

A Systematic Review: The Source of Antimicrobial Resistance Pathogenic Bacteria on Slaughtered Meat, Cross-contamination or Self-contamination?

Xin Wu¹ Fanan Suksawat² Sunpetch Angkititrakul² Chunlian Song¹ Jun Chai¹

Yifang Zhang¹ Xianghua Shu¹ Huiyan Xing¹ Wengui Li^{1*}

Abstract

Slaughtered meat has been identified as one of the major vehicles for forming antimicrobial resistance (AMR). It is still believed that AMR pathogens introduced by overusing antimicrobials in the breeding industry are directly brought in from farm animals. This disregards however the fact that many gut pathogens do not settle on muscle parts; the presence of gut pathogens on muscle products does not directly correlate to farm feeding. To investigate whether the source of AMR bacteria on slaughtered meat was cross-contamination or self-contamination, many peer-reviewed publications were studied to assess if the observational studies focused on AMR pathogenic bacteria association between farms and slaughterhouses or the contamination on the slaughter line. Using PubMed, 1919 publications on AMR bacteria in farms and slaughterhouses were collected. The 1650 papers were assembled (269 of them being repeated). From these, 92 were included in the study: 29 surveillance studies reported that AMR bacteria in slaughtered products were related to farm sources; 63 papers reported cross-contamination in the slaughter process at a significant level. Several crucial points were highlighted, including 1) the scalding, de-feathering and evisceration in the broiler slaughter line; 2) residential flora, evisceration, inappropriate meat inspection, conveyor belts, splitting, equipment in the boning hall, holding, chilling, and lairage contamination in the pig slaughter line. In this study, AMR bacteria of the two sources were genetically related. However, the majority of cases still resulted from cross-contamination (29% to 98.48%). This means that major sources of gut AMR bacteria on slaughtered meat were cross contaminated during the slaughter process.

Keywords: Antimicrobial resistance, Cross-contamination, Self-contamination, Food safety

¹College of Veterinary Medicine, Yunnan Agricultural University, Kunming 650051, China

²Faculty of Veterinary Medicine, Khon Kaen University, Khon Kaen, 40002, Thailand

*Correspondence: 909269653@qq.com (W. Li)

Received June 10, 2022

Accepted August 1, 2022

<https://doi.org/10.14456/tjvm.2022.50>

Introduction

Global health is at risk from antimicrobial resistance (AMR). AMR can lead to the failure of infectious disease treatment, to the extended duration of therapy, and to a higher rate of infection mortality (WHO, 2022a). On the other hand, unsanitary food is responsible for over 600 million food-borne illnesses and 420,000 deaths a year in the world (WHO, 2022b), and is widely recognized as the path to AMR transmission, threatening public health (Verraes *et al.*, 2013).

Foodborne pathogenic bacteria are regarded as significant vectors of antimicrobial resistance genes (ARGs) in the food chain (Huddleston, 2014), and their virulence genes can facilitate the spread of ARGs (Li *et al.*, 2019). Even worse, multidrug-resistant pathogens (MDRs) from farm animals were reported to be the predominate source for infections in humans (Shang *et al.*, 2018; Kuo *et al.*, 2014), and these ARGs could be horizontally transmitted from animal farms (Shang *et al.*, 2018; Pornsukarom *et al.*, 2017). For public health, containing the spread of AMR bacteria (especially MDRs) from farm to table is imperative.

There has been a great deal of work done to contain the transmission of AMR bacteria from farms to tables. The Hazard Analysis and Critical Control Point (HACCP) system was established in 1996 in the United States to provide safe meat products. From 1996 to 2000, around 190,000 cases were reduced (Williams and Ebel, 2012). Nevertheless, there were little further effects after the HACCP system was established (Ollinger *et al.*, 2017). This raises the question of why these improvement measures cannot prevent contamination from farm to table completely. It is therefore necessary to determine more details related to the AMR bacteria transmission route, in order to improve this situation. The first question is how the gut source AMR pathogens were spread to slaughtered meat. The common belief among many people is that the AMR pathogens at the dining table are generated from the overuse of antimicrobials among farm animals (Nógrády *et al.*, 2008; Hoelzer *et al.*, 2010; Ma *et al.*, 2017). It is ignored that there is no direct connection between the AMR bacteria on meat and dining tables, since gut pathogens do not normally inhabit muscle, and many factors can cause meat to be contaminated.

The question of whether the gut settled pathogens on slaughtered meat were directly from animal carriage or cross-contamination during the slaughter process is important to answer. A better understanding of the transmission of food-borne AMR pathogens during the slaughter process would inform appropriate intervention strategies. To determine the answer to this concern, a systematic review was proposed. A collection of publications was conducted on the association of AMR pathogenic bacteria between farms and slaughterhouses, or contamination of slaughter lines. The evidence supporting cross-contamination or self-contamination was sorted and critically analyzed, and then conclusions were proposed.

Methods

The publications reported on the AMR bacteria both in farms and slaughterhouses were searched for in PubMed. A total of 1919 peer-reviewed articles were selected including 1817 abstracts with the words “slaughter & farm, slaughterhouse & farm, and abattoir & farm” in the keywords or abstract part, and 102 articles similar to our previous work (Wu *et al.*, 2019a) (topics on contaminations in slaughterhouses). After 269 repeated items of a total of 1919 articles were excluded, the 1650 publications were further assessed. Articles were excluded concerning animal welfare, meat quality, virus foodborne diseases and parasite diseases; these article titles and abstracts imply that this series does not focus on the contamination of gut source AMR pathogens and does not discuss the food chain from farm to slaughterhouse. One hundred and thirty-two publications were left. The following reasons led to the exclusion of 132 publications because a sample comparison between two sources could not be made, the topic of the studies did not pertain to AMR pathogen transmission and contamination during slaughter, the studies did not provide any useful data for the present study, and the risk factors estimated according to the questionnaire lack direct proof. Finally, 92 cross-sectional studies, cohort studies and longitudinal studies reporting on the journey from farms to slaughterhouses, and the reports on transmission, the risk factors, and contamination during the slaughter line were included. Our search selection procedures are listed in Figure 1, following the review. Publications until 8th June 2021 were included.

In order to determine whether the source of AMR bacteria on slaughtered meat was from cross-contamination or animal carriage, these publications were sorted and summarized. 1) The publications concluded that the product contaminations were self-contaminations; 2) evidence supporting an indirect link between bacterial isolates from slaughter products and farms of each individual; 3) critical points that may prevent contamination along the food chain.

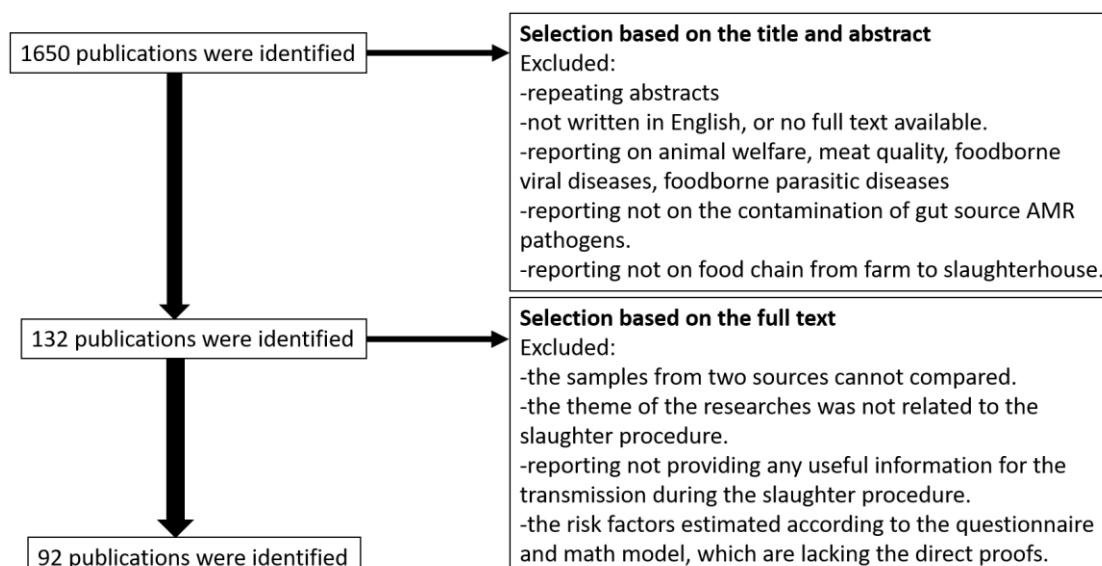


Figure 1 Flowchart of the selection steps, after the PubMed search procedures.

Note: A total of 1650 unique articles were retrieved (269 repeated publications were removed from 1919 peer-reviewed articles); the 132 publications were identified after the exclusion of irrelevant topics based on the abstract; the 92 publications were identified after exclusion of irrelevant topics based on the full text.

Results

There were 92 articles included, and an overview can be found in Table 1. There were 29 publications that reported that AMR pathogens from slaughter products were associated with farms; results are listed in Table 2. There were 30 publications that illustrated the AMR pathogens isolated from slaughtered products were indirectly from farms. Twenty-eight of these publications reported the critical points along the food chain, which are listed in Table 3.

The AMR pathogens isolated from slaughter products were associated with farms: The 29 cross-sectional studies found an association between AMR pathogens in farm animals and those in slaughtered products. They concluded that the products were contaminated from farms. However, that didn't prove that the pathogens in slaughter products were self-contaminating. The samples were both collected from farms and slaughterhouses. The isolates from pigs, chickens or others were involved (2584 from *Salmonella*, 890 from *Escherichia coli*, 189 from *Staphylococcus* spp., 7372 from *Campylobacter* spp., 147 from *Listeria* spp., 125 *Enterococcus* spp., and 101 *Carnobacterium* spp.). Data of subtype techniques such as Pulsed-field gel electrophoresis (PFGE) and Multi locus sequence typing (MLST) suggested that the isolates from the two sources had a genetic link. As a result of being the source of the contamination, the farm is important for slaughter production. Nonetheless, the same PFGE and Multiple locus variable-number tandem repeat analysis (MLVA) patterns do not indicate that the pathogens on products are self-contaminated. The data are insufficient to prove the contamination of slaughter products was due to animal carriage. The details are shown in Table 2.

