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Original Article

Longitudinal Study of *Salmonella* and *Campylobacter* Species from Two Laying Duckling Flocks in The Central Region of Thailand

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Abstract

A longitudinal study was carried out to determine the prevalence of *Campylobacter* spp. and *Salmonella* spp. in two laying duckling flocks from the same parent stock. In total, 477 samples: breeding ducks (n=100), 1-day-old female ducklings (n=160), 30-day-old female ducklings (n=178), and environmental (n=39) samples isolated from incubator, soil, water, and feed, were investigated. Results revealed that an overall isolation of *Campylobacter* spp. was 27.0% (129/477). From the total of 129 positive samples, 56.6% was *C. jejuni* and 43.4% was *C. coli*. An overall isolation of *Salmonella* spp. was 31.0% (148/477). Eight serotypes of *Salmonella enterica* were identified: *S.* Amsterdam, *S.* Chester, *S.* Dublin, *S.* Enteritidis, *S.* Hvittingfoss, *S.* Mbandaka, *S.* Montevideo, and *S.* Thompson. The three most isolated serotypes were *S.* Montevideo (42.6%), *S.* Mbandaka (36.5%), and *S.* Amsterdam (12.8%). The prevalence of *Campylobacter* spp. and *Salmonella* spp. in both 1-day-old ducklings and 30-day-old ducklings from both flocks had similar pattern. The prevalence of *Salmonella* spp. decreased when the 1-day-old ducklings grew to 30-day-old ducklings. However, the prevalence of *Campylobacter* spp. increased from the age of 1-day-old to 30-day-old. The existence of *Campylobacter* spp. and *Salmonella* serotypes in both duck feces and environmental samples was in accordance. In conclusion, our results showed that ducks were normally infected by both *Campylobacter* spp. and *Salmonella* spp. possibly originated from environmental contaminations.

Keywords: *Campylobacter* spp., egg laying duck, prevalence, *Salmonella* spp.

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Introduction

According to the findings of Ministry of Public Health of Thailand, food poisoning is one of the dangerous diseases to be emphasized. It is mainly caused by contamination of pathogens in meats, contributing to an increased morbidity rate of people. In 2011, the food-poisoning patients were 102,562 heads and the morbidity rate was 160.31 out of 100,000 heads. Major symptoms include stomach ache, nausea, and vomit (MOPH, 2012). In 2011, Center of Disease Control (CDC) of the United States of America (USA) reported that the first and the second causes of food poisoning in the USA were from *Salmonella* and *Campylobacter* (CDC, 2012). In addition, European Food Safety Authority revealed that *Campylobacter* and *Salmonella* were the first and the second causes of zoonoses in the European Union, in 2011. *Campylobacter* spp. in human is chiefly derived from the contamination in chicken and other poultry meats. As a result, strong regulations in *Salmonella* control programs in poultry populations have been launched, leading to a decline of *Salmonella* contamination in broiler meats and their products. Therefore, the salmonellosis cases in humans from 2008 to 2011 lowered (EFSA, 2013).

Epidemiological studies demonstrate that being in contact with and consumption of poultry are the major causes of campylobacteriosis, mainly from *Campylobacter jejuni* (*C. jejuni*) and *C. coli* (FSAI, 2002). In humans, *C. jejuni* is the most pathogenic species causing food poisoning. An infective dose of *C. jejuni* is 500-10,000 organisms. However, the survival of *C. jejuni* in the environment is very low; accordingly, human-to-human infection is scarcely found (Altekruse and Swerdlow, 2002). Symptoms of *C. jejuni* include watery or bloody diarrhea and stomach ache. A former study reported that patients with diarrhea from *C. jejuni* possessed reactive arthropathies and Guillain-Barre' syndrome; nervous signs and flaccid paralysis might be observed. However, the mortality rate is low (Stern and Line, 2000; Altekruse and Swerdlow, 2002).

The contamination of *Salmonella*, especially non-typhoid type, is in the gastrointestinal tract of animals, including birds, humans, pet animals, and rodents. An environmental contamination can take place in feces, soil, and water. Even though multiplication does not exist, *Salmonella* can remain in the environment for ages. Accordingly, the dispersion to humans results mainly from animal-derived food and partly from environmental contamination (Bell and Kyriakides, 2002). Salmonellosis is a pandemic disease and contributes to severe clinical signs and high morbidity rate. Its clinical signs majorly include vomit and diarrhea. The more severe signs can be found when *Salmonella* enters blood circulation and lymphatic systems, especially in immunocompromised patients such as children, the elderly, and immunodeficiency patients (Bell and Kyriakides, 2002).

