

9-1-2018

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Wenjing Yang

Dusadee Phongaran

Teerarat Prasertsee

Rendong Fang

Patchara Phuektes

See next page for additional authors

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Yang, Wenjing; Phongaran, Dusadee; Prasertsee, Teerarat; Fang, Rendong; Phuektes, Patchara; and Angkititrakul, Sunpetch (2018) "Molecular epidemiology and antimicrobial resistance of *Salmonella* spp. isolated from broilers and pigs at slaughterhouses in Thailand and China," *The Thai Journal of Veterinary Medicine*: Vol. 48: Iss. 3, Article 9.

DOI: <https://doi.org/10.56808/2985-1130.2927>

Available at: <https://digital.car.chula.ac.th/tjvm/vol48/iss3/9>

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Molecular epidemiology and antimicrobial resistance of *Salmonella* spp. isolated from broilers and pigs at slaughterhouses in Thailand and China

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Wenjing Yang, Dusadee Phongaran, Teerarat Prasertsee, Rendong Fang, Patchara Phuektes, and Sunpetch Angkititrakul

Molecular epidemiology and antimicrobial resistance of *Salmonella* spp. isolated from broilers and pigs at slaughterhouses in Thailand and China

Wenjing Yang¹ Dusadee Phongaran¹ Teerarat Prasertsee^{2,3} Rendong Fang⁴

Patchara Phuektes¹ Sunpetch Angkititrakul^{1*}

Abstract

This study aimed to compare the antimicrobial resistance patterns and DNA restriction patterns by Pulsed-Field Gel Electrophoresis (PFGE) between *Salmonella* spp. isolated from broilers and pigs in Thailand and China. One hundred and sixty six isolates were collected from broilers and pigs at slaughterhouses in Khon Kaen, Thailand (n=106) between February to August 2017 and in Chongqing, China (n=60) between March to October 2015. Antimicrobial susceptibility of the isolates was determined using the disk diffusion method with nine antimicrobial agents. Genotypic diversity of the isolates used PFGE of *Xba*I-digested chromosomal DNA to determine. Of 166 *Salmonella* isolates, 37 serotypes were identified. The Thai isolates were composed of 18 serotypes, of which *S. Rissen* was most common (34%). The Chinese isolates consisted of 23 serotypes, of which *S. Derby* was most common (22%). The antimicrobial resistance profiles of *Salmonella* isolates demonstrated that 38% (63/166) of the isolates were multidrug resistance (MDR), with 20.8% (22/106) of the Thai isolates and 68.3% (41/60) of the Chinese isolates being identified as MDR. *Salmonella* Typhimurium and *S. Give* isolated from Thailand and China were found to be clonally unrelated. It is noteworthy that a close genetic relationship, at more than 90% similarity, was observed between *S. Rissen* isolated from pigs in China and Thailand. Based on these results, better surveillance systems for *Salmonella* spp. should be implemented, and the use of antibiotics in food animal production should be more tightly regulated in both Thailand and China. The monitoring program of *Salmonella* dissemination should stay vigilant for *S. Rissen* between Thailand and China.

Keywords: *Salmonella* spp., antimicrobial resistance, PFGE, Thailand, China

¹Faculty of Veterinary Medicine, Khon Kaen University, Khon Kaen 40002, Thailand

²Graduate Program in Veterinary Science, Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai 50202, Thailand

³Integrative Research Center for Veterinary Preventive Medicine, Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai 50202, Thailand

⁴College of Animal Science and Technology, Southwest University, Chongqing, China

*Correspondence: sunpetch@kku.ac.th

Introduction

Salmonella spp. is an important foodborne pathogen causing 93.8 million cases of gastroenteritis globally each year (Majowicz et al., 2010). Pork and poultry meats are among the major sources of foodborne salmonellosis. *Salmonella* spp. can colonize the gastrointestinal tract of animals and cause enteritis. However, infected animals are commonly found to carry and shed the pathogen for a period of time without presenting any clinical signs. *Salmonella* spp. can, thus, enter the food chain during the slaughtering process. Contamination of carcasses can occur during the poor evisceration step and is linked to cross-contamination to humans through consumption of contaminated meat.