The AMR pathogens isolated from slaughtered products were indirectly from farms: Despite the genetic relationship providing evidence that the important source of AMR pathogens came from farms, it could not

confirm that the contamination in slaughtered products came directly from animals. This is because there is no direct connection of the AMR bacteria between in the muscle and in the gut. After good slaughter practices, the gut AMR pathogen should not appear on meat products. For instance, many pathogens such as *Salmonella* (non-typhoidal) settle in the animal gut rather than the muscles. The *Salmonella* (non-typhoidal) appearance on the meat products was possibly caused by contamination during slaughter. The gut pathogens that are transferred to muscles would not directly be related to animal carriage. It is possible that the genetic association of isolates in slaughterhouses and farms is due to cross-contamination. In an inappropriate slaughter practice, farm-source AMR pathogens would be transmitted from the animal gut to the environment and slaughter facilities. These contaminated facilities and the environment can lead to contamination of other meat products. The isolates from farms and slaughterhouses could also be genetically related in this case. Despite some reports of high potential self-contamination (Fois et al., 2017), the same PFGE, MLVA subtype does not show self-contamination. The explanation is presented schematically in Figure 2.

Among 1650 publications, 30 publications explored the relationship between bacterial isolates from farm sources and slaughterhouses. As a result of these studies, a considerable portion of AMR pathogens on meat products or carcasses were indirectly related to farm sources. Cross-contamination was a leading source of contamination.

As a first step, the prevalence of pathogens in the slaughterhouse was significantly higher than in the farm, indicating that cross-contamination occurred during the slaughter process (Wang et al., 2020). These studies also reported an increasing prevalence (Hurd et al., 2002; Kaneene, 2006; Kuana et al., 2008; Padungtod and Rasschaert et al., 2008; Wesley et al., 2009; Hue et al., 2010; Keelara et al., 2013; Ren et al., 2016; Zhu, et al., 2017; Djefal et al., 2018; Vinueza-

Burgos, et al., 2019). In addition, the pathogen diversity within each individual grew along with the producing line (Kuana et al., 2008; Colles et al., 2010; Mendes et al., 2020).

Additionally, several research reports indicate that certain bacteria strains isolated from slaughterhouses have not been discovered on farms. As shown by Ainslie-Garcia's study of the *Salmonella* fecal shedding at different production stages of pigs, *Salmonella* fecal shedding on-farm does not correlate with *Salmonella* in tissue at slaughter (Ainslie-Garcia et al., 2018). During the study, Gerbreyes isolated and serotyped *Salmonella* from farms and after slaughter, however, the association between isolates from farms and post-slaughter was poor (Gerbreyes et al., 2004). Zbrun found that strains of *Campylobacter* spp. isolated from slaughterhouse carcasses were not found in the previous stages of the same food chain (Zbrun et al., 2017). Masdalena identified a genotype of *Salmonella* spp. that was found in 31% of the positive carcasses of other pigs slaughtered on the same day (Vieira-Pinto et al., 2006). Nevijo isolated *Y. enterocolitica* from eight lymph nodes of pigs, but only two pigs had that organism present inside their lymph nodes (Zdolec et al., 2015). Silvia isolated the *Salmonella* from mesenteric lymph nodes of pigs and fecal materials at lairage; the 25 PFGE patterns among a total of 36 PFGE types were different (Bonardi et al., 2016). Clara reported that 14.3% of *Salmonella* strains from carcasses were also found in the slaughterhouse environments, but were not found in the animals within the batches (Marin et al., 2020). Christians isolated *Salmonella* from samples collected from feeding plants, farms, and slaughterhouses, showing that some genotypes were found only on carcasses at the slaughterhouse (Vinueza-Burgos et al., 2019).

For these studies, cross-contamination and self-contamination occurred during the slaughter process. But what are the major proportions of contamination cases among the total AMR cases on slaughtered products? Springer evaluated the transmission dynamics of Shiga toxin-producing *E. coli* (STEC) using PCR/MALDI-TOF and genome sequencing, finding that there was limited opportunity to reduce transmission on-farm, but profound effects on transport, lairage and slaughter (Browne et al., 2021). Abley used the most probable number method to count the *Campylobacter* at four different phases (on-farm, post-stunning and exsanguination, pre-chilling, and final product). There is no association of the *Campylobacter* concentration between any two phases. This lack of association indicates that the contamination of meat might be more strongly associated with slaughter practices than with animal carriage (Abley et al., 2012a; Bonardi et al., 2013). Other quantified data reported that the cross-contamination was estimated at 29% of the whole contaminated carcasses (Botteldoorn et al., 2003), while Duggan found that the cross-contamination rate reached up to 69% (Duggan et al., 2010). Similar works concluded that there is no or low association of the contamination on the slaughtered products with the farm source (animal carriage). Nauta's research showed that risk factors contributed more to the contamination of pork than the fecal source of *Salmonella* during slaughter (Nauta et al.,

2013). One survey on two slaughterhouses reported low levels of carcass contamination corresponding to its own pigs (25% and 4%) (Botteldoorn et al., 2004). According to these results, the cross-contamination percentage ranged from 29 to 96%.

These reports are consistent with our previous work. The *Salmonella* cross-contamination of carcasses from slaughterhouses in Thailand was investigated. It was shown that only a few of the carcass contaminations originated from the pig rectum (Wu et al., 2019a). Contaminations occur most often indirectly from the environment (Wu et al., 2019a; Wu et al., 2019b). The cross-contamination rate at an HACCP slaughterhouse was 60.87%, while it was 98.48% at a non-HACCP slaughterhouse (Wu et al., 2019a). Accordingly, good practices in slaughtering could keep the gut pathogen from farms from entering the food chain. Many crucial points need to be addressed further.

The critical points of the slaughter line: Over the 1650 articles, 37 publications addressed several crucial aspects of the slaughter process. Cross-contamination occurs frequently in the farm, transportation, and lairage procedure before slaughter. The critical points of slaughter procedures in the broiler slaughter line were scalding, de-feathering, eviscerating, washing, and chilling. The critical points in the pig slaughter line were scalding, polishing, eviscerating, and splitting. The surrounding environment, such as conveyor belts, boning halls and draining contributed to cross-contamination, as shown in Figure 2 or Table 3. Analyses of critical points during slaughter could provide information on reducing cross-contamination. However, more studies are needed to evaluate the effectiveness of these points (Ollinger et al., 2017).

Additionally, we found that these works could reduce contamination. In farms, the low animal carriage could result with the product at low contamination levels after slaughter. It was reported that treatment taken on-farm could reduce *Campylobacter* colonization in chickens (Georgiev et al., 2017). The improvement of biosecurity at farms would reduce *Salmonella* contamination of pork (Bolton et al., 2013). The model concluded that good farm practices were more important than slaughterhouse practices to control *Campylobacter* contamination on chicken carcasses (Hutchison et al., 2017). On the contrary, the risk of contamination is very high when large *Salmonella* carriers are slaughtered, even under hygienic handling (Corbellini et al., 2016). At the slaughterhouse level, there are several procedures that could reduce the AMR pathogen risk for humans, such as carcass decontamination (Hurd et al., 2008; Hamilton et al., 2010), chlorate treatment (Callaway et al., 2004; Tadee et al., 2014), careful slaughter procedure (good practices) (Oosterom et al., 1983; Tadee et al., 2014), changing of water in the scalding tank (Tadee et al., 2014) and water showers for animals (Giombelli et al., 2014).

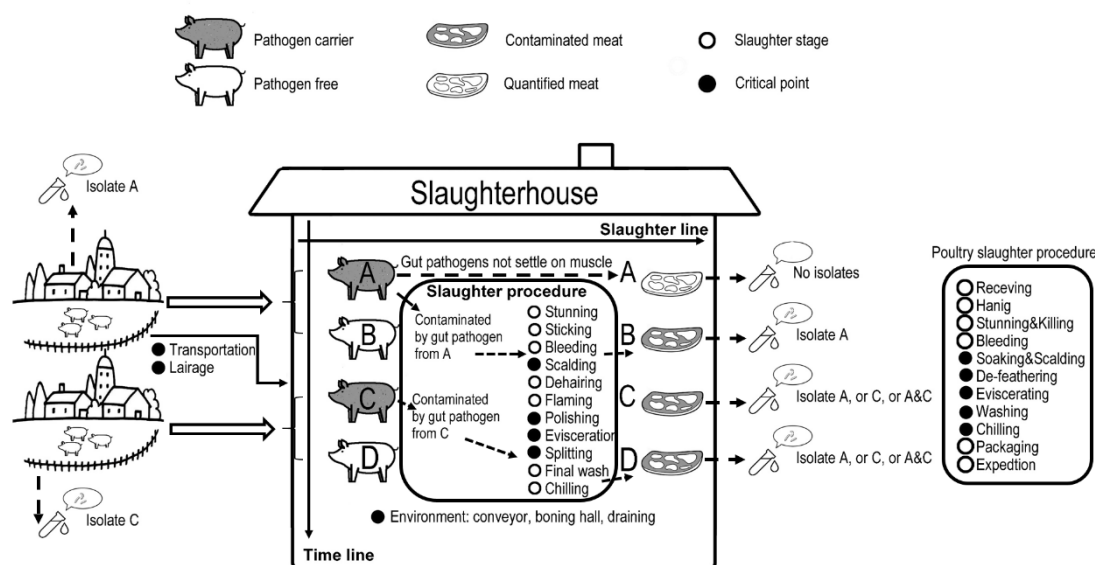


Figure 2 The cross-contamination schematic.

Discussion

Slaughtered meat is a major source of antimicrobial resistance (AMR). However, it is generally accepted that AMR pathogens are transmitted from farm animals directly when antimicrobials are overused in the breeding industry, which ignores that the presence of gut pathogens on muscle products would not directly correlate with farm feeding, since many gut pathogens do not settle on muscle parts. It was the aim of this study to determine whether AMR bacteria on slaughtered meat were caused by cross-contamination or self-contamination (animal carriage). To answer this question, a systematic review was proposed based on the database PubMed. From 1919, 92 publications were identified on AMR bacteria in farms and slaughterhouses. The 29 cross-sectional studies found that the association between AMR pathogens in farm animals and those in slaughtered products was high. However, the same PFGE and MLVA patterns do not indicate that the pathogens on products are self-contaminated. The data are insufficient to prove that slaughter products were contaminated by animal carriage. According to the published studies, which explored the relationship between bacterial isolates from farm sources and slaughterhouses, a significant portion of AMR pathogens on meat products or carcasses was related to farm sources, indicating cross-contamination was a major source of contamination. Here are the important points that were highlighted: 1) scalding, de-feathering and evisceration on the broiler slaughter line; 2) evisceration, inappropriate meat inspection, conveyor belts, splitting, equipment in the boning hall, holding, chilling and lairage contamination on the pig slaughter line. This study might lead to systematic bias towards the assumption that self-contamination rates are higher than they really are because of the limitation of discernibility in self-contamination research studies.