Ducks are considered one of the human food resources. A number of studies are conducted to survey the appearance of *Salmonella* and *Campylobacter* spp. in ducks. For instance, cloacal swabbing from 60 duck's faecal samples in California, USA, revealed 3.3% of *Salmonella* spp. and 33.0% of *Campylobacter* spp. are found. In addition, the detected *Salmonella* spp. are S. Typhimurium and *S.* Heidelberg (McCrea et al., 2006). From 2003-2005, an investigation into 2,104 samples from raw poultry meat in the United Kingdom (UK) showed 57.3% of *Campylobacter* spp. and 6.6% of *Salmonella* spp. infestations. *Campylobacter spp.* is found the highest in chicken meat (60.9%) and 50.7% in duck meat. On the other hand, *Salmonella spp.* contamination is found highest in duck meat (29.9%) and 5.6% in chicken meat (Little et al., 2008). However, comprehensive data in laying ducks both in Thailand and overseas have been scanty. Duck eggs can be directly contaminated with pathogens from feces which are the reservoir of several foodborne pathogens, especially *Salmonella* and *Campylobacter* spp. Therefore, duck eggs are one of the causes of food poisoning. Consequently, the present study aimed to survey the prevalence of *Salmonella* and *Campylobacter* spp. in laying duckling flocks in central region of Thailand.

Materials and Methods

Sampling: Proportionated sampling was conducted from cloacal swab in two duckling flocks between February and August 2011 from Kanchanaburi (Flock 1) and Nakhon Pathom (Flock 2) provinces of Thailand. The duck from both sites were produced from the same breeding duck flock. Cloacal swab was performed in breeding ducks and 30-day-old ducklings; meanwhile meconium swab by cloacal squeezing was performed in 1-day-old ducklings. In total, 438 samples (100 breeding ducks, 75 1-day-old ducklings from flock 1, 85 1-day-old ducklings from flock 2, 80 30-day-old ducklings from flock 1, and 98 30-day-old ducklings from flock 2) were investigated. Environmental samples (n=39) were pooled from soil, drinking water, and feed. In addition, samples were swabbed from incubator, egg shell, and floor after sexing of 1-day-old duckling.

Specific and serovar identifications

Identification of Campylobacter: Identification of *Campylobacter* was performed to identify *Campylobacter* genus and species by conventional method and multiplex Polymerase chain reactions (PCR)s, respectively (Denis et al., 1999). For the conventional method, the feces collected by cloacal swab and the environmental samples were applied into Preston broth 9 ml (Nutrient broth No.2 [Oxoid, USA], 5% (v/v) lysed horse blood [Oxoid], *Campylobacter* growth supplement [Oxoid] and modified Preston *Campylobacter* selective supplement [Oxoid]) and incubated for 48 h at 42°C under microaerophilic condition in anaerobic jars with gas-generating kits (Oxoid). As for environmental samples, 25 ml/g of water, soil, or feed was selected to culture in Preston broth 225 ml at 42°C for 48 h under microaerophilic condition. Following enrichment in Preston broth, then streak on Charcoal-Cefoperazone-Deoxycholate Agar (CCDA) (*Campylobacter* blood free selective agar base [Oxoid] with CCDA selective supplement [Oxoid]) at 42°C for 48 h under microaerophilic condition.

Afterwards, pick up dark-gray colony was picked up and stained with Victoria blue to investigate gull wing morphology.

mPCR could be undertaken by picking up one cultured colony of *Campylobacter* to extract deoxyribonucleic acid (DNA) by commercial DNA extraction kit (Promega, WI, USA). mPCR increased *16S* rRNA to confirm the results at generic level of *Campylobacter*. Besides, *mapA* gene and *ceuE* gene were amplified to confirm the results at specific level of *C. jejuni* and *C. coli*, respectively. PCR procedures were mainly performed according to the method described by Denis et al. (1999). Differences were that the use of dNTPs (Fermentas, MD, USA) concentration was 200 µM, the concentrations of MD16S1 and MD16S2 primer were both 0.5 µM. the use of *Taq* DNA polymerase (Invitrogen, CA, USA) 1.2 U. The examination of DNA product used gel electrophoresis by 1% (w/v) agarose gel (Seakem LE agarose; BMA, ME, USA), 100 volts for 30 min, stained with ethidium bromide (Amresco; OH, USA), and used UV light to prove DNA size.