The emergence of antimicrobial resistant bacteria (AMR) caused by improper use of antibiotics poses global health threats to both humans and animals (Landers et al., 2012). Antimicrobial resistance was observed in *Salmonella* spp. in the early 1990s, and it has dramatically increased over the past decade (Guerra et al., 2014; Clemente et al., 2015). Antibiotic drugs are used in livestock production for many purposes, including treatment, prevention and control of bacterial infections, and growth promoters (Castanon, 2007). A relationship between the practice of in-feed antimicrobials for animals and the rising problem of drug-resistant bacterial infections in humans has been demonstrated in prior studies (Witte, 2000). Overuse and misuse of antibiotics are the important keys which drive the evolution of antibiotic resistance in bacteria (Read et al., 2014). Antimicrobial resistance genes can be transferred between bacteria by horizontal gene transfer and mobile genetic elements, leading to the emergence and spread of antibiotic resistant bacteria in new geographic locations or new populations (Ventola, 2015).

Travel-associated *Salmonella* infections have become a problem globally. There are several studies indicating that human salmonellosis is related to people who have traveled overseas in the week before they became ill (Hendriksen et al., 2008; Sirichote et al., 2010). Thailand is a famous travelling destination for travelers all over the world. In 2016, there were more than 8,770,000 Chinese tourists travelling to Thailand (Manarungsan, 2009). In addition, Thailand-China bilateral trade has recently been developed and agricultural products, including live animals and meat (Thailand Ministry of Commerce, 2017), are the main products in the bilateral trade. Thus, there is an increase in the risk of foodborne pathogens spreading between Thailand and China (Pornruangwong et al., 2008; Manarungsan, 2009). In view of the current challenges over the emergence of antimicrobial resistant bacteria and a greater risk of pathogens spreading through travel and trade, the objective of this study was to determine antimicrobial resistance patterns and genetic relatedness of *Salmonella* isolates from broilers and pigs at slaughterhouses in Khon Kaen, Thailand and Chongqing, China. Comparative characterization of *Salmonella* isolates from Thailand and China would be useful for planning effective interventions for the control of *Salmonella* and AMR spread.

Materials and Methods

Sample collection: From February to August 2017, 400 samples were randomly collected from broilers (n=200) and pigs (n=200) at 3 local slaughterhouses (2 for broilers, 1 for pigs) located in Khon Kaen Province, Thailand. Cloacal and rectal swabs were collected after stunning and the swabs were put in Cary-Blair transport medium (Oxoid, England) tubes individually. All samples were kept on ice and transported to laboratory.

The Animal Science and Technology College, Southwest University, China provided 60 *Salmonella* isolates. The isolates were collected from broilers (n=21) and pigs (n=39) at 7 local slaughterhouses in Chongqing, China from March to October 2015.

The study was reviewed and approved by the Institutional Animal Care and Use Committee of Khon Kaen University, No. IACUC-KKU-97/60.

Salmonella isolation and identification: Isolation and identification of the *Salmonella* isolates were performed using standard method ISO 6579-1 (ISO, 2007). Briefly, the swabs were put in 9 ml Buffer Peptone Water (BPW, Difco, France) and incubated at 37°C for 24 hours. Bacterial suspensions were then placed on Modified Semisolid Rappaport Vassiliadis medium (MSRV, Difco, France) and incubated at 37°C for 24 hours. Presumptive colonies were streaked on Xylose Lysine Deoxycholate Agar (XLD, Difco, France) and incubated at 37°C for 24 hours. Colonies of presumptive *Salmonella* were selected and confirmed by biochemical tests, including Triple Sugar Iron Agar (TSI, Difco, France) and Motility Indole Lysine Medium (MIL, Difco, France). Serotyping was performed by slide agglutination based on the Kaufman-White scheme using a commercially available antiserum (ECDC 2012; S&A Reagents Lab, Bangkok, Thailand).

Antimicrobial susceptibility testing: The Kirby-Bauer disk diffusion method was carried out according to the Clinical and Laboratory Standards Institute (CLSI) M100 27th standard (CLSI, 2017). The nine antimicrobial agents included ampicillin (AMP, 10 µg), amoxicillin/clavulanate (AMC, 20/10 µg), chloramphenicol (CHL, 30 µg), ciprofloxacin (CIP, 5 µg), cefotazidime (CAZ, 30 µg), nalidixic acid (NAL, 30 µg), norfloxacin (NOR, 10 µg), trimethoprim/sulfamethoxazole (SXT, 1.25/23.75 µg), and tetracycline (TET, 30 µg). *Escherichia coli* ATCC-25922 were used as quality control strains.