In summary, the AMR pathogens isolated from the slaughterhouse were related to the isolates from farms. The evidence listed above illustrated that a significant proportion (from 29 to 98.48%) of AMR pathogens on meat did not come directly from the animal carriers. During the slaughtering process, cross-contamination from pathogens was significant. Considering the containment of AMR pathogen transmission within the food chain, the slaughter stage seems to be the most critical one, because an inappropriate practice would lead to cross-contamination, increasing the contamination rates. Good slaughter practices can greatly reduce meat contamination. Despite this, the improvement of the slaughter procedure is still not sufficient to prevent AMR from spreading throughout the food chain. Containment work is needed at other stages of the food chain as well.

Table 1 Overview of the selected publications.**Note:** MDR: multi-drug resistance, STEC: *Shiga toxin-producing Escherichia coli*, EPEC: *enteropathogenic Escherichia coli*, *S. aureus*: *Staphylococcus aureus*.

Author	Year	Country	Pathogens	Animal Involved	Study category	Main outcome
Nógrády	2008	Hungary	<i>Salmonella</i>	Chicken	Cross sectional study	The same multi-drug resistant <i>S. Infantis</i> clone was spread from the examined broiler farms contaminating the slaughter and the retail meat, and appeared in humans.
Hoelzer	2010	Washington, New York, USA	<i>Salmonella</i>	Bovines	Cross sectional study	Cattle are an important reservoir of multi-drug-resistant <i>Salmonella</i> infections in humans.
Ma	2017	Sichuan, China	<i>Salmonella</i>	Chicken, Pigs	Cross sectional study	<i>Salmonella</i> isolates from chicken and pig production chains frequently exhibited MDR profiles
Wu	2019a	Thailand	<i>Salmonella</i>	Pigs	Cross sectional study	The HACCP Slaughterhouses decrease <i>Salmonella</i> contaminations and reduce the AMR patterns, the non-HACCP Slaughterhouses increase contamination.
Fois	2017	Italy	<i>Salmonella</i>	Pigs	Cross sectional study	A possible self-contamination in 71.5% of <i>Salmonella</i> positive carcasses.
Wang	2020	Yangzhou, China	<i>Salmonella</i>	Geese	Cross sectional study	This study provided the evidence of <i>Salmonella</i> cross contamination in the slaughterhouse and the retail market of the goose production chain, and specific serotypes existed for a long time at a particular production link.
Kuana	2008	Brazil	<i>Campylobacter</i>	Broilers	Cross sectional study	This study highlighted the importance of programs targeted at the reduction of <i>Campylobacter</i> in poultry products.
Keelara	2013	North Carolina, USA	<i>Salmonella</i>	Pigs	Longitudinal study	This study indicated an exchange of this pathogen between the pigs and their surroundings.
Hurd	2002	Iowa	<i>Salmonella</i>	Pigs	Cross sectional study	Rapid infection during transport, and particularly during holding, is a major reason for increased <i>S. enterica</i> prevalence in swine.
Padungtod	2006	Thailand	<i>Salmonella</i>	Chicken, Pigs	Cross sectional study	The prevalence of <i>Salmonella</i> in farm, slaughterhouse and market are progressively increased.
Rasschaert	2008	Belgium	<i>Salmonella</i>	Chicken	Cross sectional study	A possible cross-contamination exists from the slaughter equipment or transport crates.
Wesley	2009	Iowa, USA	<i>Campylobacter</i>	Turkey	Cross sectional study	The overall prevalence of <i>Campylobacter</i> spp. increases in the crop and gall bladder of turkeys during the peri-marketing interval, under commercial conditions.
Djefal	2018	Algeria	<i>Salmonella</i>	Chicken	Cross sectional study	A high prevalence rate of <i>Salmonella</i> contamination was found.
Ren	2016	Guangdong, China	<i>Salmonella</i>	Chicken	Cross sectional study	Genotypes of <i>S. enterica</i> in the production chain are very diverse.
Hue	2010	France	<i>Campylobacter</i>	Chicken	Cross sectional study	At the slaughterhouse, evisceration seemed to be the operation contributing most to the spread of contamination.
Vinueza-Burgos	2019	Belgium	<i>Salmonella</i>	Poultry	Cross sectional study	Cross-contamination between stages of poultry production can occur.
Zhu	2017	Sichuan, China	<i>Salmonella</i>	Chicken	Cross sectional study	Broiler chicken products in the slaughterhouse were contaminated with MDR <i>Salmonella</i> .
Mendes	2020	Portugal	<i>Campylobacter</i>	Broilers	Longitudinal study	This study illustrated high prevalence in a sample from Portuguese poultry farms.
Colles	2010	UK	<i>Campylobacter</i>	Broilers	Cross sectional study	This study demonstrated the utility of MLST in detecting genetic diversity before and after the slaughter process.

Ainslie-Garcia	2018	Ontario, Canada	<i>Salmonella</i>	Pigs	Longitudinal study	This source of infection was in swine farms.
Gebreyes	2004	North Carolina, USA	<i>Salmonella</i>	Pigs	Cross sectional study	The slaughter plant studies based on phenotyping of <i>Salmonella</i> alone (such as serovars) may not reliably indicate the <i>Salmonella</i> status of commercial swine farms.
Zbrun	2017	Argentina	<i>Campylobacter</i>	Poultry	Cross sectional study	Evidence for transmission through the food chain and cross contamination in slaughterhouses was found.
Vieira-Pinto	2006	Portugal	<i>Salmonella</i>	Pigs	Longitudinal study	This risk may be increased by incorrect evisceration techniques and by hygienically inappropriate meat inspection procedures
Zdolec	2014	Croatia	<i>Salmonella</i> , <i>Yersinia</i> <i>Enterocolitica</i>	Pigs	Cross sectional study	The high prevalence of <i>Y. enterocolitica</i> in/on pig tonsils could be the result of cross-contamination during splitting the carcasses with head.
Bonardi	2016	Italy	<i>Salmonella</i>	Pigs	Cross sectional study	MLN contamination can be predictive of the fecal contamination.
Marin	2020	Spain	<i>Salmonella</i>	Pigs	Cross sectional study	The results showed a high level of <i>Salmonella</i> pork batch contamination upon arrival at the slaughterhouse.
Browne	2021	New Zealand	STEC	Cattle	Cross sectional study	This study illustrated the widespread STEC contamination within the farm environment, but no evidence of recent spread between farms.
Abley	2012a	Ohio, USA	<i>Campylobacter</i> , <i>Salmonella</i>	Cattle	Longitudinal study	There is an environmental reservoir that can contaminate the final meat product.
Bonardi	2013	Italy	<i>Salmonella</i> , <i>Yersinia</i>	Pigs	Cross sectional study	Carcass contamination by <i>S. enterica</i> and <i>Y. enterocolitica</i> was more likely attributable to cross-contamination than to self-contamination.
Botteldoorn	2003	Belgium	<i>Salmonella</i>	Pigs	Cross sectional study	Cross contamination was estimated to account for 29% of the positive carcasses.
Duggan	2010	UK	<i>Salmonella</i>	Pigs	Longitudinal study	Cross-contamination within the slaughter plant environment accounted for up to 69% of <i>Salmonella</i> carcass contamination.
Nauta	2013	Denmark	<i>Salmonella</i> and <i>Escherichia coli</i>	Pigs	Cohort study	Other factors than the observed fecal carriage of <i>Salmonella</i> by the individual animals brought to slaughter, play a more important role in the <i>Salmonella</i> carcass contamination of pork.
Botteldoorn	2004	Belgium	<i>Salmonella</i>	Pigs	Cohort study	Only in 4% was the same genotype or serotype detected as in the feces of the corresponding pigs.
Wu	2019b	Thailand	<i>Salmonella</i>	Pigs	Cross sectional study	There is a low rate of <i>Salmonella</i> spp. from farm <i>via</i> direct slaughter contamination, and the most reported cases could be from cross contamination during the next process of transporting and storage.
Georgiev	2016	UK	<i>Campylobacter</i>	Chicken	Cross sectional study	On-farm measures can play an important role in reducing colonization of broiler chickens with <i>Campylobacter</i> spp. and as a result human exposure.
Bolton	2013	UK	<i>Salmonella</i>	Pigs	Cross sectional study	Control activities should target improved biosecurity at farm level and better sanitation in lairage.
Hutchison	2017	UK	<i>Campylobacters</i>	Chicken	Cross sectional study	Changes to farming practices have greater potential for reducing chicken carcass microbial contamination compared with processing interventions.
Corbellini	2016	Brazil	<i>Salmonella</i>	Pigs	Cross sectional study	Despite the statistically significant association found, it may be difficult to predict when hygiene failure measured <i>via</i> <i>Enterobacteriaceae</i> count actually indicates <i>Salmonella</i> contamination, and not the inverse,
Hurd	2008	Denmark	<i>Salmonella</i>	Pigs	Risk Analysis program	Carcass decontamination was shown as the most effective means of reducing human risk.
Hamilton	2010	Australia	<i>Salmonella</i> and <i>Escherichia coli</i>	Pigs	Cross sectional study	Carcass decontamination with either hot water or sanova are effective risk management options immediately available to the pork industry.
Callaway	2004	Texas, USA	<i>Escherichia coli</i> O157:H7	Food Animals	Short Communication	Chlorate treatment will result in a dissemination of antibiotic resistance.