Identification of Salmonella: Conventional method and serotyping were used to determine *Salmonella* in the species level according to the principals of Kauffmann-White Schema. Cloacal swab, water, feed, and soil samples were taken to culture on the criterion of ISO 6579:2002 (annex D) (ISO, 2007): cloacal swabs were cultured in 25 ml Buffer Peptone Water (BPW; Oxoid), while 25 ml/g of water, feed and soil samples were cultured in 225 BPW. All samples, thereafter, were incubated at 37°C for 18 h. After incubation, 3 drops from 0.1 ml were transferred to Modified Semi-Solid Rappaport-Vassiliadis (MSRV, Difco; Becton Dickinson) agar plate with novobiocine 0.01 g/l at 42°C for 24 h. Growth on MSRV plates suspected to be *Salmonella* spp. was streaked on Brilliant-green Phenol-red Lactose Sucrose agar (BPLS; Oxoid) and Xylose Lysine Deoxycholate agar (XLD; Oxoid). After incubating at 37°C for 24 h, bacterial identification on BPLS and XLD was biochemically performed on urease agar, triple sugar iron agar, and lysine-decarboxylase broth. If the results showed *Salmonella* spp., those samples would be further analyzed for serovar by serological test on the basis of slide agglutination using with polyvalent anti-specific O antisera and specific flagellar H antisera (S.A.P. Laboratory, Thailand) to each antigen of the samples. Finally, antigen pattern was compared with Kauffmann-White Scheme (antigenic formulas of the *Salmonella* serovars) (Grimont and Weill, 2007)

Statistical analysis: Chi-squared (χ^2) or two-sided Fisher's exact tests were used to analyze data sorted by flock type, pathogen and age. A probability value of less than 1% was considered to be significant.

Results

A survey of 477 samples found 27.0% *Campylobacter* spp. and 31.0% *Salmonella* spp. As for *Campylobacter* spp., *C. jejuni* and *C. coli* were 56.5% and 43.4%, respectively. Eight serovars of *Salmonella* spp were found: *S.* Amsterdam, *S.* Chester, *S.* Dublin, *S.* Enteritidis, *S.* Hvittingfoss, *S.* Mbandaka, *S.* Montevideo, and *S.* Thompson. The outstanding species were *S.* Montevideo (42.6%), *S.* Mbandaka (36.5%), and *S.* Amsterdam (12.8%) as shown in Tables 1 and 3.

Table 1 Prevalence of *Campylobacter* and *Salmonella* from ducks and environmental samples

Flocks	Samples	*Campylobacter* spp.	95%CI	*Salmonella* spp.	95%CI	*p*-Value
Breeding	Breeding ducks	9.0%(9/100)	3.42-14.58	0.0%(0/100)	0.00	0.0021
	Breeding ducks' environment	20.0%(1/5)		0.0%(0/5)		
Flock 1	1-day-old ducklings	12.0%(9/75)	4.67-19.33	89.3%(67/75)	82.37-96.29	0.0001
	1-day-old ducklings' environment	7.7%(1/13)		84.6%(11/13)		
	30-day-old ducks	56.3%(45/80)	45.42-67.08	2.5%(2/80)	-0.91-5.91	0.0001
	30-day-old ducks' environment	14.3%(1/7)		57.1%(4/7)		
Flock 2	1-day-old ducklings	0.0%(0/85)	0.00	62.4%(53/85)	52.1-72.61	0.0001
	1-day-old ducklings' environment	0.0%(0/10)		30.0%(3/10)		
	30-day-old ducks	62.2%(61/98)	52.69-71.80	5.1%(5/98)	0.77-9.44	0.0001
	30-day-old ducks' environment	50.0%(2/4)		75.0%(3/4)		
	Total	27.0%(129/477)		31.0%(148/477)		

In the breeding ducks, 9% of *Campylobacter* spp. was detected for *C. jejuni* (33.3%) and *C. coli* (66.7%). However, no *Salmonella* spp. was detected in 100 samples. In addition, *C. jejuni* in the environment could be detected from drinking water only.