Pulsed-Field Gel Electrophoresis (PFGE) genotyping: Pulsed-Field Gel Electrophoresis (PFGE) was performed following the PulseNet protocol from the Centers for Disease Control and Prevention (CDC, 2017). Briefly, the *Salmonella* isolates were grown on Mueller-Hinton agar (MHA) at 37°C for 14-18h. Cell Suspension Buffer (100 mM Tris: 100 mM EDTA, pH 8.0) was used to suspend and adjust the bacterial concentration to an optical density (OD₆₀₀) of 1.0. Cell Lysis Buffer (50 mM Tris: 50 mM EDTA, pH 8.0 + 1% Sarcosyl) and Proteinase K (SIGMA Life Science, SL, USA) were used to lyse the bacterial cells embedded in

agarose plugs, and genomic DNA was then digested with *Xba*I restriction enzyme (New England Biolabs Ipswich, MA, USA). *Salmonella enterica* serovar Breanderup H9812 was used as a molecular standard marker. The DNA fragments were separated by CHEF-DR® III Pulsed-Field Electrophoresis System (Bio-Rad Laboratories, Hercules, CA, USA).

Data analysis: Differences in resistance rate among the isolates from pigs and chickens were analyzed between Thailand and China by chi-squared analysis using SPSS software ver.17.0 (SPSS Inc., USA). Only data about resistance to AMP, CHL, NAL, SXT and TET were used in the analysis due to distribution of the data. The analysis was done separately for each antimicrobial agent. The fingerprint analysis was carried out using Bio-Numerics software version 7.6 (Applied Maths, Belgium). Calculation of similarity between PFGE fingerprint patterns was performed using the Dice coefficient similarity index with 1% optimization and 1% tolerance. Cluster analysis was performed using unweighted-pair group method with arithmetic means (UPGMA).

Results

Salmonella detection and serotypes: One hundred and six *Salmonella* isolates were recovered from the samples collected in Thailand. The percentage of *Salmonella* positive samples for pigs (35%, 36/200) was significantly higher than that for broilers (18%, 70/200) ($p < 0.05$). Of the 166 *Salmonella* isolates from Thailand and China, a total of 37 serotypes were identified (Table 1). The Thai isolates were composed of 18 serotypes, of which *S. Rissen* (34.0%) was the most common, followed by *S. Give* (21.7%) and *S. Weltevreden* (16.0%). The Chinese isolates consisted of 23 serotypes, of which *S. Derby* (21.7%) was the most common, followed by *S. London* (15.0%) and *S. Give* (10.0%).

Antimicrobial resistance of Salmonella isolates: The antimicrobial resistance percentages of *Salmonella* from Thailand and China are shown in Table 2. Differences in resistance proportion to antimicrobials were observed between the Thai isolates from pigs and broilers. All the Thai isolates from pigs were susceptible to norfloxacin and all the isolates from broilers were susceptible to amoxicillin/clavulanate. The pig isolates were most commonly resistant to ampicillin (70.0%), followed by tetracycline (50.0%), and trimethoprim/sulfamethoxazole (27.1%), while the broiler isolates exhibited a high frequency of resistance to nalidixic acid (69.4%), followed by ciprofloxacin (16.7%), and ampicillin (13.9%). In the pig isolates from China, all isolates were susceptible to amoxicillin/clavulanate and were commonly resistant to tetracycline (79.5%), followed by ampicillin (69.2%), chloramphenicol (56.4%) and trimethoprim/sulfamethoxazole (56.4%). The majority of broiler isolates from China exhibited resistance to ampicillin (85.7%), trimethoprim/sulfamethoxazole (85.7%) and tetracycline (85.7%). The resistance proportions to ampicillin, chloramphenicol, and nalidixic acid were significantly higher for both pig

and broiler isolates from China than from Thailand ($p < 0.05$). A significantly higher resistance proportion to trimethoprim/sulfamethoxazole and tetracycline were also observed for the broiler isolates from China than from Thailand ($p < 0.05$). Overall, the Chinese isolates were more commonly found to show higher proportions of resistance to antimicrobials than the Thai isolates.

