Original Article

Sources and Disseminations of *Salmonella* spp. in an Integrated Broiler Meat Production

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Abstract

In this study, important sources and disseminations of *Salmonella* in integrated broiler meat production was conducted in the north-eastern part of Thailand during 2010-2012. Both environmental samples and chicken-related samples from three broiler meat production cycles, starting from breeder farm, hatchery, broiler farm, and slaughterhouse were collected. The chicken-related samples were tested to monitor *Salmonella* status of the chickens, eggs, or whole carcasses, whereas the environmental samples were tested to investigate the possible sources of *Salmonella* contamination. A total of 1,449 chicken-related samples and 802 environmental samples were analyzed. Results of this study showed that *Salmonella* was found in all production units. Horizontal transmission was considered as the main route of *Salmonella* contamination in this integrated broiler production. No *Salmonella* contamination was found in any of the egg samples. Important sources of *Salmonella* during the broiler production were contaminated environment and equipment in hatchery, contaminated day-old chicks, feed, and pests especially house lizards. In addition, the main factors for *Salmonella* dissemination to the chicken carcasses were contaminated transport cages, transportation of broilers to slaughterhouse, and cross-contamination during the slaughter process. Therefore, effective top-to-down *Salmonella* controlling approach should be implemented; especially for sanitary programs, feed quality control, water treatment, pest management and HACCP plan in the slaughterhouse.

Keywords: broiler, dissemination, environment, *Salmonella* spp., source

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Introduction

Salmonella is one of the most common causes of foodborne diseases worldwide (WHO, 2013; Scallan et al., 2011). Clinical signs of human salmonellosis consist of nausea, vomiting, abdominal pain, headache, chills, and diarrhea. Generally, most patients recover naturally without any antibiotic treatments. However, it has been found that serious complications do occur in infants, the elderly and immune-compromised patients.

Food from animal origin, particularly from poultry, is the major source of human salmonellosis (EFSA, 2012). In order to decrease human salmonellosis, many countries have established microbiological standard for *Salmonella* spp. in chicken meat and its products not to be detected in 25 grams. In Thailand, broiler meat and its products are one of the major agricultural exports, with up to 538,104 tons and the value over 67,000 million baht exported in year 2012 (OAE, 2013). Therefore, controlling *Salmonella* spp. contamination in the broiler meat and its products is necessary to maintain or even enhance the export volume for the poultry business in Thailand.

Controlling *Salmonella* in broiler meat and its products is a complicated, challenging and comprehensive task. The entire chain of broiler meat production needs to be taken into account as a whole. As has been observed, *Salmonella* can be introduced and disseminated during broiler meat production from several contaminated sources such as day-old chicks, litter, water supply, feed, farm workers, equipment, dust and pests, *e.g*. rodents, flies, darkling beetles and wild birds (Davies et al., 1997; Murray, 2000; Marin et al., 2010). Moreover, improper cleaning and disinfection procedure in broiler farm can cause persistence of *Salmonella* in current and consecutive batches of broiler flock (Marin et al., 2010). An evidence has shown that stress of chicks during transportation can cause *Salmonella* excretion from any latent infection in the chicks, which can then spread throughout the flock before the slaughter process (Humphrey, 2000). Finally, improper processing of chicks in slaughterhouse can spread and cross-contaminate *Salmonella* to broiler meat and its products.

In Thailand, number of the studies that focus on and aim to follow the source and dissemination route of *Salmonella* throughout the integrated broiler meat production is very limited. Therefore, the objective of this study was to comprehensively determine the major sources and disseminated routes of *Salmonella* contamination in integrated broiler meat production.

Materials and Methods

Sample collection: Samples were obtained from an integrated broiler meat operation in north-eastern Thailand. Complete production cycles of three broiler flocks were studied for *Salmonella* contamination, starting from breeding farm, hatchery, broiler farm and slaughterhouse during June 2010 to March 2012. A total of 1,449 "chicken-related" samples and 773 "environmental" samples were collected from three breeder flocks, one hatchery, three broiler flocks (from the same house), and one slaughterhouse. Ages of the breeder flocks were 55 weeks, 35 weeks, and 42 weeks at the first, second and third sampling period, respectively. Vaccination program for *Salmonella* was done by both attenuated and killed vaccine in the breeder flocks for the second and third production cycles, whereas only attenuated vaccine was used in the first production cycle.

