [12] were applied. This method is suitable for the determination of an in vitro efficacy of antibiotics by calculating the zone of inhibition diameter, which are caused by diffusion of the agent into the medium surrounding the disc. Fifteen commercially available antibacterial agents (Himedia Laboratories, India) were selected for the purpose. The pre-incubated 24-hour cultures of *Salmonella* spp. and *S. aureus* were diluted in

sterile BPW and matched with the 0.5 MacFarland turbidity standards to get 1×10^8 CFU/mL as total count. Bacterial suspensions were spread on Mueller- Hinton Agar. The antibiotic discs were placed on the agar and incubated at 37°C for 24 hours. The clear zone around each antibiotic disc was measured in millimeter. The following commonly used antibiotics were used: chloramphenicol (30 µg), amikacin (30 µg), cefotaxime (30 µg), co-trimaxole (25 µg), gentamycin (10 µg), amoxicillin (30 µg), tetracycline (10 µg), ciprofloxacin (30 µg), trimethoprim (10 µg), enrofloxacin (5 µg), ampicillin (2 µg), neomycin (10 µg), streptomycin (10 µg), ofloxacin (30 µg), erythromycin (5 µg) and trimethoprim (10 µg). The tested strains were evaluated as susceptible, intermediate, and resistant.

Determination of multiple antibiotic resistance (MAR) index: MAR index was determined for each isolate by using the formula MAR = a/b, where a represents the number of antibiotics to which the test isolate depicted resistance and b represents the total number of antibiotics to which the test isolate has been evaluated for susceptibility [20].

3. Results and Discussions

Microbiological Analysis: The study revealed the prevalence of bacteria with significance to food safety as follows: *Staphylococcus aureus* (65), *E. coli* (28), *Bacillus cereus* (41), *Salmonella* spp. (46), *Pseudomonas* spp.: Nil, *L. monocytogenes*: Nil.

The percent prevalence of *Staphylococcus aureus* in buffalo meat samples was found to be 26.00 %. This is in accordance with the prevalence study in buffalo meat samples collected from retail meat shops in and around Anand, Gujarat was 28% [21]. The prevalence of 25.27% in buffalo meat samples analyzed from Punjab, India [22]. Similar findings have been reported with 25 % [23] and 27.8 % [24] prevalence of *S. aureus* in raw retail meat samples. These findings indicate a higher potential risk of beef for human infections. Beef samples collected and analyzed from formal and informal sectors in South Africa revealed 30.3% [25]. However, 36.00% prevalence of *S. aureus* in buffalo meat samples sold at retail butcheries in Northern India, which is higher than the current study [26].

The prevalence of *Salmonella* spp. in meat samples analyzed was observed to be 18.40%, which was consistent with a report (14.3%) on *Salmonella* spp. in poultry meat samples from Egypt [27]. Similarly, 13.5% prevalence was reported in buffalo meat samples analyzed in Kathmandu [28]. Higher prevalence (35%) has been reported in buffalo meat samples collected and analyzed from Egypt with the conclusion that significant discrepancies in the prevalence results in buffalo meat analyzed by other researchers could be attributed to differences in geographic regions and hygienic conditions during slaughtering and processing as well as sampling season and isolation method [29].

The prevalence of *E. coli* was recorded to be 11.2%, which is in agreement with the study conducted in Turkey, which revealed that 15.3 % of beef samples were positive for *E. coli*, owing to the variation in the quality of the raw materials obtained from different suppliers of beef [27].

Only 16.40% of samples were revealed to be confirmed for the presence of *Bacillus cereus*, which is in concordance with the prevalence of 17.14 % in raw chicken meat analyzed in Anand, Gujarat [30]. The prevalence of *Bacillus* may be ascribed to slaughterhouse sanitation, level of food processing, cross-contamination during processing and handling of meat.