Gebreyes	2014	North Carolina, USA	<i>Salmonella</i>	Pigs	Cross sectional study	The results support recent findings that risk of exposure to <i>Salmonella</i> during transport and lairage remains a concern under contemporary industry conditions.
Oosterom	1983	Netherlands	<i>Salmonella</i>	Pigs	Cross sectional study	Slaughtering does not necessarily result in further contamination by the <i>Salmonella</i> organisms present in the intestine but a careful slaughtering procedure may even reduce the number of <i>Salmonella</i> organisms on the surfaces of the carcasses of pigs.
Giombelli	2014	Santa Catarina, Brazil	<i>Salmonella</i> and <i>Campylobacter</i>	Broilers	Cross sectional study	Control measures for preventing introduction of <i>Campylobacter</i> and the use of good hygienic conditions are needed.
Zhou	2018	Xiamen, China	<i>Staphylococcus aureus</i>	Pigs	Cross sectional study	Dominance of the scmecxii in MRSA isolates differed from previous reports, revealing the potential contribution associated with the production process.
Hellstrom	2010	Finland	<i>Listeria monocytogenes</i>	Pigs	Longitudinal study	Good farm-level practices can therefore be utilized to reduce the prevalence of this pathogen.
Tadee	2014	Northern Thailand	<i>Salmonella</i>	Pigs	Cross sectional study	<i>Salmonella</i> control programs should be implemented at slaughterhouse production lines.
Thakur	2010	North Carolina, USA	<i>Campylobacter coli</i>	Pigs	Cross sectional study	Shows the importance of testing multiple colonies to make appropriate and valid conclusions in epidemiological-based studies.
Colello	2016	Argentina	STEC	Pigs	Cross sectional study	Need to implement an integrated STEC control system based on good management practices on the farm and critical control point systems in the food chain.
Quintana-Hayashi	2012	North Carolina, USA	<i>Campylobacter</i>	Pigs	Longitudinal Study	The persistence and dissemination of AR <i>Campylobacter</i> from farm to slaughter in ABF and conventionally raised pigs and their environments.
Kich	2011	Santa Catarina, Brazil	<i>Salmonella</i>	Pigs	Cross sectional study	The ampgenkanitet profile was the most prevalent in carcass isolates and was associated with farm origin.
Abley	2012b	South charleston, USA	<i>Campylobacter coli</i>	Pigs	Cohort study	Despite high genotypic diversity of <i>C. Coli</i> on farm, retail meat products were consistently contaminated with isolates of the same.
Kirchner	2011	UK	<i>Salmonella</i>	Pigs	Cross sectional study	Shows the importance of integrated control strategies along the pork food chain.
Bersot	2019	Southern Brazil	<i>Salmonella</i>	Pigs	Cross sectional study	Showed the sources of <i>Salmonella</i> contamination in the pig production chain and highlighted the risks of antimicrobial resistance spread.
Li	2013	Sichuan, China	<i>Salmonella</i>	Pigs, Ducks and Chicken	Cross sectional study	Most isolates from different sampling sites were phenotypically and genetically diverse, and <i>Salmonella</i> was widespread and may transmit along the food production chain from farm to market.
Prachantasena	2016	Thailand	<i>Campylobacter</i>	Chicken	Cross sectional study	Broilers were the main source of <i>Campylobacter</i> contamination of chicken meat during processing.
Gwida	2020	Egypt	<i>Listeria</i>	Chicken	Cross sectional study	Chicken can be seen as a natural source of <i>Listeria</i> .
Berghaus,	2013	North Georgia, USA	<i>Salmonella</i>	Chicken	Cross sectional study	A greater proportion of the variability in carcass rinse prevalence and loads for <i>Campylobacter</i> than they found for <i>Salmonella</i> .
Pergola	2017	Italy	<i>Campylobacter</i>	Chicken	Cross sectional study	This study revealed a high prevalence of antimicrobial resistance.
Powell	2012	UK	<i>Campylobacter</i>	Broilers	Cross sectional study	Locations were highly associated with contaminated carcasses.

Lienau	2007	Germany	<i>Campylobacter</i>	Broilers	Cross sectional study	PFGE is suitable for examining epidemiological field data in the same region and time contexts.
Damjanova	2011	Hungary	<i>Campylobacter</i>	Broilers	Cross sectional study	Broilers were the major source for <i>C. jejuni</i> but not for <i>C. coli</i> in the studied area.
Lee	2019	Korea	<i>Salmonella</i>	Chicken	Cross sectional study	<i>Salmonella</i> was sequentially transmitted through the chicken slaughtering process.
Amoako	2019	South Africa	<i>Staphylococcus aureus</i>	Poultry	Cross sectional study	This study detected methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) isolates circulating in the poultry industry.
Molechan	2019	KwaZulu-Natal, South Africa	<i>Enterococcus</i>	Poultry	Longitudinal study	Isolates along the continuum were highly diverse.
Hutchinson	2017	Eastern USA	<i>Escherichia coli</i>	Cattle	Cohort study	Resistant bacteria recovered from carcasses illustrate the potential transmission of AMR to the human food supply.
Monaghan	2013	Ireland	EPEC	Cattle	Cross sectional study	Cattle are a source of EPEC, many of which have the virulence machinery necessary to be pathogenic to humans.
Yilmaz	2006	Istanbul	<i>Escherichia coli</i> O157	Cattle	Cross sectional study	HACCP systems are necessary from farm to table especially in the slaughterhouse to prevent contamination of meat and the slaughterhouse environment with intestinal content.
Mills	2018	New Zealand	<i>Carnobacterium</i>	Sheep	Cross sectional study	Shows the importance of good hygienic slaughter practices and cleaning routines to remove accumulated detritus from the handling of animals that may lead to cross contamination.
Kashoma	2014	Ohio, USA	<i>Campylobacter</i>	Turkey	Longitudinal study	Indicates the high prevalence, genotypic diversity and antimicrobial resistance of <i>Campylobacter</i> spp. in commercial turkey from farm to slaughter.
Swanenburg	2001	Netherlands	<i>Salmonella</i>	Pigs	Cross sectional study	Separate slaughter of sero-negative pig herds can be useful to decrease the prevalence of <i>Salmonella</i> contaminated pork after slaughter.
Oliveira	2005	Brazil	<i>Salmonella</i>	Pigs	Cross sectional study	The carriage of <i>S. Typhimurium</i> at slaughter might be high if pigs originate from a batch previously affected by a <i>Salmonella</i> enterocolitis outbreak.
Tadesse	2011	USA	<i>Campylobacter</i>	Pigs	Cross sectional study	Ciprofloxacin resistance, particularly from ABF herds, has significant implications on the potential role of risk factors other than mere antimicrobial use for production purposes.
Dorr	2009	North Carolina, USA	<i>Salmonella</i>	Pigs	Longitudinal Study	Demonstrates the significance of various environmental factors, including inadequate truck-washing systems, and emphasizes the role of lairage contamination.
Swanenburg	2001	Netherlands	<i>Salmonella</i>	Pigs	Cross sectional study	<i>Salmonella</i> prevalence in pigs differs a lot depending on which part of the pig is sampled.
Arguello	2013	Spain	<i>Salmonella</i>	Pigs	Longitudinal Study	Shows the lairage and slaughtering as important sources of carcass contamination.
De Busser	2011	Belgium	<i>Salmonella</i>	Pigs	Cohort study	The lairage area is a primary source of <i>Salmonella</i> in slaughtered pigs and that carcass contamination originates from the environment rather than from the pig (inner contamination) itself.
Piras	2011	Italy	<i>Salmonella</i>	Pigs	Cross sectional study	To reduce <i>Salmonella</i> prevalence some preventive measures should be encouraged.
Fajardo-Guerrero	2020	Colombia	<i>Salmonella</i>	Pigs	Cross sectional study	Indicates a higher degree of pathogen contamination at the time of consumption in meat cuts from a slaughterhouse without HACCP.
Dang-Xuan	2019	Vietnam	<i>Salmonella</i>	Pigs	Cross sectional study	Concerning the need to improve farm hygiene at the farm level, and pork hygiene practices, to avoid cross-contamination at the slaughterhouse and market levels, to reduce the risk of salmonellosis through pork consumption in northern Vietnam.
Hald	2003	European	<i>Salmonella</i>	Pigs	Cross sectional study	Temperatures of scalding water (62 °C) are appropriate for cleaning and disinfection.
Viana	2019	Brazil	<i>Salmonella</i>	Pigs	Cross sectional study	The majority of isolates were multidrug resistant.

Kureljušić	2017	Serbia	<i>Salmonella</i>	Pigs	Cross sectional study	Bacteriological examinations of carcass swabs, as well as ileal content, could be used to assess the carriage of <i>Salmonellae</i> in pigs at the time of slaughter.
Schmithausen	2015	Germany	MRSA and ESBL	Pigs	Cross sectional study	Acquisition of MRSA and ESBL-E might occur among pigs in the slaughterhouse.
Molloy	2009	Ireland	<i>Cronobacter</i>	Food Animals	Cross sectional study	<i>Cronobacter</i> spp. was not carried by food production animals but was present in a range of diverse sample types and environs with particular association to dry environments.
Genes	2020	Turkey	<i>Campylobacter</i>	Food Animals	Cross sectional study	<i>Campylobacter</i> strains isolated from slaughterhouses were resistant to most of the current antibiotics.
Gruntar	2015	Slovenia	<i>Campylobacter</i>	Broilers	Cross sectional study	The majority of <i>Campylobacter</i> contamination actually occurs before the entrance to the eviscerating room, probably during the preceding plucking stage.
Abu-Ruwaida	1994	Kuwait	Total aerobics, <i>Enterobacteriaceae</i> , Coliforms	Broilers	Cross sectional study	<i>Salmonella</i> was present in all birds examined, including those coming directly from the farm.
Gu	2020	Jiangsu, China	<i>Salmonella</i>	Chicken	Cross sectional study	Showed high prevalence of <i>Salmonella</i> in the chicken slaughter line and identified the slaughtering environment as a main source of causing <i>Salmonella</i> cross-contamination.
Dias	2016	Brazil	<i>Salmonella</i>	Chicken	Cross sectional study	Demonstrated the relevance of the initial steps of chicken slaughtering for <i>Salmonella</i> spp. contamination, and the pre-chilling of carcasses as an important controlling tool.
Lin	2020	Taiwan, China	<i>Salmonella</i>	Chicken	Cross sectional study	<i>Salmonella</i> isolates present in the environment and intestinal contents of processed birds survived in the slaughterhouse environment, resulting in subsequent carcass contamination along the processing chain including plucking, evisceration, chilling and post-chilling.
Projahn	2021	Germany	<i>Escherichia coli</i>	Chicken	Cross sectional study	Wet and dirty broiler chickens are more likely to be a vehicle for the dissemination of CTX-resistant and total <i>Enterobacteriaceae</i> into the slaughterhouses and contribute to higher rates of cross contamination during processing.

Table 2 Farms are the major source of AMR pathogen contamination during slaughter

Note: AFLP: amplified fragment length polymorphism, ERIC-PCR: enterobacterial repetitive intergenic consensus-Polymerase chain reaction, REP-PCR: repetitive extragenic palindromic elements-Polymerase chain reaction, VNTR: variable number of tandem repeats, WGS: whole genome sequencing, MDR: multi-drug resistance, STEC: *Shiga toxin-producing Escherichia coli*, EPEC: enteropathogenic *Escherichia coli*, *S. aureus*: *Staphylococcus aureus*. The cecal, fecal, lymph node, and colon content samples represented the situation of animals. The carcass, environment and lairage samples represented the situation of slaughterhouses.