After the first sampling period, difficulties in the collection procedure and interpretation of the data were identified and then corrected in subsequent sampling periods. The collection technique was adjusted to better reflect the true prevalence of the pathogen in the flock, *e.g*. changed from pooled samples to individual samples and increased the number of samples. In addition, the feather samples were changed to cloacal swab samples to reduce the time spent for collection and limit the chance of cross-contamination.

Sample collection in the breeder farm: For the first sampling period, nine pooled fecal samples (approximately 300 g per pooled sample) collected from the breeder flock were analyzed to identify contamination status of the breeder flock. For the second and third sampling period, boot swab samples were used to determine the contamination status and an addition of 120 individual cloacal swabs were tested in order to quantify the *Salmonella* prevalence in the flock. Furthermore, egg samples after being laid in the breeder farm were pooled samples (5 eggs per sample) and tested for *Salmonella* contamination in the first sampling whereas individual eggs were tested in the second and third sampling. For egg tray samples, an area of 100 square centimeters were swabbed from each tray and a pool of 10 tray swabs was combined to constitute a sample. For basket and plate samples, pooled samples were collected in the similar fashion, in which 5 baskets and 5 plates were combined to constitute a sample. Additional samples from egg transfer belts (100 square centimeters per sample) and hands of workers (before working) were collected in the second and third sampling period.

Sample collection in hatchery: Egg samples before incubation, after 18 days of incubation, and meconium in hatching trays were collected to monitor *Salmonella* contamination in eggs and baby chicks. Environmental swabs from an area of 1 square meter of egg storage room, incubating room, hatching room, egg trolleys, transferring plates, illuminating plates, transferring belts, and trucks were collected. Swabs from hooks, egg setting stands, hatching trays (before use), hands of workers (before work) and water (spraying hatching eggs) were also collected to investigate the source of *Salmonella* contamination in the hatchery.

Sample collection in broiler farm: The chicken-related and the environmental samples were collected in four different steps consecutively during the rearing period, including 1) after cleaning and

disinfection, 2) on chick arrival day, 3) during rearing period (weekly) and 4) on slaughter day. Regarding the first step, after cleaning and disinfection, swabs from an area of 1 square meter of floor and wall of the broiler house were collected. For pan feeder and water nipple, pooled swab samples from 5 pieces were combined to constitute one sample. Water, litter (after disinfection), and pests were taken to assess *Salmonella* persistence after cleaning and disinfection. In the second step, on chick arrival day, meconium on box-liners was collected to identify *Salmonella* status of new chicks. Additionally, samples from boot swabs, wall swabs, new feed in hoppers, feed in pan feeders (5 pans per samples), water nipple swabs, water and pests were taken to assess *Salmonella* contamination in the broiler house before placing the new chicks. In the third step, during rearing period, samples were collected weekly until the birds were slaughtered on week 6. Either pooled fecal samples (for the first sampling period) or cloacal swabs and boot swabs (for the second and third sampling period) were collected to monitor *Salmonella* status of the broiler flocks. In addition, samples from new feed in hoppers, feed in pan feeders (5 pans per sample), water from inlet, and water from nipples (10 nipples per sample) and pests were taken to evaluate and investigate the source of *Salmonella* contamination in the broiler flocks. As the last step, on slaughter day, water (before spraying the chicken), cage swabs, hands of workers (before work) and 1 square meter of the truck floor were collected to investigate the source of *Salmonella* contamination before the slaughtering.

Sample collection in slaughterhouse: Feathers around cloaca (for the first sampling period) or cloacal swabs (for the second and third period) were collected at the holding area of the slaughterhouse to assess contamination status of arriving birds. Whole carcass rinse samples were collected at the end of the process for final product evaluation.

