Epidemiological dynamic potential of transboundary *Salmonella* spp. in meat sold at retail markets in the middle Mekong basin area

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Abstract

Background: The surrounding areas of the middle Mekong basin, particularly along the border line between Thailand and Lao People's Democratic Republic (Lao PDR), is considered to be a high-risk area for many livestock-associated foodborne illnesses, especially salmonellosis. The aim of this study was study aimed to determine the prevalence and characteristics of Salmonella spp. contaminated in pork, beef and chicken meats sold at retail markets in the Thailand-Laos border area surrounding the Thai-Lao Friendship Bridge I from January to May 2019. This study focused on the characteristics of the serotype characteristics, antimicrobial susceptibility testing and the genotype based on multilocus sequence typing (MLST) of the relevant Salmonella strains. The findings will make a significant contribution to the current understanding of Salmonella epidemiology with the aim of enhancing food security in the region.

Results: From a total of 370 meat samples collected, 63% were found to be positive for Salmonella, with the prevalence of 73%, 60% and 56% from pork, beef and chicken meat samples, respectively. Of all the positive samples, 53 serotypes were identified. Of these, S. London accounted for the majority (27%), followed by S. Corvallis (14%), and S. Rissen (6%). Resistance against tetracycline was found at the highest frequency (50%), followed by ampicillin (35%) and sulfamethoxazole-trimethoprim (28%). MLST revealed no evidence of shared genetic relatedness of Salmonella at retail sites among Thailand-Laos border zone. However, a diverse range of Salmonella genotypes had been spread over the area. Besides, the persistence of the residential pathogen and sharing of the supply route within-country can be inferred.

Conclusions: Regular disinfecting of all working areas along with quality control checking at the pre-retail stage must be applied to reduce the transmission of Salmonella as well enhance food security.
control checking at the pre-retail stage must be applied to reduce the transmission of Salmonella and other foodborne pathogens downstream consumers.

Key words: Salmonella; retail market; MLST; Thailand-Laos border; middle Mekong basin

Introduction

Salmonella spp. is an important causative agent of certain foodborne illnesses in humans and can be found all over the world worldwide (Sirichote et al., 2010; Van Boxstael et al., 2012; Basler et al., 2016). Annually, ninety million cases resulting in 150,000 deaths among salmonellosis patients have been counted (Campioni et al., 2012). Along with the direct effects of Salmonella spp. on the gastrointestinal tract, the evidence of drug resistance is also a major public health concern (Foley & Lynne, 2008; Kurtz et al., 2017; Jajere, 2019). Consequently, a reduction in the first line of empirical treatments and limitations associated with treatment choices are listed as the main factors influencing the current situation (Van Boxstael et al., 2012).