However, *Pseudomonas* spp. and *L. monocytogenes* were absent in the buffalo samples tested. The results of the current work are in contrast with the results reported from Egypt suggesting that the prevalence of Listeria in meat was 6% from the beef samples which can be attributed to inadequate hygienic precautions followed during processing, handling, storage, and distribution of meat and meat products leading contamination [31,32,33]. A study conducted in Iran revealed that *P. aeruginosa* is predominant in raw sheep meat samples collected and analyzed from slaughterhouses [34]. All the samples were confirmed primarily by the growth characteristics on selective media and further, with biochemical testing.

Morphological Characterization: Discrete colonies were sub cultured into fresh agar plates aseptically to obtain pure cultures of the isolates. Pure isolates of the growth obtained was then stored at 4°C and used for further identification of bacteria. Colonies identified as discrete on nutrient agar were carefully examined macroscopically for cultural characteristics such as the shape, colour, size and consistency. Gram staining was performed for identification and confirmation of isolates with respect to the morphological characteristics.

Biochemical Profiling: Biochemical characterization of the bacteria was done by performing specific tests such as catalase test, oxidase test, indole test, methyl red, Voges Proskauer, Citrate tests, Sugar fermentation tests and coagulase test, according to standard procedures and compared with standard reference organisms with those of known taxa, as described in Bergey's Manual for Determinative Bacteriology (1994) [19].

The positive isolates were further subjected to antibiogram study to evaluate its antibiotic sensitivity and resistance patterns.

Antibiogram study: All the positive isolates of pathogens, namely *Bacillus* spp., *Salmonella* spp., *Escherichia coli*, *Listeria monocytogenes*, *Staphylococcus aureus* and *Pseudomonas* spp., were exposed to different antibiotics to identify the resistance pattern of significant pathogens to commonly used antibiotics were shown in Table 1. Zones of inhibition with values lower than 10 mm are designated resistant while values ≥ 10 are designated as sensitive, whereas between 5-10 mm are designated as intermediate.

Table 1. Antibiogram of pathogenic microbes against selective antibiotics

Microbes	Sensitivity (%)	CAM (30 µg)	AMK (30 µg)	CXM (30 µg)	CoT (25 µg)	GMC (10 µg)	AMX (30 µg)	TTC (10 µg)	CPX (30 µg)	TRP (10 µg)	ENR (5 µg)	AMP (2 µg)	NMC (10 µg)	STM (10 µg)	OXC (30 µg)	EMC (5 µg)
S. aureus (230)	S	220 (95.6)	200 (86.9)	197 (85.6)	173 (75.2)	114 (49.8)	92 (40)	3 (1.30)	--	--	--	--	--	--	--	--
	I	--	9 (3.91)	22 (9.56)	20 (8.69)	--	--	3 (1.30)	60 (26.08)	8 (3.47)	--	--	--	--	--	--
	R	13 (5.65)	11 (4.78)	4 (1.73)	10 (4.34)	33 (14.3)	57 (24.7)	113 (49.13)	78 (33.91)	219 (95.21)	--	--	--	--	--	--
E. coli (29)	S	23 (79.31)	29 (100)	14 (48.27)	13 (44.82)	23 (79.31)	3 (10.34)	6 (20.68)	7 (24.13)	--	13 (44.87)	--	--	--	--	--
	I	1 (3.44)	--	7 (24.13)	--	1 (4.28)		5 (17.24)	2 (6.89)	--	1 (4.28)	1 (4.28)	--	--	--	--
	R	4 (13.79)	--	7 (24.13)	15 (51.72)	4 (13.79)	25 (86.20)	16 (55.17)	19 (65.51)	22 (75.86)	15 (51.72)	27 (93.10)	--	--	--	--
Salmonella spp. (46)	S	13 (28.26)	--	--	44 (95.65)	37 (80.42)	40 (86.95)	--	6 (13.04)	--	4 (8.69)	--	45 (97.82)	25 (54.32)	--	--
	I	3 (6.52)	--	--	--	2 (4.37)	--	46 (100)	16 (34.78)	--	--	--	--	9 (19.56)	--	--
	R	30 (65.21)	--	--	2 (4.34)	7 (15.21)	6 (13.04)	--	24 (52.17)	--	42 (91.30)	--	1 (2.17)	12 (26.08)	46 (100)	46 (100)
B. cereus (41)	S	40 (97.56)	--	--	--	40 (97.56)	30 (73.17)	--	--	--	--	26 (63.41)	--	38 (92.68)	--	--
	I	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
	R	1 (2.43)	--	--	--	1 (2.43)	1 (2.43)	15 (36.58)	--	3 (7.31)	--	--	1 (2.43)	1 (2.43)	--	11 (26.82)