***Salmonella* isolation and identification:** *Salmonella* isolation was performed according to the ISO 6579:2002/Amd 1:2007 (Annex D) standard method (International Organization for Standardization, 2007). For feces, litter, and feed samples, 25 g of the sample were mixed with 225 ml of buffered peptone water (BPW, Merck KGaA, Darmstadt, Germany) and incubated at 37°C for 24 h for pre-enrichment. For swab samples, the swabs were placed in small amount of BPW (5-30 ml depending on size and number of swabs). For egg and lizard samples, the whole content was mixed with 225 ml and 100 ml of BPW, respectively. For water samples, 100 ml of the water was mixed with 100 ml of double-strength BPW for pre-enrichment. After incubation, 0.1 ml of the pre-enriched broth was inoculated into modified semi-solid Rappaport-Vassiliadis medium (MSRV, Merck KGaA, Darmstadt, Germany) and 10 ml of the Rappaport-Vassiliadis with soya broth (RVS, Merck KGaA, Darmstadt, Germany). In addition, 1 ml of the culture was inoculated into Muller-Kauffmann tetrathionate-novobiocin broth (MKTTn, Merck KGaA, Darmstadt, Germany). After the incubation of the MSRV and RVS at 42°C for 24 h and MKTTn at 37°C for 24 h, the cultures were streaked on xylose lysine deoxycholate agar plate (XLD, Merck KGaA, Darmstadt, Germany) and selective chromagar *Salmonella* medium (Microbiology, Paris, France). After incubating at 37°C for 24 h, approximately five suspected colonies were selected for biochemical testing: Triple sugar iron agar (TSI, Merck KGaA, Darmstadt, Germany), Lysine iron agar (LIA, Merck KGaA, Darmstadt, Germany), and Sulfide-Indole Motility medium (SIM, Merck KGaA, Darmstadt, Germany) as described by Ewing (Ewing, 1986). Typical colonies were further serotyped by slide agglutination test according to the Kauffmann-White-Le-Minor scheme (Grimont and Weill, 2007) at the WHO National *Salmonella* and *Shigella* Center, Bangkok, Thailand.

Results

Salmonella contamination status of the samples collected from three cycles of broiler meat production was summarized in Table 1-3. *Salmonella* recovered from chicken-related samples were 45.7% (53/116), 2.6% (18/692) and 24% (154/641) in the first, second and third sampling period, respectively. For environmental samples, the contamination levels were 34.3% (59/172), 7.1% (23/323) and 16% (49/307) in the first, second and third sampling period, respectively.

The contamination of *Salmonella* was found in all production units from the breeder farms to slaughterhouse. The result of *Salmonella* isolation in the breeding farm revealed that one out of the three production cycles was *Salmonella* positive in feces and equipment.

In the hatchery, two out of the three production cycles were *Salmonella* positive, in which the hatching baskets were the most frequently contaminated (2/3 production cycles), followed by the egg setting stand, hook, egg storage room, hands of workers and transferring belts (1/3 production cycle). Interestingly, the most common serotype isolated from the hatchery was *S. Corvallis*, which was the same serotype isolated from the meconium of the baby chicks.

In the broiler farms, *Salmonella* remained positive after cleaning and disinfection in all three production cycles. The house lizards were the most common sample contaminated (3/3 production cycles), followed by the litter (2/3 production cycles). The wall, water, water nipple, and pan feeder were occasionally contaminated (1/3 production cycle). On the chick arrival day (before releasing the day-old chicks into the broiler farm), the sample of boot swab, water nipple, and house lizards were occasionally positive for *S.* Weltevreden (Table 2).