Livestock products (farm animal-origin food), especially meats, are known to be an important source of human salmonellosis (Heyndrickx et al., 2002; Mainali et al., 2009; Rostagno & Callaway, 2012). Considering the food production chain, retail markets have been identified as the most significant point of contact for salmonellosis exposure and transmission among humans (Hauser et al., 2011; Gomes-Neves et al., 2012). Furthermore, improper management at locations ahead of the marketplace, such as farms and/or slaughterhouses, also contribute to the chances of increased pathogen loads at the retail site. This can occur either directly or through contaminated equipment due to improper handling practices or unsuitable storage conditions (Lo Fo Wong et al., 2002).
Nowadays, an increase in demand has led to an intensive transformation of the animal production industry (Guardabassi et al., 2008). Good Management Practices (GMP) must be implemented at all levels of production to ensure an optimum level of food safety for consumers. However, these practices cannot be 100% implemented in certain developing regions such as the middle Mekong basin and the surrounding area, particularly along the border between Thailand and Lao People's Democratic Republic (Lao PDR). Animal farming practices are being used extensively in traditional free-range and small-holder backyard systems, which often employ the minimum in terms of hygienic sanitation systems. Moreover, inadequate practices in slaughterhouses and retail outlets, such as on-floor slaughtering and uncontrolled storage conditions in purchasing areas, are considered incautious methods of practice. Additionally, cultural preferences and an inadequate level of awareness among local people with regard to raw meat consumption, as well as an absence of reliable and high-quality resources, such as clean water and cooking supplies, are also considered important risk factors (Wilson, 2007; Conlan et al., 2014; Okello et al., 2017). All of the above-mentioned situational conditions are acknowledged as the potential predisposing factors of several foodborne diseases such as salmonellosis (Mughini-Gras et al., 2014; Ferrari et al., 2019). In 1994, the Thai-Lao Friendship Bridge I linking Nong Khai Province, Thailand and the Vientiane Capital of Lao PDR was officially opened. More than three million people cross the bridge each year (Australian Embassy, Thailand, 2011). These people cross by way of both private and public vehicles to engage in trade and exchange various products. Therefore, the chances of pathogen transmissions between border-line communities are likely to be high. In a study of Salmonella prevalence in the meat being sold surrounding the Thailand-Laos border region, Sinwat et al., (2016) reported that the prevalence of pork contamination in the border areas of Thailand and Lao PDR was 65%. Moreover, Boonmar et al., (2013) reported...
that the prevalence of contaminated pork and beef in southern Laos PDR was 93% and 82%, respectively. Both studies reported a widespread variety of serotype distribution including S. Typhimurium, S. Derby, S. Anatum or S. Rissen. Interestingly, almost all strains of Salmonella are currently classified as multidrug-resistant strains. However, based on the data that has been studied, there is a clear lack of reported information on poultry meat, while it is well known that poultry meat is commonly consumed in this area. Additionally, in order to gain access to in-depth epidemiological information, a study of the pathogen characteristics at the genetic level should be fulfilled in order to gain access to in-depth epidemiological information. A study of the pathogen characteristics at the genetic level should be fulfilled to expand upon the scope of epidemiological knowledge of these pathogens. Multilocus sequence typing (MLST) technique is one of the methods employed in our study. This technique relies on a comparison of the sequences of allele types in a specific group for each set of housekeeping genes and focuses on the genetics to assemble data of the sequence type (ST). The resulting findings can be compared with the information presented in a number of various databases related to the study of the global bacterial dynamic distribution and their genetic evolution (Liu et al., 2011; Patchanee et al., 2017).

The purpose of the study was to investigate the prevalence of Salmonella in meat sold at retail markets in the middle Mekong Basin area along the border of Thailand and Lao PDR, surrounding the Thai-Lao Friendship Bridge I. Together with comparing the expressive and characteristics (serotypes, antimicrobial-resistant patterns and ST type) of Salmonella to expand upon the epidemiological knowledge of pathogen distribution and ST type of Salmonella to expand upon pathogen distribution epidemiological knowledge. The findings from this study would be extremely instrumental in the creation of creating...
appropriate preventive measures that would help control the spread of human salmonellosis in
the region.

Materials and methods
Sample collection
The sample size of this study was determined using the Win Epi online program
(http://www.winepi.net/uk/index.htm). For each parameter used, the degree of prevalence
identified in the previous study was used as the “expected prevalence.” The degree of prevalence
identified in the previous study was used as the “expected prevalence” for each parameter used.
Rates of 65% (Sinwat et al., 2016), 73% (Trongjit et al., 2017) and 82% (Boonmar et al., 2013)
were chosen to calculate the sample sizes for pork, chicken and beef, respectively. Furthermore,
8.5% and 95% were selected as the “accepted error” and “confidence level” values,
respectively, for the required feature inputs. For the infinite population, a minimum of 121, 105
and 79 samples of pork, chicken and beef were designated, respectively. However, in order to
achieve even greater levels of accuracy and reliability, additional samples were carefully
chosen.
During the period of time from January to May, 2019, 370 samples (121, 133 and 116 samples
of pork, chicken and beef, respectively) were carefully collected from five retail markets in
Vientiane Capital, Lao PDR and six retail markets in Nong Khai Province, Thailand. All
samples were then individually labeled, put into plastic packs and stored in an icebox for
laboratory analysis within 24 hr at the Department of Veterinary Medicine, Faculty of
Agriculture, National University of Laos, Nabong Campus, Lao PDR.

