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Review Article

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Microbial Quality of Sheep Meat and Offal: A Review

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Abstract

Sheep meat including mutton and lamb and its edible offal are regarded as important sources of high quality animal protein, essential amino acids, vitamins and minerals. However, unsanitary handling of such meat sources during the slaughtering, dressing, evisceration, or further processing might contribute to contamination of meat with a vast array of microorganisms including those with public health significance such as *E. coli*, and *Salmonella* spp. In this review, we would like to highlight the role of sheep meat and offal as potential sources of the spread of *E. coli*, and *Salmonella* spp. It was clear that adoption of strict hygienic measure during the entire steps of the carcass preparation and processing as well as efficient cooking of such meat and edible offal are among the suggested *strA*tegies to prevent the possible contamination of sheep meat with foodborne pathogens.

KEYWORDS
Sheep meat, Offal, *E. coli*, *Salmonella* spp

INTRODUCTION

Sheep meat either mutton or lamb constitutes a major part of the high quality protein sources in Egypt and around the world. Mutton with protein content reaching to about 20%, high moisture content (75%), fat (5.2%), carbohydrate (1.5%), vitamins such as vitamin B complex, and minerals such as iron, zinc, calcium, and phosphorus plain important role in the human nutrition as it can support man with part of his daily needs of such nutrients (Klobukowski *et al*., 2002; Sallam and Morshdy, 2008; Elabbasy *et al*., 2021). Mutton is regarded as a rich meat source for essential amino acids such as arginine, histidine, leucine, isoleucine, lysine, methionine, riboflavin, threonine, and valine (Löest *et al*., 1997). Moreover, sheep meat and liver were reported to contain considerable concentrations of carotenoids and retinol as compared to other meat producing animals (Darwish *et al*., 2016). However, mutton, lamb, and their products were reported to be associated with some cases of foodborne infections worldwide (Elshafie *et al*., 2022). For the following reasons, it is important to be aware that sheep meat are less frequently reported to be linked with foodborne illnesses than meat from other animal species: mutton are processed less frequently than other meats; a) lower level of production; b) less intense production, resulting in a weaker microbial contamination; c) the typical boiling or cooking operations of the final product (Pépin *et al*., 1997).

It has been discovered that meat serves as a key means of transferring foodborne pathogens to people all across the world. Food-borne illnesses in humans can be brought on by microbial meat contamination. Meat microbial loads must be studied in order to reduce the risk of consumer sickness posed by microbial meat pollutants. Recently, there has been a significant increase in public awareness about foodborne illnesses, particularly those connected to meat and animal products. The handling of the meat during preparation or consumption by the consumer is the main way that meat can spread illnesses and diseases. In addition, meat contamination by foodborne pathogens is typically caused by abattoir procedures such skinning, evisceration, and chilling. Therefore, veterinary public health officials' ongoing microbiological surveillance of slaughter carcasses is essential for preventing contamination and the emergence of meat-related foodborne disorders (Ncoko *et al*., 2020).

Foodborne illnesses are categorized into three main classes; 1st is foodborne intoxications which were associated with the ingestion of contaminated with already performed toxins, particularly those produced by *Staphylococcus aureus*, Clostridium botulinum, and mycotoxins. 2nd class is foodborne infections that associated with the ingestion of foods contaminated with some pathogens such as *E. coli*, *Salmonella* spp., Shiegella spp., Aeromonas spp., *Campylobacter* spp., Vibrio spp., and Listeria spp. The third type is Foodborne toxico-infections which are associated with ingestion of foods contaminated with Bacillus cereus, and Clostridium perfringens (Darwish *et al*., 2022).

In this review, we would like to highlight the role of sheep meat including mutton, lamb, and their products as potential sources of two major foodborne infectious agents, *E. coli*, and *Salmonella* spp.