During the broiler rearing period, the most common environmental samples contaminated with *Salmonella* from all three production cycles were the pests, especially house lizards. Other pests occasionally found in the broiler farms were small centipedes which were also positive for *Salmonella* contamination (Table 3). In this study, only one cockroach and one mouse were caught during the

Table 1 Serotypes and distribution of *Salmonella* spp. from the first sampling period

Production unit	Chicken-related sample			Environment sample		
	Type	% positive (+ ve/ Total)*	Serotype	Type	% positive (+ ve/ Total)*	Serotype
Breeding farm	Feces	100 (9/9)	Albany	Egg tray	100 (5/5)	Albany
	Egg	0 (15/15)		Basket and plate	20 (1/5)	Corvallis
Hatchery	Egg (before incubation)	0 (0/10)		Egg storage room	100 (1/1)	Corvallis
	Egg (after incubation)	0 (0/10)		Hook	100 (1/1)	Corvallis
	Meconium in hatching tray	0 (0/12)		Egg setting stand	100 (1/1)	Corvallis
				Hatching tray	8 (1/12)	Havana
				Other samples	0 (0/32)	
Broiler farm				Wall	100 (2/2)	Albany
- after cleaning				Pan feeder	100 (5/5)	Albany
and disinfection				Water nipple	60 (3/5)	Albany
				Water	100 (1/1)	Albany
				Lizard	100 (1/1)	Albany
				Other samples	0 (0/8)	
- arrival day	Meconium on box-liner	0 (0/10)		Water, Feed	0 (0/4)	
- week 1	Feces	100 (5/5)	Derby, Caen	Boot swab	100 (5/5)	Derby
				Lizard	25 (1/4)	Weltevreden
- week 2	Feces	100 (5/5)	Derby, Weltevreden	Feed	33 (2/6)	Derby, Braenderup**
				Lizard	40 (2/5)	Weltevreden
- week 3	Feces	100 (5/5)	Derby, Albany, Bovismorbifican	Boot swab	100 (5/5)	Derby
				Lizard	40 (2/5)	Derby, Hotutenae
- week 4	Feces	100 (5/5)	Derby, Senftenberg	Boot swab	100 (5/5)	Derby, Albany, kouka, Bovismorbifican
				Lizard	40 (2/5)	Weltevreden
- week 5	Feces	60 (3/5)	Derby	Boot swab	80 (4/5)	Derby
				Water	100 (1/1)	Derby
				Lizard	60 (3/5)	Weltevreden, Hotutenae
- week 6	Feces	80 (4/5)	Derby	Boot swab	100 (5/5)	Derby, Kentucky, Bovismorbifican
				Other samples (week 1-6)	0 (0/33)	
Slaughterhouse	Feather around cloaca	70 (7/10)	Kentucky, Derby, Altona, Bovismorbifican, Orion, Stockholm			
	Whole carcass (rinse)	100 (10/10)	Derby, Kentucky, Stanley, Agona, Weltevreden, Saintpaul, Paratyphi B			
Total	**Chicken-related sample**	**45.7 (53/116)**		**Envoronmental sample**	**34.3 (59/172)**	

* No. of *Salmonella* positive per total samples

** positive from new feed before putting in pan feeder

Table 2 Serotypes and distribution of *Salmonella* spp. from the second sampling period