Salmonella isolation and identification
Isolation and identification of *Salmonella* spp. from meat samples (pork, chicken, beef) were performed following ISO6579: 2002 Amendment 1:2007, Annex D technique. Accordingly, 25 g of samples were enriched with 225 ml of Buffered Peptone Water (BPW; Merck, Germany). The mixing materials were homogenized for 120 sec and incubated at 37ºC for 18-24 hr. An aliquot of 100 µl of the pre-enriched inoculum was transferred to 10 ml of Rappaport-Vassiliadis broth (RV; Oxoid, England) at 42ºC for an incubation period of 24-48 hr. The likely colonies were streaked on Xylose-Lysine-Desocholate agar (XLD; Oxoid, UK) and Brilliant-green Phenol Red Lactose sucrose agar (BPLS; Merck, Germany). After an incubation period of 18-24 hr at 37ºC, the plates were then inspected. The presumptive colonies were then placed on Triple Sugar Iron agar (TSI; Oxoid, England), urease and Motility Indole-Lysine agar (MIL; Merck, Germany). An analysis of the strains indicated a correct bio-chemical reaction as positive for *Salmonella*. Finally, all results were then recorded. *Salmonella* prevalence with a 95% confidence level along with evidence of an association between a *Salmonella* positive proportion and the relevant specifications (location or meat type) were determined by descriptive statistical analysis and Fisher’s exact test, respectively. All analyses were completed using Epi Info™ version 7. Statistically significant levels were determined at p<0.05.

**Serotyping and Antimicrobial susceptibility testing**

All detected *Salmonella* spp. specimens were serotyped using the serum-agglutination test according to the White-Kauffmann-Le Minor scheme (Popoff et al., 1993). This was made possible by a contribution from the Bacteriology Section, Veterinary Research and Development Center (Upper Northern Region), Lampang, Thailand. All strains were also run through antimicrobial susceptibility testing with agar disk diffusion using ten panels of antimicrobial agents. These agents were comprised of amoxicillin-clavulanic acid (AMC) 20/10 µg, ampicillin (AMP) 10 µg, chloramphenicol (C) 30 µg, ciprofloxacin (CIP) 5 µg,
cefotaxime (CTX) 30 µg, nalidixic acid (NA) 30 µg, norfloxacin (NOR) 10 µg, streptomycin (S) 10 µg, sulfamethoxazole-trimethoprim (SXT) 23.75/1.25 µg and tetracycline (TE) 30 µg. \cite{CLSI,2011} Strains that existed with intermediate resistance were grouped as being susceptible in order to avoid overestimation. Strains that resisted ≥ 3 of the antimicrobial agents were considered multidrug-resistant.

**Multilocus sequence typing (MLST)**

Randomly selected 38 specimens of *Salmonella* obtained from the most frequently found serotypes were genotyped using the MLST technique. Total numbers of DNA genomics were extracted according to the protocol described by Liu et al., \cite{2011}. Seven housekeeping genes, including *aroC* (chorismate synthase); *dnaN* (DNA polymerase III beta subunit); *hemD* (uroporphyrinogenIII cosynthase); *purE* (phosphoribosylaminomidazole carboxylase); *sucA* (alpha ketoglutarate dehydrogenase); *hisD* (histidinol dehydrogenase) and *thrA* (aspartokinase I/homoserine dehydrogenase), were selected for MLST profiling. PCR amplification of all 7 genes was accomplished using the method previously described by Kotetishvil et al., \cite{2002}. Subsequently, the products were sent to be sequenced at the Macrogen Service Center, Republic of Korea.