The antimicrobial resistance profiles of *Salmonella* isolates are shown in Table 3. The 166 *Salmonella* isolates displayed 32 different antimicrobial resistance profiles, with 38% (63/166) of the isolates being identified as multidrug resistance (MDR, resistance to 3 or more antimicrobial agents). In Thailand, 20.8% (22/106) of isolates were identified as MDR. The most frequent resistance profile was ampicillin/trimethoprim/sulfamethoxazole/tetracycline. In China, 68.3% (41/60) of isolates were identified as MDR, with the most common resistance pattern being ampicillin / chloramphenicol / trimethoprim / sulfamethoxazole / tetracycline.

Genetic diversity and antimicrobial resistance patterns (R-types) of Salmonella isolates: In order to investigate the relationship between the *Salmonella* isolates from Thailand and China, PFGE was performed in isolates of the serotypes commonly presented in both Thailand and China. Figure 1 shows the fingerprint patterns and R-types of 39 *Salmonella* isolates, comprising *S. Typhimurium* (n=13), *S. Rissen* (n=13) and *S. Give* (n=13). Based on 78% genetic similarity, the 39 *Salmonella* isolates were grouped into 9 genotypic clusters (A-I). The isolates of *S. Typhimurium*, *S. Rissen* and *S. Give* were distinctly grouped into 5 (A-E), 1 (F) and 3 (G-I) clusters, respectively. For *S. Typhimurium* and *S. Give*, the phylogenetic analysis revealed that the strains were clustered by geographical region. In contrast, all isolates of *S. Rissen* from Thailand and China were found to belong to the same cluster.

Most isolates in each cluster shared similar antimicrobial resistance patterns, except in the cluster F and G showing 4 diverse R-types. In terms of geographical location, distinct R-types were found for *S. Typhimurium* and *S. Give* isolated from Thailand and China. Conversely, some isolates of *S. Rissen* from Thailand and China had the same R-type such as isolates R9, R10, R11 (tetracycline) and R1, R2, R3 (ampicillin/tetracycline).

Discussion

In this study, *Salmonella* spp. was detected from pigs at a higher percentage than from broilers (35.0% versus 18.0%). For pigs, a similar percentage (34%) was reported in a previous study in northeastern Thailand (Sinwat et al., 2016). However, *Salmonella* positive proportions in this study were much higher than the studies in Sa Kaew province in eastern Thailand (35.0% versus 3%) and in two provinces in northern Thailand (35% versus 11.9%). Similarly, *Salmonella* spp. was detected from broilers at slaughterhouses at much higher percentages than the studies in Sa Kaew (18.0% versus 1.1%) and in Chiang Mai, a province located in the northern part of

Thailand (18.0% versus 3.2%) (Trongjit et al., 2017, Chotinun et al., 2014). These discrepancies may be due

to the relatively high prevalence of *Salmonella* infections in pigs and broilers in the area of this study.