Production unit	Chicken-related sample			Environment sample		
	Type	% positive (+ ve/ Total)*	Serotype	Type	% positive (+ ve/ Total)*	Serotype
Breeding farm	Cloacal swab	0 (0/120)		Boot swab	0 (0/10)	
	Egg	0 (0/50)		Other samples	0 (0/28)	
Hatchery	Eggs (before incubation)	0 (0/10)		All samples	0 (0/32)	
	Eggs (after incubation)	0 (0/50)				
	Meconium in hatching tray	0 (0/12)				
Broiler farm				Litter (after disinfection)	20 (2/10)	Weltevreden
- after cleaning				Lizard	60 (3/5)	Weltevreden
and disinfection				Other samples	0 (0/51)	
- arrival day	Meconium on box-liner	0 (0/10)		Boot swab	20 (1/5)	Weltevreden
				Water nipple	5 (1/20)	Weltevreden
				Lizard	100 (3/3)	Weltevreden
				Other samples	0 (0/30)	
- week 1-4	Cloacal swab	0 (0/240)		All samples (week1-4)	0 (0/71)	
- week 5	Cloacal swab	0 (0/60)		Boot swab	20 (1/5)	Stanley
				Lizard	80 (4/5)	IV (43;z4,z23:-)
				Other samples	0 (0/8)	
- week 6	Cloacal swab	0 (0/60)		Lizard	20 (1/5)	IV (43;z4,z23:-)
				Other samples	0 (0/13)	
- Slaughter day				Cage	50 (5/10)	Albany, Altona, Weltevreden
				Truck (floor swab)	100 (1/1)	Mbandaka
				Water (before spraying)	100 (1/1)	Falkensee
				Hands of worker	0 (0/10)	
Slaughterhouse	Cloacal swab	3 (2/60)	Albany, Derby, Virginia			
	Whole carcass (rinse)	80 (16/20)	Albany, Agona, Give, Altona			
Total	**Chicken-related sample**	**2.6 (18/692)**		**Envoronmental sample**	**7.1 (23/323)**	

*No. of *Salmonella* positive per total samples

period of the study and both were negative for *Salmonella* contamination. Another frequently positive sample was feed from both new feed and from pan feeder (2/3 production cycles).

On the slaughter day, the water used to spray the broilers before transport was found to be contaminated, whereas the transport cages and truck were also occasionally contaminated.

For the chicken-related samples, in the first production cycle, the broilers were found to be highly contaminated with *S.* Derby within the first week of rearing period. The serotype was also dominant in the subsequent production steps. For the second production cycle, the broilers were negative for *Salmonella* contamination throughout the rearing period but the contamination was found in the broilers after transportation to the slaughterhouse and the final products with several serotypes of *Salmonella*. In all three production cycles, no *Salmonella* was found in the egg samples. However, the baby chicks were found to be positive from the hatchery in the third production cycle. The same serotype (*S. Corvallis*) that was found in the baby chicks was also dominant in the subsequent broiler production steps and

Table 3 Serotypes and distribution of *Salmonella* spp. from the third sampling period

Production unit	Chicken-related sample			Environment sample		
	Type	% positive (+ ve/ Total)*	Serotype	Type	% positive (+ ve/ Total)*	Serotype
Breeding farm	Cloacal swab	0 (0/120)		Boot swab	0 (0/10)	
	Egg	0 (0/40)		Other samples	0 (0/26)	
Hatchery	Egg (before incubation)	0 (0/20)		Hatching tray (before use)	8 (1/12)	Agona
	Meconium in hatching tray	33 (4/12)	Corvallis	Hands of worker (before work)	21 (3/14)	Corvallis
				Transferring belt (before use)	50 (1/2)	Corvallis
				Other samples	0 (0/7)	
Broiler farm - after cleaning and disinfection				Litter (after disinfection)	50 (5/10)	Weltevreden, Cannstatt
				Lizard	50 (2/4)	Weltevreden
				Other samples	0 (0/21)	
- arrival day	Meconium on the box-liners	80 (8/10)	Corvallis	All samples	0 (0/31)	
- week 1	Cloacal swab	85 (51/60)	Corvallis	Boot swab	100 (5/5)	Corvallis
				Feed	57 (4/7)	Corvallis**
				Water	16 (1/6)	Weltevreden
				Pest (centipede, lizard, cockroach)	18 (2/11)	Weltevreden***
- week 2	Cloacal swab	73 (44/60)	Corvallis	Boot swab	100 (5/5)	Corvallis
				Feed	71 (5/7)	Corvallis**
				Lizard	20 (1/5)	Corvallis
				water	0 (0/6)	
- week 3	Cloacal swab	3 (2/60)	Corvallis	Feed	14 (1/7)	Corvallis**
				Other samples	0 (0/16)	
- week 4	Cloacal swab	10 (6/60)	Corvallis	All samples	0 (0/23)	
- week 5	Cloacal swab	8 (5/60)	Corvallis, Weltevreden	Boot swab	20 (1/5)	Eastbourne
				Lizard	40 (2/5)	Corvallis
				Feed, water	0 (0/13)	
- week 6	Cloacal swab	3 (2/60)	Corvallis	Boot swab	100 (5/5)	Corvallis
				Feed	29 (2/7)	Corvallis**
				Lizard	40 (2/5)	Weltevreden
				water	0 (0/6)	
- slaughter day				Water (before spraying)	100 (1/1)	Weltevreden
				Other samples	0 (0/26)	
Slaughterhouse	Cloacal swab	25 (15/60)	Corvallis			
	Whole carcass (rinse)	89 (17/19)	Corvallis			
Total	**Chicken-related sample**	**24 (154/641)**		**Envoronmental sample**	**16 (49/307)**	