The sequences obtained in each gene (Supplementary file 1) were transformed into allele numbers, and were compiled according to the sequence type (ST) data obtained from the [http://mlst.warwick.ac.uk/mlst/](http://mlst.warwick.ac.uk/mlst/) database. Finally, all data of the *Salmonella* strains acquired from this study were analysed. A phylogenetic tree was constructed using Bionumerics® software version 7.6 (Applied Maths, Belgium).

**Results**

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Commented \[D17\]: Are these sequences submitted to a public database or repository besides being supplied as supplementary material? It is advisable to deposit any sequence data to make it widely available.

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A total of 370 meat samples were collected during the period from January to May 2019. Subsequently, 135 samples from six retail markets in Nong Khai Province, Thailand and 235 samples from five in Vientiane Capital, Lao PDR were included. With regard to the meat types, 121, 133 and 116 samples of pork, chicken and beef were obtained, respectively (Table S1). The overall prevalence of *Salmonella* spp. was found to be 62.70% (232/370; 95% CI: 57.67-67.48%). In consideration of the sampling locations, the degree of prevalence of the samples collected from Laos PDR (70.21%; 165/235) was statistically higher than the samples collected from the Thai sampling sites (49.63%; 67/135) (p<0.05). In terms of measuring each meat type, the degree of prevalence of the *Salmonella* spp. positive results found in pork, chicken and beef were 72.73% (88/121), 55.64% (74/133) and 60.34% (70/116) in that order. The percentage of prevalence from the samples recovered from pork was significantly higher than from the chicken samples (p<0.05), but this figure tended to be higher compared with the beef samples (p=0.05). Table 1 demonstrates the distribution details of *Salmonella* spp. positives with 95% confidence intervals among the different locations and sample types.

From the overall *Salmonella* strains, 53 serotypes were identified by serum-agglutination according to the White-Kauffmann-Le Minor scheme (Table 2). The highest degree of frequency was found in *S. London* (26.99%; 61/232), followed by *S. Corvallis* (13.79%; 32/232), *S. Rissen* (6.47%; 15/232) and *S. Weltevreden* (6.03%; 14/232), respectively. With regard to the locations of the collected samples, those 4 serotypes were also noted as being in the majority for all locations with the exception of *S. London*, only 2 strains were identified in the Thai samples. Stratifying for each meat type, *S. London* was the most common serotype detected from the pork and beef samples. For the chicken samples, the highest degree of frequency was found for *S. Corvallis*. Interestingly, there were just three serotypes, *S. London*, *S. Rissen*, *S. Corvallis* and *S. Typhimurium*, that were distributed among all meat types.
All 232 *Salmonella* strains were submitted for antimicrobial susceptibility testing. Consequently, 76 of them (32.75%) were classified as multidrug resistant strains. Resistance to tetracycline (49.57%; 115/232) was found in the highest frequency, followed by ampicillin (35.34%; 82/232), and sulfamethoxazole-trimethoprim (28.45%; 66/232), respectively. On the other hand, 94 strains (40.52%) were found to be susceptible to all of the tested antimicrobials. Additionally, only 3 strains (1.29%) were found to be resistant to cefotaxime, while 5 (2.16%) and 6 strains (2.59%) were found to be resistant to norfloxacin and ciprofloxacin, respectively. In terms of the locations from which the samples were obtained, tetracycline (57.78%; 95/165), ampicillin (34.55%; 57/165) and sulfamethoxazole-trimethoprim (32.12%; 53/165) were also ranked in the top most three antimicrobials demonstrating a high resistant rate in Laos PDR. Then again, in Thailand, the resistant rates were ranked as follows; ampicillin (37.31%; 25/67), tetracycline (29.85%; 20/67) and streptomycin (20.90%; 14/67), respectively (Fig. 1). With regard to meat type, resistance rates were divided for each group and are also displayed in Fig. 1. Generally, those rates were found to be somewhat different. Interestingly, especially in the effective antimicrobials, strains resisted against norfloxacin or ciprofloxacin were almost originated from chicken meat. Thus related with the individual data, there were three strains resisted at least seven antimicrobials test (AMP / AMC / CIP / NA / NOR / SXT / TE, AMP / AMC / C / CIP / NA / NOR / SXT / TE and AMP / AMC / C / CIP / NA / NOR / S / SXT / TE), all three were isolated from the chicken meat from Nong Khai, Thailand. Fig. 2 demonstrates the genetic relatedness of *Salmonella* currently being detected at the Thailand-Laos border area. From the 38 *Salmonella* strains analysed, 35 genetic characters were found. The 28 genotypes could not be identified to any ST, and 11 of them could not be grouped in any ST-complex. One to five variation of housekeeping genes of those 28 unidentifies from known ST were displayed in Table 3. However, for the 7 nameable STs (ST64, ST155, ST365, ST469, ST516, ST1541, ST5706), four of those were distinct to a single strain.
Nonetheless, two strains were grouped in the ST155, ST365 and ST 469. Strains grouped in ST155 were derived from a Lao-Aussi market, one was chicken meats and the another was pork. Two strains of ST365 originated from Phonsavang market, one was chicken and the another was beef were also identified. Additionally, the strains grouped in ST469 were originated from pork and beef samples collected from different markets located in nearby areas.