Table 1 Serotypes of *Salmonella* from pigs and broilers in Thailand and China

Salmonella Group	Salmonella Serotype	Thailand			China			
		Pigs (No, %)	Broilers (No, %)	Total (No, %)	Pigs (No, %)	Broilers (No, %)	Total (No, %)	
A	S. Kiel					1, 4.8	1, 1.7	
	S. Derby				8, 20.5	5, 23.8	13, 21.7	
	S. Typhimurium	8, 11.4		8, 7.5	5, 12.8		5, 8.3	
	S. Stanley	7, 10		7, 6.6				
B	S. Bredeney				1, 2.6		1, 1.7	
	S. Fyris				1, 2.6		1, 1.7	
	S. Kunduchi				1, 2.6		1, 1.7	
	S. Indiana					1, 4.8	1, 1.7	
	S. Travis					1, 4.8	1, 1.7	
	S. Rissen	36, 51.4		36, 34.0	2, 5.1	1, 4.8	3, 5.0	
	S. Cremieu		2, 5.6	2, 1.9				
	S. Kentucky		2, 5.6	2, 1.9				
C	S. Brunei	1, 1.4		1, 0.9				
	S. Bardo		1, 2.8	1, 0.9				
	S. Bazenheid		1, 2.8	1, 0.9				
	S. Chormedey		1, 2.8	1, 0.9				
	S. Doncaster					1, 4.8	1, 1.7	
	S. Gyprus		1, 2.8	1, 0.9				
	S. Jerusalem					1, 4.8	1, 1.7	
	S. Istanbul		1, 2.8	1, 0.9				
	S. Lichfield		1, 2.8	1, 0.9				
	S. Lomita				1, 2.6		1, 1.7	
	S. Molade		1, 2.8	1, 0.9				
	S. Newport		1, 2.8	1, 0.9				
D	S. Saintpaut		1, 2.8	1, 0.9				
	S. Wippra		1, 2.8	1, 0.9				
	S. Enteritidis					1, 4.8	1, 1.7	
	S. Give	1, 1.4	22, 61.1	23, 21.7	3, 7.7	3, 14.3	6, 10.0	
	S. Weltevreden	17, 24.3		17, 16.0		1, 4.8	1, 1.7	
	S. London				7, 17.9	2, 9.5	9, 15.0	
	S. Salamae				5, 12.8		5, 8.3	
	S. Anatum				2, 5.1		2, 3.3	
	E	S. Rideau				1, 2.6	1, 4.8	2, 3.3
		S. Calaber					1, 4.8	1, 1.7
S. Newland						1, 4.8	1, 1.7	
S. Seegefeld					1, 2.6		1, 1.7	
S. Souza					1, 2.6		1, 1.7	
Total			70, 100	36, 100	106, 100	39, 100	21, 100	60, 100

S. Rissen was the most common serotype among the isolates of Thai origin, particularly in the pig samples. This finding is similar to that of a previous study in which this serotype was found to be the most common in pork carcasses (Sanguankit et al., 2010). *S. Rissen* has been reported to be among the most common serotypes found in pigs and pork products in several Asian countries including South Korea,

Vietnam, and Thailand (Lim et al., 2009; Thai et al., 2001; Hendriksen et al., 2008). In China, a recent study has shown that *S. Rissen* was the most predominant serotype in pigs at slaughterhouses in Shandong province (Zhao et al., 2017). Our results are different in that the most common serotype in pigs from China was *S. Derby*, and only 5% of *S. Rissen* were identified from pigs. *S. Derby* was also found to be the most common

among the Chinese isolates from broilers. However, this serotype was not found in the broilers in Thailand. In addition, the proportions of serotypes identified among the Thai and Chinese isolates are mostly

different, except for *S. Typhimurium* in the pig isolates. A possible explanation for all these differences is the geographical locations of sampling sites.

Table 2 Antimicrobial resistance percentages of *Salmonella* from Thailand and China

Location	Sample	Antimicrobial resistant agents*								
		AMP	AMC	CHL	CAZ	CIP	NAL	NOR	SXT	TET
Thailand	Pig	49 (70.0%) ^a	1 (1.4%)	5 (7.1%) ^a	1 (1.4%)	2 (2.9%)	2 (2.9%) ^a	0 (0%)	19 (27.1%)	35 (50.0%)
	Broiler	5 (13.9%) ^b	0 (0%)	1 (2.8%) ^b	1 (2.8%)	6 (16.7%)	25 (69.4%) ^b	2 (5.6%)	2 (5.6%) ^b	1 (2.8%) ^b
China	Pig	27 (69.2%) ^a	0 (0%)	22 (56.4%) ^a	2 (5.1%)	4 (10.3%)	14 (35.9%) ^a	3 (7.7%)	22 (56.4%)	31 (79.5%)
	Broiler	18 (85.7%) ^b	3 (13.3%)	13 (61.9%) ^b	2 (9.5%)	6 (28.6%)	10 (47.6%) ^b	2 (9.5%)	18 (85.7%) ^b	18 (85.7%) ^b

*AMP: ampicillin, AMC: amoxicillin/clavulanate, CHL: chloramphenicol, CAZ: Cefazidime, CIP: ciprofloxacin, NAL: nalidixic acid, NOR: norfloxacin, SXT: trimethoprim/sulfamethoxazole, TET: tetracycline

Table 3 Antimicrobial resistance profiles of *Salmonella* MDR from Thailand and China