In flock 1, *Campylobacter* in 1-day-old ducklings was detected by 12.0%. They were *C. jejuni* (33.3%) and *C. coli* (66.7%). When they were 30 d of age, *Campylobacter sp.* was found by 56.3%: *C. jejuni* (55.6%) and *C. coli* (44.4%). As for *Salmonella* spp. , 89.3% was found in the 1-day-old ducklings. When they were 30 days of age, it was 2.5%. There was a significant difference in the prevalence of *Salmonella* spp. and *Campylobacter* spp. among different ages of ducklings (p<0.01). As for the 1-day-old ducklings' environmental samples, 13 samples were examined: 5 from incubator, 5 from egg shell, and 3 from floor after sexing. It was found that *Campylobacter* spp. was detected only from the floor after sexing while *Salmonella* spp. was detected in 11 samples. The detected *Salmonella* spp. were *S*. Mbandaka, *S*. Montevideo, and *S*. Amsterdam, which were the same serovars as in the 1-day-old ducklings. When they were 30 d of age, 7 environmental samples: feed in duck house, soil in duck house, water in duck house, paddy in field, soil in field, watercourse, and water in field, were collected. Only *C. jejuni* was detected from the soil in field, while four species of *Salmonella* were found from the soil in duck house, water in duck house, soil in field, and water in field. In addition, the water in field contained *S*. Thompson, which was the same type as of the 30-day-old ducklings as shown in Tables 1, 2, and 3.

In flock 2, no *Campylobacter* spp. was found in all samples from the 1-day-old ducklings. Nevertheless, when they were 30 d of age, 62.2% of *Campylobacter* spp. was found. They were *C. jejuni* (67.2%) and *C. coli* (32.8%). As for *Salmonella* spp. , 62.4% was found in the 1-day-old ducklings and 5.1% was detected in the 30-day-old ducklings. There was a significant difference in the prevalence of *Salmonella* spp. and *Campylobacter* spp. among the different ages of ducklings (p<0.01). The investigation of environmental samples from the 1-day-old ducklings included 3 from incubator, 2 from egg shell, 4 from floors after sexing and 1 from incubator flushing water. It revealed that *Campylobacter* spp. were not detected, whereas two serovars of *Salmonella* (*S*. Mbandaka and *S*. Montevideo) were found in the egg shell, floor after sexing, and incubator flushing water. When they were 30 d of age, four environmental samples were collected from soil in field, water in watercourse, water in field, and paddy in field. It was found that *C. jejuni* was detected from the water in watercourse and *C. coli* was detected from the water in field. *Salmonella* was found in the soil in field, water in watercourse, and water in field. In addition, *S*. Thompson was found both in the soil in field and water from watercourse, similar to that found in the 30-day-old ducklings as shown in Tables 1, 2, and 3.

Table 2 *Campylobacter* spp. isolated from ducks and environmental samples

Flock	Samples	*C. jejuni*	*C. coli*
Breeding	Breeding ducks	33.3% (3/9)	66.7% (6/9)
	Breeding ducks' environment	100.0% (1/1)	0.0% (0/1)
Flock 1	1-day-old ducklings	33.3% (3/9)	66.7% (6/9)
	1-day-old ducklings' environment	0.0% (0/1)	100.0% (1/1)
	30-day-old ducks	55.6% (25/45)	44.4% (20/45)
	30-day-old ducks' environment	100.0% (1/1)	0.0% (0/1)
Flock 2	1-day-old ducklings	0.0% (0/0)	0.0% (0/0)
	1-day-old ducklings' environment	0.0% (0/0)	0.0% (0/0)
	30-day-old ducks	67.2% (41/61)	32.8% (20/61)
	30-day-old ducks' environment	50.0% (1/2)	50.0% (1/2)
	Total	56.6% (74/129)	43.4% (55/129)