Discussion

The findings obtained from this study represent scientific information on the burden and intensity of *Salmonella* in livestock meats in a 30 km radius surrounding the Thai-Lao Friendship Bridge I. It is well known that this bridge is the primary place for the expansion of trade that has occurred along the Thailand and Laos PDR border since 1994.

Overall degree of prevalence of *Salmonella* spp. in all meat samples was found to be 63%. With regard to each meat type, pork, chicken and beef were found to be contaminated with pathogens at rates of 73%, 56% and 60%, respectively. The degree of contamination in pork had a tendency to be higher in all collected samples in a study conducted by Sinwat et al., (2016). The degree of intensity was recorded at 65.06% (95% CI: 59.26-70.47%). However, for beef samples, the degree of prevalence in this study was lower when compared to the results of a study conducted by Boonmar et al., (2013), in which the prevalence was recorded at 82.35% (95% CI: 58.97-93.81%). Actually, comprehensive figures related to *Salmonella* contamination in the chicken meat being sold in the border area of Thailand and Laos have not yet been reported. A study conducted by Trongjit et al., (2017) reported on the degree of prevalence of *Salmonella* infection at the Thai-Cambodia border, which was found to be 73.43% (95% CI: 66.65-79.42%). This figure is quite a bit higher when compared with our results. In general, most studies have not demonstrated much difference when reporting numbers, which has been proven by an overlap in the 95% confidence intervals. Variations in
the results might depend upon the time period of the sampling along with any existing geographical factors. Nevertheless, high levels of *Salmonella* contamination still persist, even though some intervention has been implemented in some of these areas. *Salmonella* remains a problem in the meat being sold in this region, which has been an important public health concern for the last half decade.