Antimicrobial resistant profile	Thailand			China		
	Pig (No, %)	Broiler (No, %)	Total (No, %)	Pig (No, %)	Broiler (No, %)	Total (No, %)
AMP-CAZ-NAL	1, 5.0		1, 4.5			
AMP-NAL-SXT					1, 5.6	1, 2.4
AMP-SXT-TET	13, 65.0		13, 59.1	1, 4.3	2, 11.1	3, 7.3
CHL-SXT-TET	2, 10.0		2, 9.1			
AMP-AMC-SXT-TET	1, 5.0		1, 4.5			
AMP-CHL-SXT-TET	2, 10.0		2, 9.1	10, 43.5	6, 33.3	16, 39.0
AMP-CIP-NAL-TET	1, 5.0		1, 4.5			
CHL-NAL-SXT-TET				1, 4.3		1, 2.4
CAZ--CIP-NAL-NOR		1, 50.0	1, 4.5			
AMP-CHL-NAL-SXT-TET				6, 26.1	1, 5.6	7, 17.1
AMP-AMC-CHL-SXT-TET					1, 5.6	1, 2.4
AMP-CAZ-NAL-SXT-TET				1, 4.3	1, 5.6	2, 4.9
AMP-CIP-NAL-SXT-TET					1, 5.6	1, 2.4
AMP-CIP-NAL-NOR-TET		1, 50.0	1, 4.5			
AMP-CHL-CIP-NOR-SXT-TET				1, 4.3		1, 2.4
AMP-CHL-CIP-NAL-SXT-TET					3, 16.7	3, 7.3
AMP-CHL-CAZ-CIP-NAL-TET				1, 4.3		1, 2.4
AMP-CHL-CIP-NAL-NOR-SXT-TET				2, 8.7		2, 4.9
AMP-AMC-CHL-CIP-NAL-NOR-SXT-TET					1, 5.6	1, 2.4
AMP-CHL-CAZ-CIP-NAL-NOR-SXT-TET					1, 5.6	1, 2.4
Total	20, 100	2, 100	22, 100	23, 100	18, 100	41, 100

In Thailand, the highest resistance proportion was observed for ampicillin, followed by tetracycline. This finding is similar to that in China where bacteria were most commonly resistant to ampicillin and tetracycline. This may be attributed to the global usage of ampicillin and tetracycline in food-animals against bacterial infections for long periods, causing selective pressure. Chloramphenicol has already been banned in food-animal productions for more than 10 years in most countries including Thailand and China. However, *Salmonella* isolates of Thai and Chinese

origins were found to have resistance to chloramphenicol, particularly the Chinese isolates. Resistance to chloramphenicol is related to the presence of chloramphenicol resistance gene (*cmIA*) located in gene cassettes in class 1 integrons. Thus, *Salmonella* carrying class 1 integrons may display chloramphenicol resistance phenotype (Chuanchuen et al., 2009, Shousha et al., 2015, Prasertsee et al., 2016). Another reason mentioned in a previous study is that the use of related classes of antibiotics such as florfenicol, commonly used in livestock production,

attributes to co-selective pressure (Pornsukarom et al., 2015). High resistance proportions to nalidixic acid (first generation quinolones antibiotics) were detected in pigs from China (35.9%) and in broilers from both Thailand (69.4%) and China (47.6%). Quinolones are

commonly used for the treatment of multi-drug resistant salmonellosis in humans and animals (Dalhoff, 2012). Thus, increasing quinolone resistance means increased difficulty in controlling bacterial infections caused by *Salmonella* spp. (Pribul et al., 2017).