(S: Sensitivity, I: Intermediate, R: Resistant

***Antibiotics used in the study**:* CAM: chloramphenicol, AMK: amikacin, CXM: cefotaxim, CoT: co-trimaxole, GMC: gentamycin, AMX: amoxicillin, TTC: tetracycline, CPX: ciprofloxacin, TRP: trimethoprim, ENR: enrofloxacin, AMP: ampicillin, NMC: neomycin, STM: streptomycin, OXC: ofloxacin, EMC: erythromycin, --: No Activity)

Table 2. MAR Index of Resistant pathogens

Sr. No	Resistant pathogens under the study	MAR Index
1.	*S. aureus*	0.6
2.	*E. coli*	0.66
3.	*Salmonella* spp.	0.66
4.	*B. cereus*	0.53

Out of the 15 antibiotics tested in the study, *E. coli* and *Salmonella* spp. predominantly exhibited resistance to 66.6% of the antibiotics tested, followed by *S. aureus* (60%). The lowest resistance was recorded in *B. cereus* (53.3%).

In the current study, out of the 65 *S. aureus* isolates, 95.6% were sensitive to chloramphenicol which is in agreement with 94.4% susceptibility [35]. Intermediate sensitivity was exhibited to ciprofloxacin (26.08%), whereas 95.21% were resistant to trimethoprim. This is in accordance with results reporting 92% resistance against *S. aureus* [36]. Food producing animals harbour *S. aureus* and influence the level of contamination due to the multitude of small slaughter and meat processing [37].

Cent percent sensitivity to amikacin was noted in all the 29 isolates of *E. coli*, and is in accordance with the study designed to determine the antibiogram pattern of *E. coli* with 88.89 % sensitivity to amikacin. Intermediate sensitivity exhibited by cefotaxime (24.13%) whereas 93.10% were resistant to ampicillin [38]. Likewise, high resistance pattern for ampicillin against *E. coli* spp. was observed in clinical samples, collected from Bangladesh and Nagpur, India [39,40] respectively, indicative of indiscriminate use of ampicillin in healthcare centres. Poor management practices and general hygienic conditions contribute to higher infection of *E. coli* [41].

Among the 46 isolates of *Salmonella* spp., 97.82% was sensitive to neomycin and was in agreement with the data obtained from analyzing isolates collected from animal and human sources in Southern Taraba, North-East, Nigeria who reported 100% sensitivity to neomycin in *Salmonella* spp. [42]. The resistance pattern was followed by ciprofloxacin (34.78%) whereas highest resistance (100%) was exhibited with ofloxacin and erythromycin. Similarly, high resistance trends with respect to use of fluoroquinolones (83.3%) and erythromycin (100%), respectively for treatment of *Salmonella* spp. infections have been reported [43,44]. However, in contrast to the current study, cent percent sensitivity against ofloxacin from *Salmonella* spp. isolates had been reported from slaughtered cattle and the processing environment in Abuja abattoirs, Nigeria [45]. The odds of *Salmonella* isolation were 7.8 times higher when meat handlers are illiterate, and similarly was also reported to be higher among workers of butcher and restaurants without any training on food safety and hygiene [46].