Host	Bacteria	AMR	No. of isolates/samples animal	slaughterhouse	Sampling design	Association relationship between farm and slaughterhouse/ confirmed technique	Reference
Pigs	<i>S. aureus</i>	MRSA	13/1485	31/1485	randomly from farms, slaughterhouses and markets	associated	PCR (Zhou <i>et al.</i> , 2018)
	<i>Salmonella</i>	MDR	20/361	97/349	randomly from farms and slaughterhouses	no mention	(Padungtod <i>et al.</i> , 2006)
	<i>Listeria</i>		4/364	107/1421	from the same pigs in farm and slaughterhouse	associated	(Hellström <i>et al.</i> , 2010)
	<i>Salmonella</i>	MDR	39 isolates	47 isolates	from pigs, farm and slaughterhouse workers and the local environment	associated	(Tadee <i>et al.</i> , 2015)
	<i>Campylobacter</i>	MDR	497/908	114/757	randomly from farm and slaughterhouse	associated	(Thakur <i>et al.</i> , 2010)
	STEC		348 isolates	147 isolates	randomly from farm and slaughterhouse	no mention	(Colello <i>et al.</i> , 2016)
	<i>Campylobacter</i>	MDR	2561/501	314/1363	randomly from pigs and environment in farm and slaughterhouse	similar MDR patterns	(Quintana-Hayashi <i>et al.</i> , 2012)
	<i>Salmonella</i>	MDR	181/382	307/876	farm samples were from floor pens, feces, pooled feces and feed; slaughterhouse samples were from lairage, pre-chill & post-chill carcasses, and lymph nodes	associated	(Kich <i>et al.</i> , 2011)
	<i>Campylobacter</i>	MDR	90/100	320/400	cohort study, five points from each individual	no associations	(Abley <i>et al.</i> , 2012)
	<i>Salmonella</i>		286 isolates	159 isolates	randomly collected from farm and slaughterhouse	associated	(PFGE/VNTR (Kirchner <i>et al.</i> , 2011)
Chicken	<i>Salmonella</i>	MDR	120/1298	40/270	samples were tracked from farm until slaughter	associated	(Dos <i>et al.</i> , 2019)
	<i>Salmonella</i>	MDR	27/112	40/128	randomly collected from farm and slaughterhouse	associated	(Ma <i>et al.</i> , 2017)
	<i>Salmonella</i>	MDR	71/433	21/196	randomly collected from farm and slaughterhouse	associated	(PFGE (Li <i>et al.</i> , 2013)
	<i>Campylobacter</i>	flaA SVR	267/1627	252/579	randomly from breeder flock, hatchery, broiler farm and slaughterhouse	associated	(Prachantasena <i>et al.</i> , 2016)
	<i>Salmonella</i>	MDR	0/199	0/127	randomly collected from farm and slaughterhouse	associated	(PFGE (Li <i>et al.</i> , 2013)
	<i>Salmonella</i>	MDR	24/109	28/110	randomly collected from farm and slaughterhouses	associated	(PFGE (Ma <i>et al.</i> , 2017)
	<i>Salmonella</i>	MDR	18/425	31/73	randomly collected from farm and slaughterhouse	not mention	(Padungtod <i>et al.</i> , 2006)
	<i>Listeria</i>		7/25	29/185	randomly collected from farm and slaughterhouse	associated	(WGS (Gwida <i>et al.</i> , 2020)
	<i>Salmonella</i>		177/549	513/1650	randomly from boot sock, drag, fecal and litter in farm, and from the outside plant, rehang, pre-chill and post-chill in slaughterhouse	associated	(Berghaus <i>et al.</i> , 2013)
	<i>Campylobacter</i>		262/549	995/1650	randomly from boot sock, drag, fecal and litter in farm, and from the outside plant, rehang, pre-chill and post-chill in slaughterhouse	associated	(Berghaus <i>et al.</i> , 2013)
	<i>Campylobacter</i>	MDR	116 isolates	24 isolates	randomly from farms	associated with other reports	AFLP (Pergola <i>et al.</i> , 2017)
	<i>Salmonella</i>	class 1 integron	52/534	55/219	from environment, floor feces in farms, and from environmental, carcass and meat in slaughterhouse	no mention	PFGE (Nógrády <i>et al.</i> , 2008)

Poultry	<i>Campylobacter</i>	303/400 isolates	349/400	cohort study, randomly from cecal and carcass	associated	(Powell et al., 2012)
	<i>Campylobacter</i>	45 isolates	192 isolates	randomly collected from farm and slaughterhouse	associated	(Lienau et al., 2007)
	<i>Campylobacter</i>	114 isolates	101 isolates	randomly collected from farm and slaughterhouse	associated	(Damjanova et al., 2011)
	<i>Salmonella</i>	MDR	11/25	collected from 10 sampled slaughtering sites	associated	(Lee et al., 2019)
	<i>Salmonella</i>	MDR	3/129	randomly collected from farm, slaughterhouse and retail	associated	(Nógrády et al., 2008)
	<i>S. aureus</i>	MRSA	120 isolates	randomly from poultry and occupational workers	associated	(Amoako et al., 2019)
	<i>Enterococcus</i>	MDR	83/100	along the continuum (growth phase, transport and post-slaughter)	associated	(Molechan et al., 2019)
	<i>Salmonella</i>	MDR	6/49	randomly collected from farm and slaughterhouse	associated	(Li et al., 2013)
	<i>E. coli</i>	MDR	161/166	A cohort design, from farm and slaughterhouse	associated	(Hutchinson et al., 2017)
	<i>EPEC</i>		59/1800	randomly from farm and slaughterhouse	associated	(Monaghan et al., 2013)
bovine	<i>E. coli</i>	14 isolates	18 isolates	randomly from farms and slaughterhouse	associated	(Yilmaz et al., 2006)
	<i>Carnobacterium</i>		81/150	randomly from farm and slaughterhouse	associated	(Mills et al., 2018)
	<i>Campylobacter</i>	MDR	423/750	randomly from farm and slaughterhouse	associated	(Kashoma et al., 2014)
			33/60			

Table 3 Critical stage of contamination in slaughter procedure

Slaughter line type	Critical stage of contamination	reference
Pig slaughter line	The farm origin, the transportation, and the lairage, incorrect evisceration techniques, and hygienically inappropriate meat inspection procedures	(Vieira-Pinto <i>et al.</i> , 2006)
Pig slaughter line	Animal infection, and residential flora of the slaughterhouse	(Swanenburg <i>et al.</i> , 2001a)
Pig slaughter line	Lairage, evisceration operatives, environment: conveyor belts, and equipment in the boning hall	(Duggan <i>et al.</i> , 2010)
Pig slaughter line	Rapid infection during transport and holding	(Hurd <i>et al.</i> , 2002)
Pig slaughter line	Pathogen outbreak at the pre-harvest pork production chain	(Oliveira <i>et al.</i> , 2005)
Pig slaughter line	The antimicrobial free use in herds	(Tadesse <i>et al.</i> , 2011)
Pig slaughter line	Environmental factors, including inadequate truck-washing systems, and lairage contamination	(Dorr <i>et al.</i> , 2009)
Pig slaughter line	The splitting stage	(Zdolec <i>et al.</i> , 2015)
Pig slaughter line	Pig rectal content, environment: the drain water, and the carcass splitter machine	(Swanenburg <i>et al.</i> , 2001b)
Pig slaughter line	The lairage and slaughtering	(Arguello <i>et al.</i> , 2006)
Pig slaughter line	The lairage area is a primary source	(De <i>et al.</i> , 2011)
Pig slaughter line	Water temperature at drains	(Piras <i>et al.</i> , 2011)
Pig slaughter line	At different processing stages	(Fajardo-Guerrero <i>et al.</i> , 2020)
Pig slaughter line	The slaughter area close to lairage is without hygienic measures	(Dang-Xuan <i>et al.</i> , 2019)
Pig slaughter line	The scalding water, the polishing, and the splitter	(Hald <i>et al.</i> , 2003)
Pig slaughter line	The pig carriage	(Viana <i>et al.</i> , 2019)
Pig slaughter line	The lairage area and the transportation vehicle are primary sources	(Kureljusic <i>et al.</i> , 2017)
Pig slaughter line	The stable air and lairage	(Schmithausen <i>et al.</i> , 2015)
Pig and cattle	Slaughterhouse environment	(Molloy <i>et al.</i> , 2009; Huzisoy <i>et al.</i> , 2020)
Poultry slaughter line	Before evisceration possibly in the plucking stage	(Gruntar <i>et al.</i> , 2015)
Poultry slaughter line	The chilled carcasses after immersed in chlorinated water (1-2 parts per million)	(Kuana <i>et al.</i> , 2008)
Poultry slaughter line	Scalding and defeathering	(Abu-Ruwaida <i>et al.</i> , 1994)
Poultry slaughter line	Evisceration	(Hue <i>et al.</i> , 2010)
Poultry slaughter line	The scalding, unhairing stage to subdividing stage. The main source of contamination was from the slaughtering environment	(Gu <i>et al.</i> , 2020)
Poultry slaughter line	The reception of contaminated animals and the pre-chilling of carcasses	(Dias <i>et al.</i> , 2016)
Poultry slaughter line	The plucking, evisceration, chilling and post-chilling	(Lin <i>et al.</i> , 2020)
Poultry slaughter line	The wet and dirty broiler chickens	(Projahn <i>et al.</i> , 2021)

Acknowledgements

The authors thank the Yunnan Provincial Major Science and Technology Special Project "Construction and Application of Important Pig Disease Prevention and Control Technology System in Yunnan Province" (No. 202102AE090007) for financial help.

Funding: This study was funded by the Major Science and Technology Projects in Yunnan Province, "Construction and Application of Technical System for Prevention and Control of Important Pig Diseases in Yunnan Province" [NO. 202102AE090007], "Animal Disease Prevention and Control Technology Innovation Center of Kunming" [NO. 20191N25318000003525], "Science and Technology Planning Project of Yunnan Science and Technology Department" [NO. 202201AU070181], and "Scientific Research Fund Project of Yunnan Education Department" [NO. 2022J0288].

Author Contributions: XW, FS and SA conceived and designed the study. CS, YZ, JC and XS performed the data collection. XW, HX and WL analyzed the data. XW and WL completed the manuscript. FS edited the writing. All authors have read and approved the final manuscript.