* No. of *Salmonella* positive per total samples
** positive from pan feeder
***positive from centipede

the final product produced from this production cycle.

Discussion

It has been known that the main route of *Salmonella* spread in the broiler production chain can be either vertical or horizontal transmission (vd Giessen et al., 1991; Heyndrickx et al., 2002). However, in this study we did not find any *Salmonella* positive in the egg samples, indicating that the vertical transmission was not the main route of *Salmonella* contamination in this integrated broiler production. It was possible that the attenuated and killed vaccine used in the second and third breeder flocks were highly effective since no *Salmonella* was detected in either of the breeders or in the eggs produced from these flocks. According to previous studies, an effective vaccination program can prevent vertical transmission of *Salmonella* to eggs as well as prevent colonization in internal organs and shedding in feces (Okamura et al., 2007; Penha Filho et al., 2009). For the first breeder flock, although no egg was positive for *Salmonella*, the breeders and farm environment were contaminated with *S.* Albany. It is possible that only attenuated vaccine used in this flock may not be enough to protect the breeders from the infection. In addition, the age of the breeders which were older than others (55 weeks old) may also contribute to the higher chance of contamination from the environment.

In the hatchery, *Salmonella* was found in the environment and equipment before being used indicating insufficient cleaning and disinfection of this production unit. Transfer of *Salmonella* from the contaminated hatchery environment and equipment to the baby chicks and subsequent production units was evident from the third production cycle. In this production cycle, the most frequent serotype contaminated in this hatchery was *S. Corvallis*, which was also found in the baby chicks and persisted throughout the rearing period and whole carcasses. A previous study demonstrated that contaminated egg trolleys and trays in a hatchery can lead to widespread dissemination of *Salmonella* within integrated poultry production (Davies et al., 1997). However, in the current study, no contamination in the egg trolleys was found. In addition, although the hatching trays were found contaminated on several occasions, they were positive with the serotypes different from those in the baby chicks and subsequent production units. In this work, the possible source of contamination were the worker's hands and transferring belts, which were contaminated with *S. Corvallis* before work, and the same serotype was found in the baby chicks from this production cycle.

In the broiler farms, various serotypes of *Salmonella* were isolated from water on several occasions. For example, in the first sampling cycle, the water was contaminated with *S.* Albany at farm preparation step and suspected to be the source of contamination of this serotype in the house and other equipment during cleaning and disinfection. During subsequent production steps, the water was found occasionally contaminated with *S.* Derby, *S.* Weltevreden and *S.* Falkensee. These results indicated that there was a problem in the water treatment system. However, there is no direct evidence that water was the source of *Salmonella* contamination in

the broiler since the serotypes isolated from the water samples were found later or not presented in the broiler samples. Similar finding was also reported that the contaminated water may not be related to *Salmonella* contamination status of the broiler (Marin et al., 2010).

After cleaning and disinfection of the broiler farms, positive results were found with the same *Salmonella* serotype, *S.* Weltevreden, in both litter and house lizards in two production cycles, indicating possible cross-contamination between these two types of samples. Additional serotype, *S.* Cannstatt, was also found in the litter after disinfection. This result revealed that the spraying of liquid disinfectant commonly practiced in this production unit was not enough to get rid of *Salmonella* in the litter.