Sheep meat as a source of *E. coli*

In Egypt, Abdul-Raouf *et al*. (1996) mentioned that in order to find out if *Escherichia coli* O157:H7 was detected in 175 samples of raw ground beef, poultry, lamb, and unpasteurized milk, a survey was conducted in middle Egypt. The pathogen was found in 3 of 50 (6%) samples of beef, 2 of 50 (4%) samples of poultry, 1 of 25 (4%) samples of lamb, and 3 of 50 (6%) milk samples that were taken from slaughterhouses, grocery stores, and farmer's homes. Moreover, A total of 50 carcasses, including 10 each of beef, buffalo, camel, sheep, and goat, as well as 20 freezer beef samples, yielded 220 random meat samples from various animal species. Four cut samples from the neck, shoulder, abdomen, and thigh were used to represent each carcass. In order to evaluate their microbiological status and compare the degrees of contamination among animal species and carcass slices, all samples were obtained from a random sampling of retail and butcher shops in the Beni-Suef governorate. This study presented and compared the means of counts (CFU/g) of total aerobic bacteria, coliforms, faecal coliforms, *E. coli*, *Staphylococcus aureus*, in each of the corpses from beef, buffalo, camel, sheep, and goats, as well as imported frozen beef. In addition to the prevalence of *Salmonella* spp., *E. coli*, and coagulase-positive *Staphylococcus aureus*. The results showed that the samples of beef, buffalo, and mutton that were under examination were more contaminated than those of other types of meat. *Escherichia coli* O157:H7, *Campylobacter* jejuni, and Clostridium perfringens was linked to eating meat from the small ruminants including the sheep as reported in several European countries (Pépin *et al*., 1997). For the purpose of determining the prevalence of virulence determinants, Verotoxin 1 (VT1), Verotoxin 2 (VT2), Intimin (*eae*) genes, and enterohemolysin synthesis, 93 *Escherichia coli* isolates from market mutton in India belonging to 35 serotypes were investigated. SYBR green format Real Time PCR was used to detect virulence genes, and amplicons were verified by melt curve analysis. The prevalence of the VT1 gene was substantially higher (38.70%) in these isolates than the VT2 gene (0%) or the *eae* gene (3.22%), which were both much less common. When tested on washed sheep blood agar enriched with CaCl(2), isolates that produced enterohemolysin were detected in 31.18% of cases. The VT1 gene was present in all isolates that produced enterohemolysin (Bhong *et al*., 2008). In Norway, 17 Children diarrheal cases were found between 20 February and 6 April 2006, of which 10 children, including one fatal case, developed HUS. Following pilot interviews, a matched case-control research was conducted and revealed a link between a traditional cured banger and STEC infection (odds ratio 19.4 (95% CI: 2.4-156)). The product included *E. coli* O103:H25 that was identical to the outbreak strain identified by the MLVA profile and was linked to tainted mutton. They described an outbreak that was brought on by an uncommon STEC variant (O103:H25, *stx2*-positive). The fact that more than half of the individuals with a diagnosis went on to develop HUS suggests that the etiological agent is particularly pathogenic. STEC, a human pathogen, continues to have a significant reservoir in small ruminants. To reduce the likelihood, better slaughtering cleanliness and good production procedures for cured sausage products are required (Schimmer *et al*., 2008). Hiko *et al*. (2008) recorded that out of the 738 meat samples analyzed, 31 (4.2%) contained *E. coli* O157:H7. The highest prevalence (8%) was found in beef among the meat samples sampled in Ethiopia, followed by lamb and mutton (2.5%) and goat meat (2%). The identified strains were discovered to be completely sensitive to trimethoprim-sulfamethoxazole, amikacin, chloramphenicol, gentamicin, nalidixic acid, and norfloxacin. In 7/31 (22.6%) isolates, multidrug resistance to three or more medicines was found. Kagambèga *et al*. (2011) examined the hygienic status of the meat sold at outdoor markets in Ouagadougou, Burkina Faso, as well as the prevalence of *Salmonella* and *Escherichia coli*. From four neighborhood markets, a total of 150 samples of beef meat (n = 45), beef intestine (n = 45), mutton (n = 30), and chicken (n = 30) were gathered for the study. The incidence of *Salmonella enterica* subsp. enterica was 9.3%, and six serotypes—Derby, Tilene, Hato, Bredeney, Agona, and Senftenberg—all previously unreported in Burkina Faso—were found. The majority of the 12 antimicrobial medications tested were effective against the *Salmonella* isolates. All meat varieties have a 100% prevalence of *E. coli*. Unhygienic conditions were found when the manufacturing, transportation, presentation, and sale of the meat were examined for hygiene practises. meat vendors. Meat vendors had little education and little understanding of how foodborne diseases spread. The results demon*strA*ted the urgent need for food handlers to receive training in safe food handling procedures. The major reservoir of the hig*hly* contagious foodborne bacterium *Escherichia coli* O157:H7 has been identified as cattle. Nevertheless, growing evidence demonstrates the significance of sheep as an *E. coli* O157:H7 carrier. In Iran, The presence of *E. coli*, its serogroups, virulence factors, and antibiotic resistance qualities in ruminant meat were examined using culture, PCR, and disc diffusion methods on a total of 820 raw meat samples. There were 238 (29.02%) positive *E. coli* test results overall. *Stx1*, *Stx2*, *eaeA*, and e*hly* were among the many virulence genes present in all of the isolates. All of the examined serogroups, with the exception of O145, O121, and O128, were discovered in beef, sheep, and goat. Camels contained the O91, O113, O111, O103, O26, and O157 serogroups. Overall, the combination of the genes *aadA*1 and *bla*$_{SHV}$ was the most common source of antibiotic resistance. Penicillin exhibited the highest level of STEC strain resistance, whilst nitrofurantoin and ciprofloxacin showed only moderate resistance. These results demon*strA*ted the need to reevaluate meat inspection and health care at Iranian slaughterhouses and butchers (Momtaz *et al*., 2013). Likely, Over the course of a year, the presence of *E. coli* O157/O157:H7 in 100 sheep taken to the abattoir in Kirikkale, Turkey was examined in recto-anal mucosal exchange and carcass sponge samples. Molecular characteristics (*stx1*, *stx2*, *eaeA*, *hly*, *lpfA1-3*, *espA*, *eae-α1*, *eae-α2*, *eae-β*, *eae-β1*, *eae-β2*, *eae-γ1*, *eae-γ2/θ*, *stx1*c, *stx1*d, *stx2*c, *stx2*d, *stx2*e, *stx2*f, *stx2*g, blaampC, *tet*(A), *tet*(B), *tet*(C), *tet*(D), *tet*(E), *tet*(G), *sul1*, *sul2*, *floR*, *cmlA*, *strA*, *strB* and *aadA*) of 79 isolates were determined and minimum inhibitory concentrations of 20 different antibiotics were investigated. *E. coli* O157/O157:H7 was discovered in 18% of the sheep tested. Despite the fact that none of the categories (season, sex, or age range) had a discernible impact on prevalence, and was more common in yearlings than lambs and adult sheep, as well as male sheep than female sheep. Shiga-toxigenic *E. coli* (STEC) O157:H7 was also found in 2% and 8%, respectively, of sheep carcasses and feces. Additionally, all isolates showed evidence of *lpfA1-3* and *eae*-1. Despite the fact that four isolates of sorbitol-fermenting *E. coli* O157 tested positive for *tet*(A), *sul1*, and *aadA*, none of the isolates shown resistance to the tested antibiotics (Gencay, 2014). In Saudi Arabia, Hessain *et al*. (2015) mentioned that *Escherichia coli* O157:H7, which causes diarrhoea and hemolytic-uremic syndrome (HS), is one example of a pathogenic bacteria that may be present in raw meat and may be dangerous to humans. In order to assess the prevalence and molecular detection characterization of *E. coli* serotype O157:H7 recovered from raw meat and meat products collected in Saudi Arabia, 200 raw meat samples and 170 meat products totaling 370 meat samples were gathered from abattoirs and markets in Riyadh, Saudi Arabia, between January 25, 2013, and March 25, 2014. It was discovered that 11 (2.97%) strains of *E. coli* O157:H7 had been recovered through bacterial investigation of the meat samples and serotyping of the isolated *E. coli*. In raw beef, chicken, and mutton, *E. coli* O157:H7 isolation rates were 2%, 2.5%, and 2.5%, respectively. However, the incident never happened with raw turkey. Ground beef, beef burgers, beef sausage, ground chicken and chicken burgers all had *E. coli* O157:H7 incidences that were, correspondingly, 