The prevalence of *Salmonella* in the Laos PDR-originated samples was statistically and significantly high. Normally, sanitation practices are different at each location. In fact, there is no supermarket in Laos DPR. All fresh food, such as meat, can only be bought from fresh markets and mini-grocery stores. The lack of covering materials, unsuitable storage conditions and inadequate disinfection practices at the purchasing areas during the meat cutting and handling processes can substantially increase the risk of bacterial colonization (Gomes-Neves et al., 2012; Patchanee et al., 2016). In Thailand, supermarkets are the preferred place to purchase meat. One-sixth of the Thai samples collected in our study were obtained from supermarkets. It is known for stringently regulating their facilities, as well as for implementing biosecurity and hygienic policies along with quality control practices at the pre-harvesting and harvesting stages along the supply chain. However, in general, standard protocols for every type of retail outlet (supermarkets, mini-grocery stores and fresh markets) tend to be higher in bigger cities (Trongjit et al., 2017). With a focus on meat type, pork was found to be the most prevalent when compared with the other types of meat. The reason for this may not be clear. It could be due to the high bacterial loads that emerge during previous production stages, which can then lead to instances of contamination at retail outlets. According to the information obtained from previous studies, *Salmonella* prevalence at pig farms and during pig slaughtering processes was higher than in chicken and beef production (Padungtod & Kaneene, 2006; Trongjit et al., 2017; Phongaran et al., 2019). Another possible explanation for this is that pork is the most common type of meat consumed in this region of study (Napasirth & Napasirth, 2019).
295 The amount of dressing required, along with any other forms of manipulation that are
296 required before meat is sold, would likely increase the opportunity for contamination or re-
297 contamination by product exposure at the final.
298 Based on the findings of previous studies, S. Typhimurium and S. Rissen are the majority
299 serotypes identified in pork (Patchanee et al., 2016; Sinwat et al., 2016). For chicken meat, S.
300 Corvallis and S. Enteritidis are known to be the dominant serotypes (Trongjit et al., 2017).
301 Additionally, S. Stanley and S. Typhimurium have been reported as the most commonly
302 recorded serotypes in beef (Boonmar et al., 2013). At the moment, these serotypes have not
303 been universally matched to each meat type, but low frequencies were recorded in some
304 instances. However, S. Corvallis is still noted as being the dominant serotype in chicken meat.
305 Consequently, new typical sero-characteristics for this region should be set for pork and beef.
306 As the data indicates, S. London is presently the most common serotype. Furthermore, as
307 several serotypes have been detected, some of them several serotypes have been detected, such
308 as S. Altona, S. Cerro, S. Elisabethville, S. Itami, S. Mikamasima, S. Ruzizi, etc., have been
309 reported for the very first time with regard to the isolation of Salmonella in the region.
310 Time factor and sample picking, as well as the cross-contamination that occurs from
311 other sources, are notable factors. Furthermore, even though the same serotype might be
312 present at several meat origins, it cannot be concluded that two or three meat types would be
313 representative of a sharing pool for Salmonella identified from similar sources
314 (Sinwat et al., 2016). All of which would need to be proven later.
315 Salmonella specimens isolated in this study displayed a relatively high degree of frequency of
316 resistance against tetracycline and ampicillin, which is consistent with the findings of previous
317 investigations (Padungtod & Kaneene, 2006; Pulsrikarn et al., 2012; Boonmar et al., 2013).
318 From the past until now, the antimicrobials have been widely used for treatment and
319 prophylaxis in livestock. However, excessive or inappropriate use is considered to be a key
critical factor that has led to the current situation of resistance (Jajere, 2019). On the contrary, low resistance rates have been recorded for cefotaxime, norfloxacin and ciprofloxacin. Instances of resistance should be of particular concern in resource-limited countries because these are the drugs of choice that are recommended to treat human salmonellosis. Particularly for quinolones (norfloxacin and ciprofloxacin), the antimicrobial class is now often used as the first line of treatment (Kurtz et al., 2017). Of course, all of the quinolone-resistant strains discovered in these study areas originated from chicken meat collected in Thailand, and all were found to be resistant to 7-9 of the tested antimicrobials. Selective pressures such as those associated with antimicrobial use, unsuitable temperatures or pH levels, could be considered sub-lethal stress factors during the short production cycle in broiler farms. Additionally, the chicken’s gut ecology should be taken into account when developing resistance to bacterial pathogens (Shang et al., 2018; Yang et al., 2019).