Gentamycin and chloramphenicol were 100% sensitive to *B. cereus*, and is in accordance with 97.63% and 100% sensitivity to *B. cereus*, [30,47] respectively. The antibiogram study of isolated *B. cereus* from raw meat products revealed gentamicin (100%) and chloramphenicol (89.69%) to be the most sensitive [48]. Intermediate resistance was not exhibited by any of the antibiotics under the study. Tetracyclines revealed 36.58% resistance in the current study, which is in line with the 22.6% resistance to tetracyclines obtained on analysis and isolation of *B. cereus* isolated from dairy samples [49].

Multiple Antibiotic Resistance (MAR) index: The MAR Index of organisms are as enlisted in Table 2. *E. coli* and *Salmonella* spp. reported to have high MAR index of 0.66, whereas *Bacillus* spp. was found to have the lowest MAR index (0.55). The MAR Index > 0.2 is suggestive of multidrug resistance due to high-risk application and contamination of antibiotics [50]. In compliance with the findings of the current study, the MAR index of *S. aureus* and *Salmonella* spp. reported to be 0.6 each when isolated from raw buffalo meat [51]. The MAR index for *E. coli* isolated from meat products was 0.5 and is in line with the findings of the current research. [52]. The MAR index of *S. aureus* was found to be 0.6 in cow meat [53], whereas that of *B. cereus* was in the range of 0.27–0.73 when isolated from several meat and meat products [54]. High MAR value corresponds to exposure of the bacteria to a wide range of antibiotics.

Staphylococcus aureus is the most predominant

microbe detected in buffalo meat, in the current study, followed by *Salmonella* spp. and *E. coli*. They contribute significantly to prevalence of foodborne diseases and mortality in underdeveloped and developing nations, costing the health and social sectors billions of dollars [55]. The most important factor for development of antibiotic resistance is the extended utilization of antimicrobial agents in food animal production and humans [46]. Judicious antimicrobial use includes use of antimicrobials for treatment of diseased cattle individually to maximize therapeutic efficacy and reduce the spread of AMR instead of administering antimicrobials at sub-therapeutic doses to the entire herds for production purposes [56]. Indiscriminate use of antibiotics for treatment of animals, along with environmental contamination of residues lead to development of antibiotic resistance [57]. These endogenous pathogens cause meat-borne diseases that threaten consumer health and undermine the integrity of consumer protection [15].

4. Conclusion

The presence of pathogenic *Staphylococci*, *E. coli*, *Salmonella* and *Bacillus* spp. revealed the fact that the meat maybe contaminated owing to inadequate sanitation and hygiene measures or probable cross-contamination at the source, which could significantly endanger public health. The prevalence of various microorganisms in 250 buffalo meat samples was reported such as *Staphylococcus aureus* in 65 samples, *Salmonella* spp. in 46 samples, *Bacillus cereus* in 41 samples, *E. coli* in 28 samples, while no growth was observed for the *Listeria monocytogenes* and *Pseudomonas* spp. *Staphylococcus aureus* was found to be the most prevalent pathogen in buffalo meat (26.00 %), followed by *Salmonella* spp. (18.40 %), *Bacillus cereus* (16.40 %) and *E. coli*. (11.2 %), while *Pseudomonas* spp. and *Listeria monocytogenes* was not present in any of the samples. The bacterial isolates were further subjected to antibiotic susceptibility testing which revealed that conventionally used antibiotics such as chloramphenicol, amikacin, cefotaxim, co-trimaxole and gentamicin exhibited maximum resistance against microbes isolated from buffalo meat, which illustrates the effects of widespread use of antibiotics in healthcare posing a risk to the development of resistance factors which in turn endangers public health. Thus, implementation of good hygienic practices (GHP) and good manufacturing practices (GMP) for hygienic slaughtering, meat processing, transportation and storage is extremely significant to deliver wholesome meat.

Author's Contributions

All the authors contributed effectively to this work. The authors contributed actively to analyzing the results and writing the article.

Conflict of Interest

All the authors declare that they have no conflict of interest.

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References

[1] Carbas, B., Cardoso, L., & Coelho, A. C. (2012). Investigation on the knowledge associated with foodborne diseases in consumers of northeastern Portugal. *Food Control, 30* (1), 54-57.