5%, 10%, 0.0%, 5% and 0.0%. The results of the multiplex PCR assay showed that 5 (45.45%) *E. coli* O157:H7 isolates from ground beef, ground chicken, and raw beef had both *stx1* and *stx2*, while 3 (27.27%) of the 11 *E. coli* O157:H7 isolates from raw beef, chicken, and mutton contained *stx1*, *stx2*, and *eae*. Only one *E. coli* O157:H7 isolate from beef burgers carried the *stx1* gene, whereas two of them had the *hly*A gene. These findings highlight the urgent need for effective controls and hygienic handling of raw meat. In South Africa, *E. coli* and *Salmonella* spp. were found in meat and water from specific slaughterhouses, as well as the aerobic plate count (APC) and enterobacteria*ceae* count. For this study, the Provincial Veterinary Department of the Eastern Cape Province used retrospective data (n=100) from abattoirs gathered in 2017 and prospective survey data of meat (n=50) collected from abattoirs in the Eastern Cape Province in 2018. From the samples, APC and Enterobacteria*ceae* were counted. *E. coli* and *Salmonella* were also identified using selective media. Both retrospective and prospective studies found that the APC for all samples varied between 2 and 4.50 log CFU/cm^2, but Enterobacteria*ceae* levels were similar at 2-4.00 log CFU/cm^2. APC and Enterobacteria*ceae* count across all meat kinds did not differ significantly (p>0.05). In 50% of the beef, *Salmonella* and *E. coli* were discovered. *Salmonella* was identified in 66.7% of the mutton, while *E. coli* was not. And whereas *Salmonella* was absent from any water sample, *E. coli* was present in 91.7% of them (Ncoko *et al*., 2020). In addition, Rani *et al*. (2023) mentioned that there are few studies examining the microbial loads in South African beef. They compared the microbiological contamination of various meat kinds coming from low-throughput (LTA) and high-throughput (HTA) abattoirs at three points along the supply chain, from the slaughterhouse to retail outlets. It has been discovered that meat is a key means of spreading poo. Carcasses of beef, hog, and mutton (n = 216) were sampled at three different phases in the process: loading at the abattoirs, unloading at the supply points, and marketing. Total bacterial count (TBC), coliform count (CC), presumptive *Escherichia coli* (*E. coli*) (PEC), and *Staphylococcus aureus* (*S. aureus*) detection were performed on all samples. In mutton, PEC predominated at the offloading stage at the HTA, while TBC dominated at loading, CC was similar across distribution chain stages, and *S. aureus* predominated at the display stage at the LTAs. However, TBC was affected at loading, CC was similar across distribution chain stages, PEC was affected at loading, and TBC was affected at loading. In China, Hu *et al*. (2022) reported that foodborne pathogen shiga toxin-producing *Escherichia coli* (STEC) can cause serious human illnesses such hemolytic uremic syndrome (HUS). STEC infections in humans are frequently brought on by eating contaminated food, particularly raw meats. The purpose of this study was to characterize the meat-derived STEC strains using whole genome sequencing and to ascertain the prevalence of STEC in raw meats. According to our research, 7.5% of raw beef samples and 26.6% of raw mutton samples were positive for STEC by culture. The virulent serotypes O157:H7 and O26:H11 were among the thirteen serotypes found in this study's 22 meat-derived isolates. 22 isolates had seven different Shiga toxin (Stx) subtypes, with *stx1*c and *stx1*c + *stx2*b predominating. Three isolates from mutton were discovered to have the previously described *stx2*k subtype. Intimin (*eae*), enterohemorrhagic *E. coli* (EHEC) hemolysin (*ehxA*), EHEC factor for adherence (*efa1*), heat-stable enterotoxin 1 (*astA*), and type III secretion system effectors were among the additional virulence genes found in meat-derived STEC strains. One isolate from mutton was resistant to tetracycline, chloramphenicol, and trimethoprim-sulfamethoxazole, three antibiotics. The genetic diversity of the meat-derived strains in this investigation was shown by whole-genome phylogeny. The fact that the isolates of O157:H7 and O26:H11 in this investigation were phylogenetically related to germs from HUS patients suggests that they have the potential to be harmful.