Pests existing in broiler farm such as rodents and beetles were reported as possible risk factors or reservoirs of *Salmonella* contamination in broiler flocks (Rose et al., 2000; Skov et al., 2004). However, in this study, we did not find any beetles or contaminated rodents in the broiler house. Interestingly, the majority of the pest found in this study was house lizards which always persisted in the farm environment throughout the rearing period for all three production cycles. Moreover, the house lizards were found to be highly contaminated with *Salmonella*, especially *S*. Weltevreden. Other serotypes occasionally found in the house lizards were *S.* Albany, *S.* Derby, *S.* Hotutenae, *S*. IV 43;z_4,z_{23}:-, and *S. Corvallis*. On many instances, the same serotypes were also found in the chicken-related samples at the same time period. This result clearly showed that the house lizards acted as the reservoir of *Salmonella,* which could persist in the farm environment and transmit Salmonella within and between production cycles.

Contaminated feed has been shown as another source of *Salmonella* in the broiler production unit. In the first production cycle, the new feed was positive for *S.* Derby, the same serotype identified in the broiler in this production cycle. Although the fact that the new feed was positive after the positive broiler was detected, it could not be ruled out as the source of *Salmonella* since the contamination might occur only intermittently and was unevenly distributed in the feed stock. In addition, feed may also act as a vehicle distributing the pathogen among broilers within the flock. As seen in the third production cycle, *S. Corvallis* was found in the day-old chicks before being placed in the broiler house and the same serotype was subsequently found in the feed from pan feeder on several occasions. It is possible that the infected chicks can shed *Salmonella* in feces and contaminate the feed in the pan feeder. Consequently, the fecal-oral route can cause *Salmonella* transmission among broilers and spread throughout the flock. Significant relationship between the contaminated feed and positive status of the broiler were also previously reported (Heyndrickx et al., 2002).

On the slaughter day, the water sprayed to the chicken for reducing heat stress and the transport cages were found to be *Salmonella* positive. Although the serotypes identified in the water were different from those found in the broilers and whole carcasses, a significance of water treatment should be emphasized. In the case of transport cages, two serotypes found in the cages were also found in the final carcasses. The results suggested that the cages were one of the sources contributing to *Salmonella* dissemination in the carcasses. A high frequency of contaminated cages after cleaning and disinfection was also reported in a previous study in which improper concentration and temperature of disinfectant and contaminated water were reported as the main factors responsible for the contamination (Corry et al., 2002).

After transportation to the slaughterhouse, the prevalence of *Salmonella* in the broilers increased. We hypothesized that the stress from the withdrawal of feed and water, catching, and transportation may contribute to the higher rate of *Salmonella* shedding and subsequent horizontal transfer to the uncontaminated chickens. A previous study showed that stress from water and feed withdrawal increased the number of *S.* Enteritidis shedding in chicken faeces (Nakamura et al., 1994). In addition, the feces excreted during transportation may cause widespread contamination of *Salmonella* among the broilers before slaughter. A previous study also demonstrated that the *Salmonella* negative flock during the rearing period in the broiler farm turned out to be *Salmonella* positive in feces after transport to the slaughterhouse (Heyndrickx et al., 2002).

After slaughtered, several serotypes of *Salmonella* which had never been detected in any prior production units were found from the whole carcasses. This result clearly indicated that cross-contamination during the slaughter process in the slaughterhouse played an important role in *Salmonella* dissemination among the broiler carcasses.

In conclusion, this study revealed that the important sources of *Salmonella* contamination could be found in all broiler production units such as from contaminated environment and equipment in the hatchery, contaminated day-old chicks, feed and pests in broiler farm. In addition, the other factors associated with *Salmonella* dissemination to the chicken carcasses were contaminated transport cages, transportation of broilers to slaughterhouse and cross-contamination during the slaughter process. Therefore, it is imperative that a top-to-down *Salmonella* control approach should be implemented, especially in the form of sanitary programs, for example, cleaning and disinfection of the equipment and environment from the hatchery to the slaughterhouse, implementing feed quality control, ensuring effective water treatment and pest management. Additionally, Hazard analysis and critical control points (HACCP) should be revised in the slaughterhouse in order to reduce the cross-contamination.