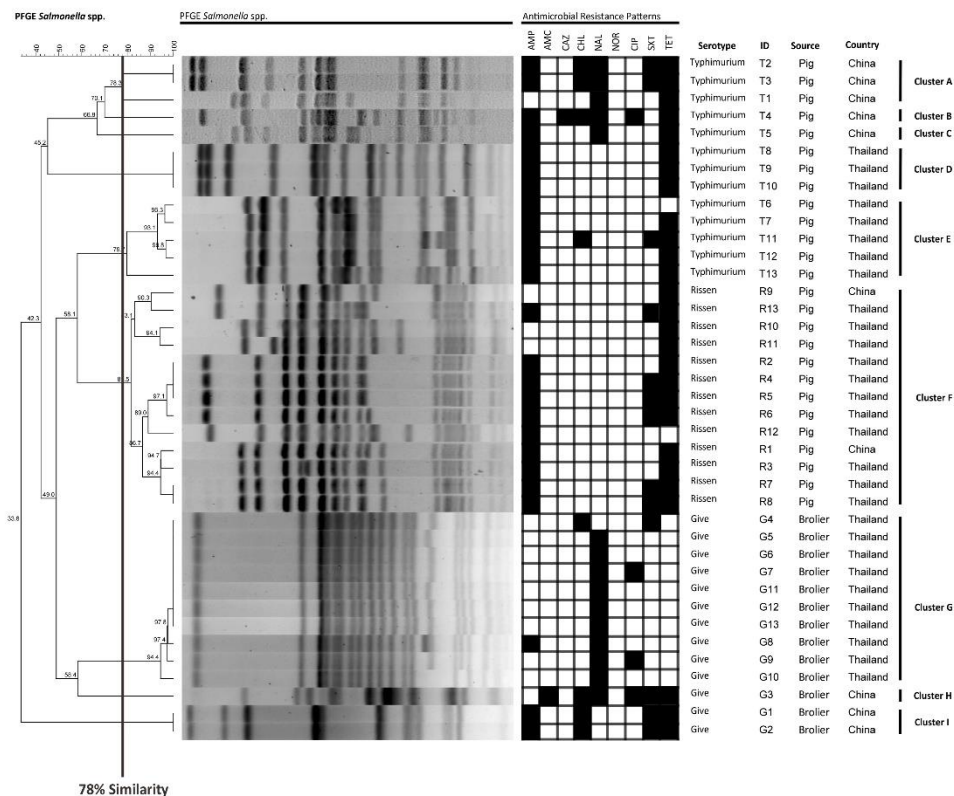


Figure 1 Dendrogram of 39 PFGE-*Xba*I profiles of *Salmonella* spp. isolated from broilers and pigs at slaughterhouses in Thailand and China (■ = resistance, □ = susceptibility)

The serotyping results demonstrated that *S. Typhimurium*, *S. Rissen*, *S. Give* and *S. Weltevreden* were present in both Thailand and China. Pulsed-Field Gel Electrophoresis (PFGE) has been used as an epidemiological tool to identify the genetic relatedness of *Salmonella* across different geographical regions (Zheng et al., 2014). In this study, *S. Typhimurium*, *S. Rissen* and *S. Give* were genetically analyzed by PFGE in order to investigate the relationship between the *Salmonella* isolates from Thailand and China. The pulsotypes and also R-types of *S. Typhimurium* and *S. Give* isolates did not show a relationship between these two different geographical regions. However, these findings are different from those found in *S. Rissen*. The pulsotype of *Salmonella* isolates revealed the genetic relatedness between *S. Rissen* from Thailand and China. This finding differs from a previous study that demonstrated no clonal relatedness between *S. Rissen* isolates from Thailand and United States (Pornsukarom et al., 2015). It could be due to a wider spectrum of clonal diversity among *S. Rissen* in the US than in Thailand and China. However, the epidemiological link between *S. Rissen* in Thailand and China is possible and calls for further investigations.

In conclusion, this is the first study that compares molecular epidemiology and antimicrobial resistance of *Salmonella* spp. between Thailand and China. It indicated that *S. Rissen* was the most important serotype for implementation of active surveillance systems to monitor and control cross-circulation and spread of AMR between Thailand and China through various means such as bilateral trade and tourism.

Acknowledgements

The authors would like to thank Asst. Prof. Seri Khang-Air from Khon Kaen University for collecting the samples; Assoc. Prof. Dr. Rungtip Chuanchuen and staff from Faculty of Veterinary Medicine, Chulalongkorn University for serotyping technique; and staff from Veterinary Diagnostic Laboratory Research and Academic Service Unit, KKU Animal Hospital for helping with the isolation.