Sheep meat as a source of *Salmonella* spp.

Several reports investigated the occurrence of *Salmonella* spp., in sheep meat and offal and its direct impact on human health. For instances, Purvis *et al*. (2005) recorded that a *Salmonella* Typhimurium DT120 outbreak that affected patients in the north of England in the summer of 1999 was uncommon in that it was responsive to antimicrobial medications. The epidemic was traced to mutton and lamb from a nearby butchery, and four holding paddocks where sheep were kept before being killed came under the spotlight. These paddocks and the concrete course running from them were sampled for dirt and excrement in November 1999, as well as for faeces. 59 out of the 100 samples yielded *Salmonella* Typhimurium isolates. Seven visits to the abattoir were performed between January 2000 and October 2000, during which 100 samples from the concrete race and paddocks were collected and tested for the presence of *Salmonella*. *S.* Typhimurium DT120 was still extensively present in the paddocks until April, when the organism's recovery was noticeably reduced. By June, the contamination had decreased significantly, and by August, it had completely vanished. Wong *et al*. (2007) documented that in order to generate baseline proportionality data, a national quantitative survey of *Salmonella* in five different types of uncooked retail meats in New Zealand was conducted from August 2003 to May 2005. *Salmonella* was present in 1,108 samples of meat with a rate of 1.1% (95% confidence interval, 0.6 to 1.9). Low *Salmonella* prevalences were found in all meat types, with chicken having the lowest prevalence (1.2–6.1%), lamb and mutton having the most (0.3–3.8%), unweaned veal having the lowest (0–3.0%), beef having the lowest (0–2.4%), and pork having the lowest (0–1.6%). *Salmonella* Infantis from beef, *Salmonella* Typhimurium PT1 from veal and fowl that hadn't been weaned, *Salmonella* sp. 6,7:k:-, *Salmonella* Enteritidis PT9a, *Salmonella* sp. 4,5,12:-, *Salmonella* sp. 4,12:- and *Salmonella* Typhimurium PT160 from poultry were the *Salmonella* serotypes that were isolated. *Salmonella* sp. 4,5,12:- (two isolates), *Salmonella* sp. 4,12:-, and *Salmonella* Typhimurium PT1 were four chicken isolates that shared a great deal of phenotypic and serological similarities with the attenuated *Salmonella* vaccine strain used in MeganVacl for poultry. *Salmonella* Brandenburg was found in one lamb sample with a level of 4.24 most probable numbers (MPN)/g, while the MPN/g of all other positive samples was less than 1.0. In light of other information, such as consumption statistics that can be utilized for risk characterisation, the results give baseline proportionality data for *Salmonella* in retail uncooked meats, which will be invaluable to future risk assessment. Similarly, Little *et al*. (2008) tested 3959 raw red meats for *Campylobacter* and *Salmonella* in the UK between 2003 and 2005. *Campylobacter* contamination of meats was more common (7.2%) than *Salmonella* contamination (2.4%). In comparison to pork (6.3%) and beef (4.9%), lamb and other meats (such as mutton, rabbit) had the highest