References

Abley MJ, Wittum TE, Funk JA, Gebreyes WA 2012a. Antimicrobial Susceptibility, Pulsed-Field Gel Electrophoresis, and Multi-Locus Sequence Typing of *Campylobacter coli* in Swine before, during, and after the Slaughter Process. *Foodborne Pathog Dis.* 9(6): 506-512.

Abley MJ, Wittum TE, Zerby HN, Funk JA 2012b. Quantification of *Campylobacter* and *Salmonella* in Cattle before, during, and after the Slaughter Process. *Foodborne Pathog Dis.* 9(2): 113-119.

Abu-Ruwaida AS, Sawaya WN, Dashti BH, Murad M, Al-Othman HA 1994. Microbiological Quality of Broilers during Processing in a Modern Commercial Slaughterhouse in Kuwait. *J Food Prot.* 57(10): 887-892.

Ainslie-Garcia MH, Farzan A, Newman JE, Friendship RM, Lillie BN 2018. *Salmonella* Fecal Shedding in Pigs from Birth to Market and its Association with the Presence of *Salmonella* in Palatine Tonsils and Submandibular Lymph Nodes at Slaughter. *Can J Vet Res.* 82(4): 249-255.

Amoako DG, Somboro AM, Abia ALK, Allam M, Ismail A, Bester L, Essack SY 2019. Genomic Analysis of Methicillin-Resistant *Staphylococcus aureus* Isolated from Poultry and Occupational Farm Workers in Umgungundlovu District, South Africa *Sci Total Environ.* 670: 704-716.

Arguello H, Carvajal A, Naharro G, Arcos M, Rodicio MR, Martin MC, Rubio P 2013. Sero- and Genotyping of *Salmonella* in Slaughter Pigs, from Farm to Cutting Plant, with a Focus on the Slaughter Process. *Int J Food Microbiol.* 161(1): 44-52.

Berghaus RD, Thayer SG, Law BF, Mild RM, Hofacre CL, Singer RS 2013. Enumeration of *Salmonella* and

Campylobacter spp. in Environmental Farm Samples and Processing Plant Carcass Rinses from Commercial Broiler Chicken Flocks. *Appl Environ Microbiol.* 79(13): 4106-4114.

Bolton DJ, Ivory C, McDowell D 2013. A study of *Salmonella* in Pigs from Birth to Carcass: Serotypes, Genotypes, Antibiotic Resistance and Virulence Profiles. *Int J Food Microbiol.* 160(3): 298-303.

Bonardi S, Bassi L, Brindani F, D'Incau M, Barco L, Carra E, Pongolini S 2013. Prevalence, Characterization and Antimicrobial Susceptibility of *Salmonella enterica* and *Yersinia Enterocolitica* in Pigs at Slaughter in Italy. *Int J Food Microbiol.* 163(2-3): 248-257.

Bonardi S, Alpigiani I, Bruini I, Barilli E, Brindani F, Morganti M, Cavallini P, Bolzoni L, Pongolini S 2016. Detection of *Salmonella enterica* in Pigs at Slaughter and Comparison with Human Isolates in Italy. *Int J Food Microbiol.* 218: 44-50.

Botteldoorn N, Heyndrickx M, Rijpens N, Grijspeerd K, Herman L 2003. *Salmonella* on Pig Carcasses: Positive Pigs and Cross Contamination in the Slaughterhouse. *J Appl Microbiol.* 95(5): 891-903.

Botteldoorn N, Herman L, Rijpens N, Heyndrickx M 2004. Phenotypic and Molecular Typing of *Salmonella* Strains Reveals Different Contamination Sources in Two Commercial Pig Slaughterhouses. *Appl Environ Microbiol.* 70(9): 5305-5314.

Browne AS, Midwinter AC, Withers H, Cookson AL, Biggs PJ, Marshall JC, Benschop J, Hathaway S, Rogers L, Nisa S, Hranac CR, Winkelman T, French NP 2021. Evaluating Transmission Dynamics of Shiga Toxin-Producing *E. coli* (STEC) in New Zealand Cattle from Farm to Slaughter Using PCR/MALDI-TOF and Genome Sequencing. *Appl Environ Microbiol.*

Callaway TR, Anderson RC, Edrington TS, Bischoff KM, Genovese KJ, Poole TL, Byrd JA, Harvey RB, Nisbet DJ 2004. Effects of Sodium Chlorate on Antibiotic Resistance in *Escherichia coli* O157:H7. *Foodborne Pathog Dis.* 1(1): 59-63.

Colello R, Cáceres ME, Ruiz MJ, Sanz M, Etcheverría AI, Padola NL 2016. From Farm to Table: Follow-up of Shiga toxin-Producing *Escherichia coli* throughout the Pork Production Chain in Argentina. *Front Microbiol.* 7(93).

Colles FM, McCarthy ND, Sheppard SK, Layton R, Maiden MC 2010. Comparison of *Campylobacter* Populations Isolated from a Free-Range Broiler Flock Before and after Slaughter. *Int J Food Microbiol.* 137(2-3): 259-264.

Corbellini LG, Júnior AB, De FCE, Duarte AS, Albuquerque ER, Kich JD, Cardoso M, Nauta M 2016. Effect of Slaughterhouse and Day of Sample on the Probability of a Pig Carcass being *Salmonella*-Positive according to the *Enterobacteriaceae* Count in the Largest Brazilian Pork Production Region. *Int J Food Microbiol.* 228: 58-66.

Damjanova I, Jakab M, Farkas T, Mészáros J, Galántai Z, Turcsányi I, Bisttyák A, Juhász A, Pásztai J, Kiss I, Kardos G 2011. From Farm to Fork Follow-Up of Thermotolerant *Campylobacters* throughout the Broiler Production Chain and in Human Cases in a Hungarian County during a Ten Month Period. *Int J Food Microbiol.* 150(2-3): 95-102.

- Dang-Xuan S, Nguyen-Viet H, Pham-Duc P, Unger F, Tran-Thi N, Grace D, Makita K 2019. Risk Factors associated with *Salmonella* spp. Prevalence along Smallholder Pig Value Chains in Vietnam. *Int J Food Microbiol.* 290: 105-115.
- De Busser EV, Maes D, Houf K, Dewulf J, Imberechts H, Bertrand S, De ZL 2011. Detection and Characterization of *Salmonella* in Lairage, on Pig Carcasses and Intestines in Five Slaughterhouses. *Int J Food Microbiol.* 145(1): 279-286.
- Dias MR, Cavicchioli VQ, Camargo AC, Lanna FG, Pinto PS, Bersot LS, Nero LA 2016. Molecular Tracking of *Salmonella* spp. in Chicken Meat Chain: from Slaughterhouse Reception to End Cuts. *J Food Sci Technol.* 53(2): 1084-1091.
- Djeffal S, Mamache B, Elgroud R, Hireche S, Bouaziz O 2018. Prevalence and Risk Factors for *Salmonella* spp. Contamination in Broiler Chicken Farms and Slaughterhouses in the Northeast of Algeria. *Vet World.* 11(8): 1102-1108.
- Dorr PM, Tadesse DA, Zewde BM, Fry P, Thakur S, Gebreyes WA 2009. Longitudinal Study of *Salmonella* Dispersion and the Role of Environmental Contamination in Commercial Swine Production Systems. *Appl Environ Microbiol.* 75(6): 1478-1486.
- Dos SBL, Quintana CV, Viana C, Konrad BRC, Camargo AC, de ANPJP, Nero LA, Destro MT 2019. Prevalence, Antimicrobial Resistance, and Diversity of *Salmonella* along the Pig Production Chain in Southern Brazil. *Pathogens.* 8(4).
- Duggan SJ, Mannion C, Prendergast DM, Leonard N, Fanning S, Gonzales-Barron U, Egan J, Butler F, Duffy G 2010. Tracking the *Salmonella* Status of Pigs and Pork from Lairage through the Slaughter Process in the Republic of Ireland. *J Food Prot.* 73(12): 2148-2160.
- Fajardo-Guerrero M, Rojas-Quintero C, Chamorro-tobar I, Zambrano C, Sampedro F, Carrascal-Camacho AK 2020. Exposure Assessment of *Salmonella* spp. in Fresh Pork Meat from Two Abattoirs in Colombia. *Food Sci Technol Int.* 26(1): 21-27.
- Fois F, Piras F, Torpdahl M, Mazza R, Consolati SG, Spanu C, Scarano C, De SEP 2017. Occurrence, Characterization, and Antimicrobial Susceptibility of *Salmonella enterica* in Slaughtered Pigs in Sardinia. *J Food Sci.* 82(4): 969-976.
- Gebreyes WA, Davies PR, Turkson PK, Morrow WE, Funk JA, Altier C 2004. *Salmonella enterica* Serovars from Pigs on Farms and after Slaughter and Validity of Using Bacteriologic Data to Define Herd *Salmonella* Status. *J Food Prot.* 67(4): 691-697.
- Georgiev M, Beauvais W, Guitian J 2017. Effect of Enhanced Biosecurity and Selected on-Farm Factors on *Campylobacter* Colonization of Chicken Broilers. *Epidemiol Infect.* 145(3): 553-567.
- Giombelli A, Gloria MB 2014. Prevalence of *Salmonella* and *Campylobacter* on Broiler Chickens from Farm to Slaughter and Efficiency of Methods to Remove Visible Fecal Contamination. *J Food Prot.* 77(11): 1851-1859.
- Gruntar I, Biasizzo M, Kušar D, Pate M, Ocepek M 2015. *Campylobacter jejuni* Contamination of Broiler Carcasses: Population Dynamics and Genetic Profiles at Slaughterhouse Level. *Food Microbiol.* 50: 97-101.
- Gu D, Wang Z, Tian Y, Kang X, Meng C, Chen X, Pan Z, Jiao X 2020. Prevalence of *Salmonella* Isolates and their Distribution Based on Whole-Genome Sequence in a Chicken Slaughterhouse in Jiangsu, China. *Front Vet Sci.* 7(29).
- Gwida M, Lüth S, El-Ashker M, Zakaria A, El-Gohary F, Elsayed M, Kleta S, Al DS 2020. Contamination Pathways can be traced along the Poultry Processing Chain by Whole Genome Sequencing of *Listeria innocua*. *Microorganisms.* 8(414): 1-11.
- Hald T, Wingstrand A, Swanenburg M, Von AA, Thorberg BM 2003. The Occurrence and Epidemiology of *Salmonella* in European Pig Slaughterhouses. *Epidemiol Infect.* 131(3): 1187-1203.
- Hamilton D, Holds G, Lorimer M, Kiermeier A, Kidd C, Slade J, Pointon A 2010. Slaughter Floor Decontamination of Pork Carcasses with Hot Water or Acidified Sodium Chlorite - a Comparison in Two Australian Abattoirs. 57(s1): 16-22. D
- Hellström S, Laukkanen R, Siekkinen KM, Ranta J, Majjala R, Korkeala H 2010. *Listeria monocytogenes* Contamination in Pork Can Originate from Farms. *J Food Prot.* 73(4): 641-648.
- Hızlısoy H, Al S, Ertaş ON, Yıldırım Y, Gönülalan Z, Barel M, Güngör C, Dışhan A, Dişli HB, Farklı KİE 2020. Virulence Genes, Antibiotic Susceptibility Profiles and Molecular Characterization of *Campylobacter* Species Isolated from Different Slaughterhouses. *Mikrobiyol Bul.* 54(1): 11-25.
- Hoelzer K, Soyer Y, Rodriguez-Rivera LD, Cummings KJ, McDonough PL, Schoonmaker-Bopp DJ, Root TP, Dumas NB, Warnick LD, Gröhn YT, Wiedmann M, Baker KN, Besser TE, Hancock DD, Davis MA 2010. The Prevalence of Multidrug Resistance is Higher among Bovine than Human *Salmonella enterica* Serotype Newport, Typhimurium, and 4,5,12:i:- Isolates in the United States but Differs by Serotype and Geographic Region. *Appl Environ Microbiol.* 76(17): 5947-5959.
- Huddleston JR 2014. Horizontal Gene Transfer in the Human Gastrointestinal Tract: Potential Spread of Antibiotic Resistance Genes. *Infect Drug Resist.* 7: 167-176.
- Hue O, Le BS, Laisney MJ, Allain V, Lalande F, Petetin I, Rouxel S, Quesne S, Gloaguen PY, Picherot M, Santolini J, Salvat G, Bougeard S, Chemaly M 2010. Prevalence of and Risk Factors for *Campylobacter* spp. Contamination of Broiler Chicken Carcasses at the Slaughterhouse. *Food Microbiol.* 27(8): 992-999.
- Hurd HS, McKean JD, Griffith RW, Wesley IV, Rostagno MH 2002. *Salmonella enterica* Infections in Market Swine with and without Transport and Holding. *Appl Environ Microbiol.* 68(5): 2376-2381.
- Hurd HS, Enøe C, Sørensen L, Wachmann H, Corns SM, Bryden KM, Greiner M 2008. Risk-Based Analysis of the Danish Pork *Salmonella* Program: Past and Future. *Risk Anal.* 28(2): 341-351.
- Hutchinson H, Finney S, Muñoz-Vargas L, Feicht S, Masterson M, Habing G 2017. Prevalence and Transmission of Antimicrobial Resistance in a Vertically Integrated Veal Calf Production System. *Foodborne Pathog Dis.* 14(12): 711-718.