An overview of the phylogenetic tree reveals that most of the strains obtained in this study were diverse. Five-sixths of all strains could not be named to any ST. Microevolution or mutation is a possible explanation for the finding (Harbottle et al., 2006; Liu et al., 2011). This may be proven if some unidentified strains differed in only one or two loci from the other known nomenclatures. Moreover, the variation of 3-5 housekeeping genes of known related ST were also denoted. Therefore, of those, many strains cannot be grouped in any clonal complexes. Those that were unidentified may be newly detected STs that have not yet been recorded in the MLST database.

At this moment, shared genetical relatedness of Salmonella among Thai-Laos border area was not evidenced. The finding infers that the transboundary food supply chain from locations ahead of the marketplace (farm and/or slaughterhouse) are not involve to contamination. However, since only 38 strains were analysed, it cannot 100% prove that Salmonella contamination from both countries are not related. An analysis
together with information of all geographical matching strains previously submitted in MLST database should be recommended fulfilled the gap. Interestingly, various specimens of the *Salmonella* genotypes collected from a single market were remarked. In details, 9 and 6 *Salmonella* genotypes were detected in various meat types collected from Phonsavang and Chensavang markets, respectively. These findings evidence that more than one infection source can exist at a given location. Contamination can occur by itself in the purchasing area or as a result of inadequate processing when the meat product may have already been contaminated. Unhygienic practices at previous production sites, such as on farms and at slaughterhouses, or at transportation hubs may be causes of transmission in the present situation (Heyndrickx et al., 2002; Campioni et al., 2012).

According to the findings of the ST155 and ST365 clonal strains, both were detected on different sampling dates from the same marketplaces. Persistence of residential *Salmonella* flora could therefore be inferred. Moreover, two strains of ST469 were recovered from different markets at in nearby areas. Consequently, the sharing of supply routes at the nearby areas could play a significant role in the dissemination of *Salmonella* spp.

**Conclusions**

As has been demonstrated, the presence of *Salmonella* in meat sold in the middle Mekong basin area was relatively high in terms of prevalence. Standard hygienic protocols are known to be maintained at a higher level in administrative areas. The findings from the molecular MLST indicate that extensive quality control checking at pre-retail stages should be implemented. Furthermore, regular disinfecting of all equipment, as well as at working areas, must be applied. Future efforts in the strengthening of food safety education...
and awareness programs would help authorities to strengthening food safety education and awareness programs would help authorities establish strategies that could potentially reduce the transmission of *Salmonella* and other foodborne pathogens to downstream consumers.

Acknowledgements

This study was financially supported by the Faculty of Veterinary Medicine, Chiang Mai University (Project ID: CMU-MIS R00017502). The authors would like to thank the Bacteriology Section, Veterinary Research and Development Center (Upper Northern Region), Lampang, Thailand and the Vientiane Capital Agriculture and Forestry Department, Vientiane, Laos PDR for their valuable contributions. We would like to thank the Department of Veterinary Medicine, Faculty of Agriculture, National University of Laos for allowing us to use their laboratory facilities for the purposes of diagnosis. Finally, we would like to thank the people who operate the [http://mlst.warwick.ac.uk/mlst/](http://mlst.warwick.ac.uk/mlst/) website which made our regional analysis possible.

Disclosure Statement

No competing financial interests exist.

Figure Legends

**Figure 1**: Percent resistant against antimicrobials of *Salmonella* isolated from various meat types in the Thai-Lao border area.

Antibiotic abbreviations: amoxicillin-clavulanic acid (AMC); ampicillin (AMP); chloramphenicol (C); ciprofloxacin (CIP); cefotaxime (CTX); nalidixic acid (NA); norfloxacin (NOR); sulfamethoxazole-Trimethoprim (SXT); streptomycin (S); tetracycline (TE).
Figure 2: Dendrogram generated using UPGMA algorithms based on MLST profiles with their phenotypic characterizations and the epidemiological data of *Salmonella* circulating in the Thai-Laos border area.

References