Campylobacter infection (12.6% and 19.8%, respectively). *Salmonella* infection was highest in pork (3.9%), then lamb (2.0%), various meats (2.0%), and beef (1.3%). Muscle tissue (7.0%) was more commonly contaminated than offal (36.6%) by *Campylobacter* or *Salmonella*. All varieties of meat were dominated by *C. jejuni*. Compared to *C. jejuni*, *C. coli* isolates were more likely to show signs of quinolone and other antimicrobial drug resistance. The most common *Salmonella* serotype found in meat samples was *S.* Typhimurium, namely *S.* Typhimurium DT104/104b. In India, a total of 284 samples, including chevon and mutton (112 samples each), as well as 60 samples (20 each of the environment samples from retail meat shops, such as butchers' hands, knives, and log swabs), were taken under aseptic conditions from the retail meat shops in and around Anand City. All of the samples were enriched using Rappaport-vassiliadis soy bean meal broth and tetrathionate broth, and inoculations were carried out on brilliant green agar and xylose lysine deoxycholate agar. The confirmation of isolates using biochemical assays came next. Isolates were delivered to the Central Research Institute's National *Salmonella* and Escherichia Centre in Kasauli, Himachal Pradesh, for serotyping. Using the PCR method, virulence genes were found. 13 (4.58%) of 284 meat and retail meat store environment samples tested positive for *Salmonella*. It was fascinating to learn that mutton has a higher prevalence of *Salmonella* (6.25%) than chevon (3.57%). One (5.00%) sample from each of the 20 samples evaluated from the butchers' hands and blades was found to be positive for *Salmonella* in the case of the environmental samples from the meat shops. Only two of the 13 isolates were found to contain *Salmonella* Enteritidis, compared to eleven isolates that did. All *Salmonella* isolates have the invA and stn genes, but only five of the isolates showed the presence of the *spvC* gene, according to in vitro virulence gene detection by PCR. Nine isolates had the spvR gene present (Makwana *et al*., 2015). In Ghana, Adzitey *et al*. (2020) conducted a study that characterized five different varieties of meat (mutton, beef, chevon, guinea fowl, and local chicken) that were purchased from Tamale, Ghana. The disc diffusion approach was used to characterize the *S. enterica* phenotypically (n = 44), based on their pattern of antibiotic resistance, and genetically (n = 16), using whole-genome sequencing (WGS), as well as bioinformatic analysis to forecast their clonal and phylogenomic relationship. 107 (47.56%) of the 225 meat samples evaluated were positive for *S. enterica*. Local chicken was the least infected meat variety, whereas mutton was the most contaminated. The 44 *S. enterica* isolates displayed five distinct patterns of antibiotic resistance, with MAR indices ranging from 0.13 to 0.63.

In Iran, in order to report the isolation of *Salmonella* among products in Tehran, along with its serotypes and antibiogram pattern, the current study used 400 samples from several slaughterhouses. From samples of fermented meat gathered at slaughterhouses, including chicken, beef, veal, mutton, roast beef, and sausage, *Salmonella* was recovered. Serotyping and tests for antimicrobial susceptibility helped identify the isolates. 80 *Salmonella enterica* isolates from 19 different serotypes, including S. adelaide and S. agona With an overall incidence of 20%, S. abortus ovis, S. abortus bovis, S. derby, S. dublin, S. enteritidis, S. havana, S. heidelberg, S. indiana, S. infantis, S. kentucky, S. montevideo, S. newport, S. saint paul, S. senftenberg, *S.* Typhimurium, S. Roast beef was the source of the most identified *Salmonella enterica* strains (Mehrabian and Jaberi, 2007). Besides, serotype, antibiotic resistance, and biofilm forming capabilities of *Salmonella* isolates collected from beef and mutton and meat contact surfaces at retail were examined. Out of 120 samples, 29 (24.17%) had *Salmonella*, including 14/50 (28%) of beef, 10/40 (25%) of mutton, and 5/30 (16.67%) of surfaces that came into contact with meat. The remaining isolates were thought to be different *Salmonella* spp., however seven isolates were determined to be S. Enteritidis, three to be *S.* Typhimurium, and two to be S. Typhi. 48.27% of the isolates were found to be multidrug-resistant (MDR) *Salmonella*, and all of them exhibited resistance to at least one antimicrobial agent. *Salmonella* isolates from all (100%) meat contact surfaces, 42.8% of beef, and 30% of mutton were discovered to be MDR *Salmonella*. Three drugs were found to be resistant: sulphamethoxazole/trimethoprim (44.8%), tetracycline (79.3%), and nalidixic acid (100%). Of the 29 isolates, the gyrA gene was found in 19, but *tet*A was only discovered in one strain. S. Enteritidis produced the most biofilm out of all the serotypes (75.66% moderate and 24.14% strong), and all of them were capable of doing so. The results showed that MDR and biofilm-producing *Salmonella* isolates made up the bulk of those used in this investigation (Manafi *et al*., 2020).