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บทคัดย่อ

แหล่งที่มาและการแพร่กระจายเชื้อแซลโมเนลลาในการผลิตไก่เนื้อแบบครบวงจร

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การศึกษานี้มีวัตถุประสงค์เพื่อหาแหล่งที่มาและการแพร่กระจายของเชื้อแซลโมเนลลาในการผลิตไก่เนื้อแบบครบวงจร ในเขตภาคตะวันออกเฉียงเหนือของประเทศไทย ระหว่างปี พ.ศ. 2553-2555 โดยทำการเก็บตัวอย่างจากสิ่งแวดล้อมและตัวอย่างที่มาจากไก่ทั้งหมด 3 วงรอบการผลิตไก่เนื้อ ตั้งแต่ระดับฟาร์มพ่อแม่พันธุ์ โรงฟัก ฟาร์มไก่เนื้อ และโรงเชือด เพื่อติดตามสถานะการปนเปื้อนของเชื้อแซลโมเนลลาในตัวไก่ ไข่ฟักหรือซากไก่ และหาแหล่งที่เป็นไปได้ของการปนเปื้อนเชื้อจากสิ่งแวดล้อม โดยตัวอย่างทั้งหมดที่มาวิเคราะห์ประกอบด้วยตัวอย่างที่มาจากไก่ 1,449 ตัวอย่างและตัวอย่างที่มาจากสิ่งแวดล้อม 802 ตัวอย่าง ผลการศึกษาครั้งนี้พบการปนเปื้อนเชื้อแซลโมเนลลาในทุกหน่วยของการผลิต และพบว่าการแพร่กระจายเชื้อแบบ Horizontal transmission เป็นเส้นทางหลักที่ทำให้เกิดการปนเปื้อนเชื้อแซลโมเนลลาในระหว่างการผลิตไก่เนื้อแบบครบวงจรนี้ เนื่องจากไม่พบการปนเปื้อนเชื้อแซลโมเนลลาในตัวอย่างที่มาจากไข่ทั้งหมดที่ทำการตรวจ ทั้งนี้พบว่าแหล่งสำคัญของการปนเปื้อนเชื้อแซลโมเนลลาในระหว่างการผลิตไก่เนื้อคือการปนเปื้อนเชื้อในสิ่งแวดล้อมและอุปกรณ์ในโรงฟัก การปนเปื้อนเชื้อในลูกไก่วันแรก อาหาร และสัตว์พาหะ โดยเฉพาะอย่างยิ่ง จิ้งจก นอกจากนี้ยังพบว่าปัจจัยที่ทำให้เกิดการแพร่กระจายเชื้อแซลโมเนลลาไปยังซากไก่คือ การปนเปื้อนเชื้อในกล่องขนส่งไก่ การขนส่งไก่เนื้อไปยังโรงเชือด และการปนเปื้อนข้ามระหว่างกระบวนการเชือด ดังนั้นจึงควรมีมาตรการเพื่อควบคุมการปนเปื้อนของเชื้อแซลโมเนลลาอย่างมีประสิทธิภาพตลอดกระบวนการผลิตตั้งแต่ที่ฟาร์มพ่อแม่พันธุ์ไปจนถึงการแปรรูปในโรงเชือด โดยเฉพาะการจัดการด้านโปรแกรมสุขอนามัย ระบบการควบคุมคุณภาพอาหารสัตว์ ระบบการฆ่าเชื้อน้ำ การควบคุมและกำจัดสัตว์พาหะ รวมถึงการจัดการแผน HACCP ภายในโรงเชือดให้มีประสิทธิภาพมากยิ่งขึ้น

คำสำคัญ: ไก่เนื้อ การแพร่กระจาย สิ่งแวดล้อม เชื้อแซลโมเนลลา แหล่งที่มา

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