[2] Angenent, L. T., Mau, M., George, U., Zahn, J. A., & Raskin, L. (2008). Effect of the presence of the antimicrobial tylosin in swine waste on anaerobic treatment. *Water Research, 42*, 2377–2384.

[3] Kemper, N., Färber, H., Skutlarek, D., & Krieter, J. (2008). Analysis of antibiotic residues in liquid manure and leachate of dairy farms in northern Germany. *Agricultural Water Management, 95*, 1288–1292.

[4] Landers, T. F., Cohen, B., Wittum, T. E., & Larson, E. L. (2012). A review of antibiotic use in food animals: Perspective, policy, and potential. *Public Health Reports, 127* (1), 4-22.

[5] Visa, I. (Ed.). (2014). *Sustainable Energy in the Built Environment-Steps Towards NZEB: Proceedings of the Conference for Sustainable Energy (CSE) 2014*. [Viewed on 10th July, 2024].

[6] Saud, B., Paudel, G., Khichaju, S., Bajracharya, D., Dhungana, G., Awasthi, M. S., & Shrestha, V. (2019). Multidrug-resistant bacteria from raw meat of buffalo and chicken in Nepal. *Veterinary Medicine International, 1*, 7960268.

[7] Ondon, B. S., Li, S., Zhou, Q., & Li, F. (2021). Sources of antibiotic resistant bacteria (ARB) and antibiotic resistance genes (ARGs) in the soil: A review of the spreading mechanism and human health risks. *Reviews of Environmental Contamination and Toxicology, 256*, 121-153.

[8] Thakur, S. D., & Panda, A. K. (2017). Rational use of antimicrobials in animal production: A prerequisite to stem the tide of antimicrobial resistance. *Current Science, 113*(10), 1846-1857.

[9] Hao, H., Cheng, G., Iqbal, Z., Ai, X., Hussain, H. I., Huang, L., & Yuan, Z. (2014). Benefits and risks of antimicrobial use in food-producing animals. *Frontiers in Microbiology, 5*, 288.

[10] Hower, S., Phillips, M. C., Brodsky, M., Dameron, A., Tamargo, M. A., Salazar, N. C., & Plano, L. R. (2013). Clonally related methicillin-resistant *Staphylococcus aureus* isolated from short-finned pilot whales (*Globicephala macrorhynchus*), human volunteers, and a bayfront cetacean rehabilitation facility. *Microbial Ecology, 65*(4), 1024-1038.

[11] Verkade, E., & Kluytmans, J. (2014). Livestock-associated *Staphylococcus aureus* CC398: Animal reservoirs and human infections. *Infection, Genetics and Evolution, 21*, 523-530.

[12] Clinical Laboratory and Standards Institute. (2019). *Performance standards for antimicrobial susceptibility testing* (29th ed).

[13] Kabir, A. B. M. (2017). *A study on the prospect of Escherichia coli isolated from raw beef samples as a potential reservoir of antibiotic resistance* (Doctoral dissertation, BRAC University). Retrieved on 15th July, 2024, from [BRAC University Digital Repository].

[14] Naas, H. T., Edarhoby, R. A., Garbaj, A. M., Azwai, S. M., Abolghait, S. K., Gammoudi, F. T., & Eldaghayes, I. M. (2019). Occurrence, characterization, and antibiogram of *Staphylococcus aureus* in meat, meat products, and some seafood from Libyan retail markets. *Veterinary World, 12*(6), 925.

[15] Hassan, M. K., Jahan, L., Sultana, P., Hasan, A., & Siddique, M. P. (2021). Detection and antibiogram of different bacterial agents from market goat meat. *Research in Agriculture Livestock and Fisheries, 8*(1), 135-143.

[16] Swati Singh, S. S., Kshirsagar, D. P., Brahmbhatt, M. N., Nayak, J. B., & Chatur, Y. A. (2015). Isolation and characterization of *Salmonella* spp. from buffalo meat samples. *Buffalo Bulletin, 34*(3), 301-302.