In China, from 2015 to 2016, meat from livestock and poultry from 8 counties in Huaian, China, was gathered and examined for the presence of *Salmonella*. 37 (or 10.05%) of the 368 total samples were positive for *Salmonella*. And the respective positive rates for chicken, duck, pork, beef, and mutton were 14.14%(14/99), 11.11%(10/90), 10.34%(12/116), and 1.59%(1/63). *Salmonella* enteritidis and *Salmonella* typhimurium were the two most prevalent serotypes among the 37 *Salmonella* isolates that were divided into 8 different groups. According to the antimicrobial resistance test, *Salmonella* isolates were least resistant to cefoxitin (8. 11%) and most resistant to ampicillin and nalidixic acid (72. 97%) (Li *et al*., 2018). In addition, Yang *et al*. (2019) reported that the most common bacterial foodborne illness in China is still caused by *Salmonella*. Although it is widely acknowledged that meat products are one of the main causes of human salmonellosis, there aren't any detailed statistics available on the extent to which these foods are contaminated with the *Salmonella*. Therefore, the goals of this study were to look at the distribution, bacterial burden, and antimicrobial resistance profiles of different *Salmonella* serovars in retail meat throughout the entire country of China. A total of 807 retail meat samples, which included the majority of Chinese province capitals, were gathered between July 2011 and June 2016. *Salmonella* was detected in 159 samples (19.7%) overall. Pork had the highest level of contamination (37.3%, n = 287), followed by beef (16.1%, n = 161), mutton (10.9%, n = 92), dumplings (6.6%, n = 212), and smoked pork (6.6%, n = 212). In the 83 samples that tested positive using this approach, the most probable number (MPN) analysis showed that the majority of contamination was in the range of 0.3–10 MPN/g, with eight samples surpassing 110 MPN/g. 29 serovars and 33 multilocus sequence typing patterns were found among the 456 *Salmonella enterica* subsp. enterica isolates included in this investigation, with S. Derby, *S.* Typhimurium, S. London, S. Rissen, S. 1,4,[5],12:i:-, S. Weltevreden, and S. Enteritidis being the most common. Furthermore, Sun *et al*. (2022) reported that *Salmonella* is a prevalent disease that can be found in food, particularly in meat and meat products. *Salmonella* Typhimurium was isolated from chilled mutton retiled in China. The authors reported that lytic phages provide potential improvements over current techniques for controlling *Salmonella* in food and food processing. In their study, a virulent bacteriophage (PSDA-2) against *Salmonella enterica* serovar Typhimurium was isolated from sewage.

From such reports, it is clear that using contaminated water and cross contamination from the abattoir environment during slaughtering, dressing, evisceration, or further processing and handling of meat with contaminated hands, equipment or utensils is the major source of the contamination of sheep meat and offal with foodborne pathogens such as *E. coli*, and *Salmonella* spp (Darwish *et al*., 2018; Darwish and Thompson, 2023).

CONCLUSION

In this review, we highlighted the potential role of sheep meat and offal as sources for the transmission of some foodborne pathogens such as *E. coli*, and *Salmonella* spp. Therefore, adoption of strict hygienic measures during preparation and processing of such meat sources and efficient cooking of sheep meat and offal are mandatory to avoid the possible intake of the foodborne pathogens via their consumption.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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