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บทคัดย่อ

ระบาดวิทยาทางโมเลกุลและการดื้อสารต้านจุลชีพของเชื้อซัลโมเนลลาที่แยกได้จากไก่และสุกรที่โรงฆ่าสัตว์ของประเทศไทยและประเทศสาธารณรัฐประชาชนจีน

เวณิจ ยัง¹ ดุษฎี ผ่องอรุณ¹ อีร์รัตน์ ประเสริฐศรี^{2,3} เรนดอง ฟิง⁴ พัชรา เมือกเทศ¹ สรรเพชญ์ อังกิติตระกูล^{1*}

วัตถุประสงค์ของการศึกษานี้ เพื่อเปรียบเทียบรูปแบบการดื้อสารต้านจุลชีพและ DNA restriction pattern โดยใช้วิธี Pulsed-Field Gel Electrophoresis (PFGE) ของเชื้อ *Salmonella* spp. ที่แยกได้จากไก่และสุกรที่โรงฆ่าสัตว์ในประเทศไทยและประเทศสาธารณรัฐประชาชนจีน จำนวนตัวอย่างทั้งหมด 166 ตัวอย่าง โดยสุ่มเก็บจากไก่และสุกรที่โรงฆ่าสัตว์ในจังหวัดขอนแก่น ประเทศไทย (n=106) ระหว่างเดือนกุมภาพันธ์ถึงสิงหาคม 2560 และเมืองฉิ่ง ประเทศสาธารณรัฐประชาชนจีน (n=60) ระหว่างเดือนมีนาคมถึงตุลาคม 2558 การทดสอบการดื้อสารต้านจุลชีพจำนวน 9 ชนิดด้วยวิธี Disk diffusion method การเปรียบเทียบความหลายหลายทางพันธุกรรมของเชื้อซัลโมเนลลาด้วยวิธี PFGE ด้วยเอนไซม์ XbaI การศึกษาพบเชื้อซัลโมเนลลา 37 ซีโรไทป์จาก 166 ตัวอย่าง เชื้อที่แยกจากประเทศไทยพบ 18 ซีโรไทป์ โดยเป็น *S. Rissen* สูงสุด (34%) ส่วนประเทศจีนพบ 23 ซีโรไทป์ โดยเป็น *S. Derby* มากที่สุด (22%) พบการดื้อสารต้านจุลชีพทั้งหมดร้อยละ 38 (63/166) โดยเป็นเชื้อที่ดื้อสารต้านจุลชีพสามชนิดขึ้นไปของประเทศไทยและประเทศจีนจำนวน 20.8% (22/106) และ 68.3% (41/60) ตามลำดับ อย่างไรก็ตาม อย่างไม่พบความสัมพันธ์ของ *S. Typhimurium* และ *S. Give* ที่แยกได้จากประเทศไทยและประเทศจีน แต่ซีโรไทป์ *S. Rissen* พบว่ามีความสัมพันธ์กันมากกว่าร้อยละ 90 ดังนั้น การเฝ้าระวังเชื้อซัลโมเนลลาอย่างเป็นระบบ โดยเฉพาะ *S. Rissen* และการใช้สารต้านจุลชีพอย่างเหมาะสมในสัตว์บริโภคทั้งประเทศไทยและประเทศจีนจะช่วยลดการแพร่กระจายและการดื้อสารต้านจุลชีพของเชื้อนี้ได้

คำสำคัญ: ซัลโมเนลลา การดื้อสารต้านจุลชีพ PFGE ประเทศไทย ประเทศสาธารณรัฐประชาชนจีน

¹คณะสัตวแพทยศาสตร์ มหาวิทยาลัยขอนแก่น จังหวัดขอนแก่น 40002 ประเทศไทย

²หลักสูตรบัณฑิตศึกษา สาขาวิชาวิทยาศาสตร์การสัตวแพทย์ คณะสัตวแพทยศาสตร์ มหาวิทยาลัยเชียงใหม่ จังหวัดเชียงใหม่ 50202 ประเทศไทย

³ศูนย์บูรณาการวิจัยวิทยาศาสตร์ป้องกันทางสัตวแพทย์ คณะสัตวแพทยศาสตร์ มหาวิทยาลัยเชียงใหม่ จังหวัดเชียงใหม่ 50202 ประเทศไทย

⁴College of Animal Science and Technology, Southwest University, Chongqing, China

*ผู้รับผิดชอบบทความ E-mail: sunpetch@kku.ac.th