[17] Eruteya, O. C., Odunfa, S. A., & Lahor, J. (2014). *Listeria* spp. in raw cow and goat meat in Port Harcourt, Nigeria. *British*

Biotechnology Journal, 4(2), 204-214.

[18] Arslan, S., Eyi, A., & Özdemir, F. (2011). Spoilage potentials and antimicrobial resistance of *Pseudomonas* spp. isolated from cheeses. *Journal of Dairy Science, 94*(12), 5851-5856.

[19] Holt, J. G., Krieg, N. R., Sneath, P. H. A., Staley, J. T., & Williams, S. T. (1994). *Bergey's Manual of Determinative Bacteriology* (9th ed.). Williams and Wilkins Press.

[20] Singh, S. K., Ekka, R., Mishra, M., & Mohapatra, H. (2017). Association study of multiple antibiotic resistance and virulence: a strategy to assess the extent of risk posed by bacterial population in aquatic environment. Environmental monitoring and assessment, 189, 1-12.

[21] Likhitha, P., Nayak, J. B., & Thakur, S. (2022). Prevalence of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* in retail buffalo meat in Anand, India. *The Pharma Innovation Journal, 11*(6), 17-20.

[22] Zehra, A., Gulzar, M., Singh, R., & Kaur, S. (2019). Methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* from the retail meat shops and customers. *International Journal of Current Microbiology and Applied Sciences, 8*, 1929-1939.

[23] Raji, M. A., Garaween, G., Ehricht, R., Monecke, S., Shibl, A. M., & Senok, A. (2016). Genetic characterization of *Staphylococcus aureus* isolated from retail meat in Riyadh, Saudi Arabia. *Frontiers in Microbiology, 7*, 911.

[24] Thapaliya, D., Forshey, B. M., Kadariya, J., Quick, M. K., Farina, S., O'Brien, A., Nair, R., & Smith, T. C. (2017). Prevalence and molecular characterization of *Staphylococcus aureus* in commercially available meat over a one-year period in Iowa, USA. *Food Microbiology, 65*, 122-129.

[25] Jaja, I. F., Jaja, C. J. I., Chigor, N. V., Anyanwu, M. U., Maduabuchi, E. K., Oguttu, J. W., & Green, E. (2020). Antimicrobial resistance phenotype of *Staphylococcus aureus* and *Escherichia coli* isolates obtained from meat in the formal and informal sectors in South Africa. *BioMed Research International, 2020*(1), 3979482.

[26] Khan, J. A., Rathore, R. S., Ahmad, I., Gill, R., Husain, F. M., & Akhtar, J. (2022). High prevalence of multidrug-resistant *Staphylococcus aureus* from buffalo beef sold at retail butcheries in Northern India. *Acta Scientific Microbiology, 5*(10), 2581-3226.

[27] Eyi, A., & Arslan, S. (2012). Prevalence of *Escherichia coli* in retail poultry meat, ground beef, and beef. *Medycyna Weterynaryjna Veterinary Medicine Science and Practice, 68*(4), 237-240.

[28] Maharjan, M., Joshi, V., Joshi, D. D., & Manandhar, P. (2006). Prevalence of Salmonella species in various raw meat samples of a local market in Kathmandu. *Annals of the New York Academy of Sciences*, 1081(1), 249-256.

[29] Mohammed, T., Zakaria, A., Abd-Elghany, S., & Sallam, K. (2023). Prevalence, genetic characterization, and antibiogram of *Salmonella enterica* recovered from buffalo meat. *Mansoura Veterinary Journal, 24*(1), 14-21.

[30] Suthar, A. P., Kumar, R., Savalia, C. V., Nayak, D. N., & Kalyani, I. H. (2022). Determination of prevalence and multidrug resistance phenotypes of *Bacillus cereus* in raw chicken meat and swabs of human subjects. *Pharma Innovation, 11*(12), 1159-1164.