- Hutchison ML, Taylor MJ, Tchörzewska MA, Ford G, Madden RH, Knowles TG 2017. Modelling-based Identification of Factors Influencing *Campylobacter* in Chicken Broiler Houses and on Carcasses Sampled after Processing and Chilling. *J Appl Microbiol.* 122(5): 1389-1401.
- Kashoma IP, Kumar A, Sanad YM, Gebreyes W, Kazwala RR, Garabed R, Rajashekara G 2014. Phenotypic and Genotypic Diversity of Thermophilic *Campylobacter* spp. in Commercial Turkey Flocks: a Longitudinal Study. *Foodborne Pathog Dis.* 11(11): 850-860.
- Keelara S, Scott HM, Morrow WM, Gebreyes WA, Correa M, Nayak R, Stefanova R, Thakur S 2013. Longitudinal Study of Distributions of Similar Antimicrobial-Resistant *Salmonella* Serovars in Pigs and Their Environment in Two Distinct Swine Production Systems. *Appl Environ Microbiol.* 79(17): 5167-5178.
- Kich JD, Coldebella A, Morés N, Nogueira MG, Cardoso M, Fratamico PM, Call JE, Fedorka-Cray P, Luchansky JB 2011. Prevalence, Distribution, and Molecular Characterization of *Salmonella* Recovered from Swine Finishing Herds and a Slaughter Facility in Santa Catarina, Brazil. *Int J Food Microbiol.* 151(3): 307-313.
- Kirchner M, Marier E, Miller A, Snow L, McLaren I, Davies RH, Clifton-Hadley FA, Cook AJ 2011. Application of Variable Number of Tandem Repeat Analysis to Track *Salmonella enterica* spp. Enterica Serovar Typhimurium infection of Pigs Reared on Three British Farms through the Production Cycle to the Abattoir. *J Appl Microbiol.* 111(4): 960-970.
- Kuana SL, Santos LR, Rodrigues LB, Borsoi A, Moraes HL, Salle CT, Nascimento VP 2008. Occurrence and Characterization of *Campylobacter* in the Brazilian Production and Processing of Broilers. *Avian Dis.* 52(4): 680-684.
- Kuo HC, Lauderdale TL, Lo DY, Chen CL, Chen PC, Liang SY, Kuo JC, Liao YS, Liao CH, Tsao CS, Chiou CS 2014. An Association of Genotypes and Antimicrobial Resistance Patterns among *Salmonella* Isolates from Pigs and Humans in Taiwan. *PLoS One.* 9(4): e95772.
- Kureljusic JM, Dmitrić MP, Vidanović DS, Teodorović VB, Kureljušić BI, Velhner MJ, Karabasil NR 2017. Prevalence of *Salmonella enterica* in Slaughtered Pigs in Serbia: Serotyping, PFGE-Genotyping and Antimicrobial Resistance. *J Infect Dev Ctries.* 11(08): 640-645.
- Lee HJ, Youn SY, Jeong OM, Kim JH, Kim DW, Jeong JY, Kwon YK, Kang MS 2019. Sequential Transmission of *Salmonella* in the Slaughtering Process of Chicken in Korea. *J Food Sci.* 84(4): 871-876.
- Li Q, Yin J, Li Z, Li Z, Du Y, Guo W, Bellefleur M, Wang S, Shi H 2019. Serotype Distribution, Antimicrobial Susceptibility, Antimicrobial Resistance Genes and Virulence Genes of *Salmonella* Isolated from a Pig Slaughterhouse in Yangzhou, China. *AMB Express.* 9(1): 210.
- Li R, Lai J, Wang Y, Liu S, Li Y, Liu K, Shen J, Wu C 2013. Prevalence and Characterization of *Salmonella* Species Isolated from Pigs, Ducks and Chicken in Sichuan Province, China. *Int J Food Microbiol.* 163(1): 14-18.
- Lienau JA, Ellerbroek L, Klein G 2007. Tracing Flock-Related *Campylobacter* Clones from Broiler Farms through Slaughter to Retail Products by Pulsed-Field Gel Electrophoresis. *J Food Prot.* 70(3): 536-542.
- Lin CH, Huang JF, Sun YF, Adams PJ, Lin JH, Robertson ID 2020. Detection of Chicken Carcasses Contaminated with *Salmonella enterica* Serovar in the Abattoir Environment of Taiwan. *Int J Food Microbiol.* 325: 108640.
- Ma S, Lei C, Kong L, Jiang W, Liu B, Men S, Yang Y, Cheng G, Chen Y, Wang H 2017. Prevalence, Antimicrobial Resistance, and Relatedness of *Salmonella* Isolated from Chickens and Pigs on Farms, Abattoirs, and Markets in Sichuan Province, China. *Foodborne Pathog Dis.* 14(11): 667-677.
- Marin C, Chinillac MC, Cerdà-Cuellar M, Montoro-Dasi L, Sevilla-Navarro S, Ayats T, Marco-Jimenez F, Vega S 2020. Contamination of Pig Carcass with *Salmonella enterica* Serovar Typhimurium Monophasic Variant 1,4[5],12:I:- Originates Mainly in Live Animals. *Sci Total Environ.* 703: 1-27.
- Mendes ÂJ, Santos-Ferreira NL, Costa FM, Lopes EP, Freitas-Silva J, Inácio ÂS, Moreira F, Martins DCP 2020. External Contamination of Broilers by *Campylobacter* spp. Increases from the Farm to the Slaughterhouse. *Br Poult Sci.* 61(4): 400-407.
- Mills J, Horváth KM, Reynolds AD, Brightwell G 2018. Farm and Abattoir Sources of *Carnobacterium* Species and Implications for Lamb Meat Spoilage. *J Appl Microbiol.* 125(1): 142-147.
- Molechan C, Amoako DG, Abia ALK, Somboro AM, Bester LA, Essack SY 2019. Molecular Epidemiology of Antibiotic-Resistant *Enterococcus* spp. from the Farm-to-Fork Continuum in Intensive Poultry Production in Kwazulu-Natal, South Africa. *Sci Total Environ.* 692: 868-878.
- Molloy C, Cagney C, O'Brien S, Iversen C, Fanning S, Duffy G 2009. Surveillance and Characterisation by Pulsed-Field Gel Electrophoresis of *Cronobacter* spp. in Farming and Domestic Environments, Food Production Animals and Retail Foods. *Int J Food Microbiol.* 136(2): 198-203.
- Monaghan Á, Byrne B, Fanning S, Sweeney T, McDowell D, Bolton DJ 2013. Serotypes and Virulence Profiles of Atypical Enteropathogenic *Escherichia coli* (EPEC) Isolated from Bovine Farms and Abattoirs. *J Appl Microbiol.* 114(2): 595-603.
- Nauta M, Barfod K, Hald T, Sørensen AH, Emborg HD, Aabo S 2013. Prediction of *Salmonella* Carcass Contamination by a Comparative Quantitative Analysis of *E. coli* and *Salmonella* during Pig Slaughter. *Int J Food Microbiol.* 166(2): 231-237.
- Nógrády N, Kardos G, Bistyák A, Turcsányi I, Mészáros J, Galántai Z, Juhász A, Samu P, Kaszanyitzky JE, Pászti J, Kiss I 2008. Prevalence and Characterization of *Salmonella infantis* Isolates Originating from Different Points of the Broiler Chicken-Human Food Chain in Hungary. *Int J Food Microbiol.* 127(1-2): 162-167.
- Oliveira CJ, Carvalho LF, Fernandes SA, Tavechio AT, Domingues FJJ 2005. Prevalence of Pigs Infected by *Salmonella* Typhimurium at Slaughter after an