[31] Al-Humam, N. A., Reda, L., Mohamed, R. E., El-Ghareeb, W. R., Darwish, W. S., & Ibrahim, N. A. (2021). Prevalence and antibiogram of *Listeria monocytogenes* in retailed buffalo raw meat and mince with a protection trial using nisin, and gingerol. *Buffalo Bulletin, 40*(4), 47-57.

[32] De Cesare, A., Parisi, A., Mioni, R., Comin, D., Lucchi, A., & Manfreda, G. (2017). *Listeria monocytogenes* circulating in rabbit meat products and slaughterhouses in Italy: Prevalence data and comparison among typing results. *Foodborne Pathogens and Disease, 14*(3), 167-176.

[33] Liu, Y., Sun, W., Sun, T., Gorris, L. G., Wang, X., Liu, B., & Dong, Q. (2020). The prevalence of *Listeria monocytogenes* in meat products in China: A systematic literature review and novel meta-analysis approach. *International Journal of Food Microbiology, 312*, 108358.

[34] Poursina, S., Ahmadi, M., Fazeli, F., & Ariaii, P. (2022). Prevalence and antibiotic resistance of *Pseudomonas aeruginosa* isolates from raw meat samples of small ruminants. *Journal of Pharmaceutical Negative Results, 13*(9), 9742-9748.

[35] Al-Zoubi, M. S., Al-Tayyar, I. A., Hussein, E., Al Jabali, A., & Khudairat, S. (2015). Antimicrobial susceptibility pattern of *Staphylococcus aureus* isolated from clinical specimens in Northern area of Jordan. *Iranian Journal of Microbiology, 7*(5), 265.

[36] Nurjadi, D., Schäfer, J., Friedrich-Jänicke, B., Mueller, A., Neumayr, A., Calvo-Cano, A., & Zanger, P. (2015). Predominance of *dfrG* as determinant of trimethoprim resistance in imported *Staphylococcus aureus*. *Clinical Microbiology and Infection, 21*(12), 1095-e5.

[37] Thwala, T., Madoroba, E., Basson, A., & Butaye, P. (2021). Prevalence and characteristics of *Staphylococcus aureus* associated with meat and meat products in African countries: A review. *Antibiotics, 10*(9), 1108.

[38] Khanal, S., Kandel, M., & Shah, M. P. (2019). Antibiogram pattern of *Escherichia coli*, *Salmonella* spp., and *Staphylococcus* spp. isolates from broiler chicken. *Nepalese Veterinary Journal, 36*, 105-110.

[39] Alipourfard, I., & Nili, N. Y. (2010). Antibiogram of extended spectrum beta-lactamase (ESBL) producing *Escherichia coli* and *Klebsiella pneumoniae* isolated from hospital samples. *Bangladesh Journal of Medical Microbiology, 4*(1), 32-36.

[40] Kamble, G. A., Shah, R. C., & Tumane, P. M. (2013). Characterization and antibiogram study of *Escherichia coli* clinical isolates. *Blood, 25*(1), 24.

[41] Zanella, A., Alborali, G. L., Bardotti, M., Candotti, P., Guadagnini, P. F., Martino, P. A., & Stonfer, M. (2000). Severe *Escherichia coli* O111 septicaemia and polyserositis in hens at the start of lay. *Avian Pathology, 29*(4), 311-317.

[42] Abhadionmhen, A. O., Imarenezor, E. P. K., Brown, S. T. C., Lana, O. E., & Usiabulu, O. Q. (2024). Molecular identification of *invA* gene from *Salmonella* species isolated from human sources in Southern Taraba, North-East Nigeria. *Asian Journal of Research in Infectious Diseases, 15*(3), 7-16.

[43] Abdeen, E., Elmonir, W., Suelam, I. I. A., & Mousa, W. S. (2018). Antibiogram and genetic diversity of *Salmonella enterica* with zoonotic potential isolated from morbid native chickens and pigeons in Egypt. *Journal of Applied Microbiology, 124*(5), 1265-1273.

[44] Akhtar, F., Hussain, I., Khan, A., & Rahman, S. U. (2010). Prevalence and antibiogram studies of *Salmonella enteritidis* isolated from human and poultry sources. *Pakistan Veterinary Journal, 30*(1), 25-28.

[45] Shaibu, A. O., Okolocha, E. C., Maikai, B. V., & Olufemi, O. T. (2021). Isolation and antibiogram of *Salmonella* species from slaughtered cattle and the processing environment in Abuja abattoirs, Nigeria. *Food Control, 125*, 107972.

[46] Gebremedhin, E. Z., Soboka, G. T., Borana, B. M., Marami, L. M., Sarba, E. J., Tadese, N. D., & Ambecha, H. A. (2021). Prevalence, risk factors, and antibiogram of nontyphoidal *Salmonella* from beef in Ambo and Holeta Towns, Oromia Region, Ethiopia. *International Journal of Microbiology, 2021*(1), 6626373.

[47] Weber, D. J., Saviteer, S. M., Rutala, W. A., & Thomann, C. A. (1988). In vitro susceptibility of *Bacillus* spp. to selected antimicrobial agents. *Antimicrobial Agents and Chemotherapy, 32*(5), 642-645.

[48] Rather, M. A., Aulakh, R. S., Gill, J. P., & Ghatak, S. (2012). Enterotoxin gene profile and antibiogram of *Bacillus cereus* strains isolated from raw meats and meat products. *Journal of Food Safety, 32*(1), 22-28.

[49] Osama, R., Ahmed, M., Abdulmawjood, A., & Al-Ashmawy, M. (2020). Prevalence and antimicrobial resistance of *Bacillus cereus* in milk and dairy products. *Mansoura Veterinary Medical Journal, 21*(2), 11-18.

[50] Joseph, A. A., Odimayo, M. S., Olokoba, L. B., Olokoba, A. B., & Popoola, G. O. (2017). Multiple antibiotic resistance index of *Escherichia coli* isolates in a tertiary hospital in southwest Nigeria. *Medical Journal of Zambia, 44*(4), 225-232.

[51] Nwankwo, C. C., Ezeonuegbu, B. A., & Owei, M. D. (2024). Antibiogram of foodborne pathogenic bacteria isolated from raw pork and beef meat. *Magna Scientia Advanced Research and Reviews, 11*(1), 325-338.

[52] Hassanien, F. M., Nada, S. M., & Abd-Elsattar, A. M. (2016). Incidence of *E. coli* in some meat products. *Benha Veterinary Medical Journal, 30*(1), 104-108.

[53] Jolapamo, O. T., & Osatoyinbo, O. O. (2023). Isolation, identification, and antibiogram of bacterial pathogens from cow meat obtained from different market sources. *Achievers Journal of Scientific Research, 5*(2), 72-79.

[54] Algammal, A. M., Eid, H. M., Alghamdi, S., Ghabban, H., Alatawy, R., Almanzalawi, E. A., & El-Tarabili, R. M. (2024). Meat and meat products as potential sources of emerging MDR *Bacillus cereus*: *groEL* gene sequencing, toxigenic and

antimicrobial resistance. *BMC Microbiology*, *24*(1), 50.

[55] Abdel-Atty, N. S., Abdulmalek, E. M., Taha, R. M., Hassan, A. H., & Adawy, A. A. (2023). Predominance and antimicrobial resistance profiles of *Salmonella* and *E. coli* from meat and meat products. *Journal of Advanced Veterinary Research*, *13*(4), 647-655.

[56] Cameron, A., & McAllister, T. A. (2016). Antimicrobial usage and resistance in beef production. *Journal of Animal Science and Biotechnology*, *7*(68), 1-22.

[57] Argudín, M. A., Deplano, A., Meghraoui, A., Dodémont, M., Heinrichs, A., Denis, O., & Roisin, S. (2017). Bacteria from animals as a pool of antimicrobial resistance genes. *Antibiotics*, *6*(2), 12.