- Enterocolitis Outbreak. Int J Food Microbiol. 105(2): 267-271.
- Ollinger M, Wilkus J, Hrdlicka M, Bovay J 2017. Public Disclosure of Tests for *Salmonella*: The Effects on Food Safety Performance in Chicken Slaughter Establishments. United States Department of Agriculture, Economic Research Service.
- Oosterom J, Notermans S 1983. Further Studies on the Practicability of Fattening and Slaughtering Pigs Free from *Salmonella*. Vlaams Diergeneeskundig Tijdschrift. 108(5): 177-186.
- Padungtod P, Kaneene JB 2006. *Salmonella* in Food Animals and Humans in Northern Thailand. Int J Food Microbiol. 108(3): 346-54.
- Pergola S, Franciosini MP, Comitini F, Ciani M, De LS, Bellucci S, Menchetti L, Casagrande PP 2017. Genetic Diversity and Antimicrobial Resistance Profiles of *Campylobacter coli* and *Campylobacter jejuni* Isolated from Broiler Chicken in Farms and at Time of Slaughter in Central Italy. J Appl Microbiol. 122(5): 1348-1356.
- Piras F, Brown DJ, Meloni D, Mureddu A, Mazzette R 2011. Investigation of *Salmonella* Enterica in Sardinian Slaughter Pigs: Prevalence, Serotype and Genotype Characterization. Int J Food Microbiol. 151(2): 201-209.
- Pornsukarom S, Thakur S 2017. Horizontal Dissemination of Antimicrobial Resistance Determinants in Multiple *Salmonella* Serotypes following Isolation from the Commercial Swine Operation Environment after Manure Application. Appl Environ Microbiol. 83(20).
- Powell LF, Lawes JR, Clifton-Hadley FA, Rodgers J, Harris K, Evans SJ, Vidal A 2012. The Prevalence of *Campylobacter* spp. in Broiler Flocks and on Broiler Carcasses, and the Risks Associated with Highly Contaminated Carcasses. Epidemiol Infect. 140(12): 2233-2246.
- Prachantasena S, Charununtakorn P, Muangnoicharoen S, Hankla L, Techawal N, Chaveerach P, Tuitemwong P, Chokesajjawatee N, Williams N, Humphrey T, Luangtongkum T 2016. Distribution and Genetic Profiles of *Campylobacter* in Commercial Broiler Production from Breeder to Slaughter in Thailand. Plos One. 11(2): 1-16.
- Projahn M, Sachsenroeder J, Correia-Carreira G, Becker E, Martin A, Thomas C, Hobe C, Reich F, Robé C, Roesler U, Kaesbohrer A, Bandick N 2021. Impact of on-Farm Interventions against CTX-Resistant *Escherichia coli* on the Contamination of Carcasses before and during an Experimental Slaughter. Antibiotics (Basel). 10(3).
- Quintana-Hayashi MP, Thakur S 2012. Longitudinal Study of the Persistence of Antimicrobial-Resistant *Campylobacter* Strains in Distinct Swine Production Systems on Farms, at Slaughter, and in the Environment. Appl Environ Microbiol. 78(8): 2698-2705.
- Rasschaert G, Houf K, Godard C, Wildemaue C, Pastuszczyk-Frak M, De ZL 2008. Contamination of Carcasses with *Salmonella* during Poultry Slaughter. J Food Prot. 71(1): 146-52.
- Ren X, Li M, Xu C, Cui K, Feng Z, Fu Y, Zhang J, Liao M 2016. Prevalence and Molecular Characterization of *Salmonella enterica* Isolates throughout an Integrated Broiler Supply Chain in China. Epidemiol Infect. 144(14): 2989-2999.
- Schmithausen RM, Schulze-Geisthoevel SV, Stemmer F, El-Jade M, Reif M, Hack S, Meilaender A, Montabauer G, Fimmers R, Parcina M, Hoerauf A, Exner M, Petersen B, Bierbaum G, Bekereditjan-Ding I 2015. Analysis of Transmission of MRSA and ESBL-E among Pigs and Farm Personnel. PLoS one. 10(9): e0138173.
- Shang K, Wei B, Kang M 2018. Distribution and Dissemination of Antimicrobial-Resistant *Salmonella* in Broiler Farms with or without Enrofloxacin Use. BMC Vet Res. 14(1): 257.
- Swanenburg M, Van DWPJ, Urlings HA, Snijders JM, van KF 2001a. *Salmonella* in Slaughter Pigs: the Effect of Logistic Slaughter Procedures of Pigs on the Prevalence of *Salmonella* in Pork. Int J Food Microbiol. 70(3): 231-242.
- Swanenburg M, Urlings HA, Snijders JM, Keuzenkamp DA, Van KF 2001b. *Salmonella* in Slaughter Pigs: Prevalence, Serotypes and Critical Control Points during Slaughter in Two Slaughterhouses. Int J Food Microbiol. 70(3): 243-254.
- Tadee P, Boonkhot P, Patchanee P 2014. Quantification of Contamination Levels and Particular Risk of *Salmonella* spp. in Pigs in Slaughterhouses in Chiang Mai and Lamphun Provinces, Thailand. Jpn J Vet Res. 62(4): 171-9.
- Tadee P, Boonkhot P, Pornruangwong S, Patchanee P 2015. Comparative Phenotypic and Genotypic Characterization of *Salmonella* spp. in Pig Farms and Slaughterhouses in Two Provinces in Northern Thailand. PLoS one. 10(2): e0116581.
- Tadesse DA, Bahnson PB, Funk JA, Thakur S, Morrow WE, Wittum T, DeGraves F, Rajala-Schultz P, Gebreyes WA 2011. Prevalence and Antimicrobial Resistance Profile of *Campylobacter* spp. Isolated from Conventional and Antimicrobial-Free Swine Production Systems from Different U.S. Regions. Foodborne Pathog Dis. 8(3): 367-374.
- Thakur S, Gebreyes WA 2010. Phenotypic and Genotypic Heterogeneity of *Campylobacter coli* within individual Pigs at Farm and Slaughter in the US. Zoonoses Public Health. 57 supply 1: 100-106.
- Verraes C, Van BS, Van ME, Van CE, Butaye P, Catry B, de SMA, Van HX, Imberechts H, Dierick K, Daube G, Saegerman C, De BJ, Dewulf J, Herman L 2013. Antimicrobial Resistance in the Food Chain: A Review. Int J Environ. 10(7): 2643-2669.
- Viana C, Sereno MJ, Pegoraro K, Yamatogi RS, Call DR, Dos SBL, Nero LA 2019. Distribution, Diversity, Virulence Genotypes and Antibiotic Resistance for *Salmonella* Isolated from a Brazilian Pork Production Chain. Int J Food Microbiol. 310: 108310.
- Vieira-Pinto M, Tenreiro R, Martins C 2006. Unveiling Contamination Sources and Dissemination Routes of *Salmonella* spp. in Pigs at a Portuguese Slaughterhouse through Macrorestriction Profiling by Pulsed-Field Gel Electrophoresis. Int J Food Microbiol. 110(1): 77-84.
- Vinueza-Burgos C, Baquero M, Medina J, De ZL 2019. Occurrence, Genotypes and Antimicrobial Susceptibility of *Salmonella* Collected from the

- Broiler Production Chain within an Integrated Poultry Company. *Int J Food Microbiol.* 299: 1-7.
- Wang M, Zhang M, Lu Y, Kang X, Meng C, Zhou L, Li A, Li Z, Song H 2020. Analyses of Prevalence and Molecular Typing of *Salmonella* in the Goose Production Chain. *Poult Sci* 99(4): 2136-2145.
- Wesley IV, Rostagno M, Hurd HS, Trampel DW 2009. Prevalence of *Campylobacter jejuni* and *Campylobacter coli* in Market-Weight Turkeys on-Farm and at Slaughter. *J Food Prot.* 72(1): 43-48.
- Williams MS, Ebel ED 2012. Estimating Changes in Public Health Following Implementation of Hazard Analysis and Critical Control Point in the United States Broiler Slaughter Industry. *Foodborne Pathog Dis.* 9(1): 59-67.
- World Health Organization 2022. Antibiotic resistance. <https://www.who.int/news-room/fact-sheets/detail/antibiotic-resistance>. Accessed 2022 8th Feb.
- World Health Organization 2022. Food safety. <https://www.who.int/news-room/fact-sheets/detail/food-safety>. Accessed 2022 8th Feb.
- Wu X, Suksawat F, Richards AL, Phommachanh S, Phongaran D, Angkititrakul S 2019a. Evaluation of the Containment of Antimicrobial-Resistant *Salmonella* Species from a Hazard Analysis and Critical Control Point (HACCP) and a Non-HACCP Pig Slaughterhouses in Northeast Thailand. *Pathogens.* 9(1).
- Wu X, Angkititrakul S, Prasertsee T, Adsanychan N, Suksawat F 2019b. A Monitoring Report for *Salmonella* spp. in an HACCP Standard Pig Slaughterhouse. *Thai J Vet Med.* 49(2): 161-165.
- Yilmaz A, Gun H, Ugur M, Turan N, Yilmaz H 2006. Detection and Frequency of VT1, VT2 and EaeA Genes in *Escherichia coli* O157 and O157:H7 Strains Isolated from Cattle, Cattle Carcasses and Abattoir Environment in Istanbul. *Int J Food Microbiol.* 106(2): 213-217.
- Zbrun MV, Romero-Scharpen A, Olivero C, Zimmermann JA, Rossler E, Soto LP, Astesana DM, Blajman JE, Berisvil A, Frizzo LS, Signorini ML 2017. Genetic Diversity of Thermotolerant *Campylobacter* spp. Isolates from Different Stages of the Poultry Meat Supply Chain in Argentina. *Rev Argent Microbiol.* 49(3): 235-241.
- Zdolec N, Dobranić V, Filipović I 2015. Prevalence of *Salmonella* spp. and *Yersinia enterocolitica* in/on Tonsils and Mandibular Lymph Nodes of Slaughtered Pigs. *Folia Microbiol (Praha).* 60(2): 131-5.
- Zhou W, Li X, Shi L, Wang HH, Yan H 2018. Novel Scmec Type XII Methicillin-Resistant *Staphylococcus aureus* Isolates Identified from a Swine Production and Processing Chain. *Vet Microbiol.* 225: 105-113.
- Zhu Y, Lai H, Zou L, Yin S, Wang C, Han X, Xia X, Hu K, He L, Zhou K, Chen S, Ao X, Liu S 2017. Antimicrobial Resistance and Resistance Genes in *Salmonella* Strains Isolated from Broiler Chickens along the Slaughtering Process in China. *Int J Food Microbiol.* 259: 43-51.