Table 3 *Salmonella* serotypes isolated from ducks and environmental samples

Flock	Samples	*Salmonella* spp.	*Salmonella* serotype
Breeding	Breeding ducks	0	
	Breeding ducks' environment	0	
Flock 1	1-day-old ducklings	67	*S*. Amsterdam 20.9% (14), *S*. Mbandaka 47.76% (32), *S*. Montevideo 31.34% (21)
	1-day-old ducklings' environment	11	*S*. Amsterdam 9.1% (1), *S*. Mbandaka 54.5% (6), *S*. Montevideo 36.3% (4)
	30-day-old ducks	2	*S*. Enteritidis 50% (1), *S*. Thompson 50% (1)
	30-day-old ducks' environment	4	*S*. Amsterdam 75% (3), *S*. Thompson 25% (1)
Flock 2	1-day-old ducklings	53	*S*. Chester 5.66% (3), *S*. Mbandaka 26.42% (14), *S*. Montevideo 67.92% (36)
	1-day-old ducklings' environment	3	*S*. Mbandaka 33.33% (1), *S*. Montevideo 66.67% (2)
	30-day-old ducks	5	*S*. Chester 20% (1), *S*. Dublin 20% (1), *S*. Hvittingfoss 20% (1), *S*. Mbandaka 20% (1), *S*. Thompson 20% (1)
	30-day-old ducks' environment	3	*S*. Amsterdam 33.33 (1), *S*. Thompson 66.67% (2)
	Total	148	

Discussion

We found the significant difference in the prevalence of *Salmonella* and *Campylobacter* spp. among the different ages of ducklings and breeding ducks (p<0.01). The present study demonstrated that the prevalence of *Campylobacter* spp. in the breeding ducks and 1-day-old ducklings in flock 1 were 9.0% and 12.0%, respectively. The infestation of *Campylobacter* in the 1-day-old ducklings might have been from vertical transmission: *Campylobacter* at the oviduct of the breeding ducks transmitted to the eggs before embryo development. Besides, it might be oral transmission from *C. jejuni,* which penetrate egg contents by fecal contamination of egg shells (Newell and Fearnley, 2003). The prevalence of *Campylobacter* and *Salmonella* in the ducks aged 1 and 30 days from both flocks was in the similar pattern: the prevalence of *Salmonella* in 1-day-old ducklings was higher than that of *Campylobacter*, whereas prevalence of *Campylobacter* was higher than that of *Salmonella* in 30-day-old ducklings (p<0.01) (Table 1). This similar pattern of *Campylobacter* infection might be due to the fact that both flocks accommodated the ducks in houses with high density. Moreover, the houses had been used to accommodate a number of duck flocks; those pathogens might contaminate the environment. The pathogens might be released from ducks' feces and contaminated other materials such as bedding materials, fomites, rats, insects which, finally, orally infect the ducks in new flocks. This contributed to the enhanced rate of *Campylobacter* infection when the ducks' age increased (Newell and Fearnley, 2003). On the other hand, the prevalence of *Salmonella* in both flocks tended to decline when the ducks were older. This might result from the development of immunological system, causing the enhanced protective immunity in the gastrointestinal tract of the ducks (S.-Y. Cha et al., 2013).

A previous study revealed that the global prevalence of *Campylobacter* infection between 1990 and 2011 was 53.0% (range 0.0-83.3%) in ducks and was 94.4% (range 92.0-96.7%) in rearing and processing environment. In the UK, the prevalence of *Campylobacter* spp. in ducks and environment was 83.3% and 96.7%, respectively. Moreover, the prevalence of *Campylobacter* spp. in ducks was 33.0%, 63.5%, and 80.0% in the USA, Nigeria, and Tanzania, respectively (Adzitey et al., 2012[a]). In Taiwan, the prevalence of *Campylobacter* spp. in ducks was 43.5% and 92% out of all duck farms; 991 (94.8%) samples of them were *C. jejuni* (94.8%) and *C. coli* (5.2%) (Tsai and Hsiang, 2005). In Malaysia, the prevalence of *Campylobacter* spp. in ducks was 7.0% (Adzitey et al., 2012[b]). In the present study, the prevalence of *C. jejuni* was detected more than that of *C. coli*, which corresponded with the results from other region of the world (Adzitey et al., 2012[a]).

The environment is one of the important factors dominating in the dispersion of *Campylobacter* spp. and *Salmonella* spp. to the ducks. The current study demonstrated that *C. jejuni* in the breeding ducks was found both in duck feces and drinking water in container. Since the drinking water container was the place where all ducks consumed and ran activities, the appearance of *C. jejuni* took place in all ducks. The existence of *C. jejuni* or *C. coli* in both feces and environment of 1- and 30-day-old ducklings was in accordance. For instance, the environmental samples such as the soil in field, watercourse, and water in field from the 30-day-old ducklings from both flocks were contaminated with *C. jejuni* or *C. coli*; the pathogens could be transmitted to the ducks orally. In contrast, the infected ducklings could also spread *Campylobacter* into the environment. These implied that *Campylobacter* could survive in the environment by contaminating any kind of birds. This was supported by a survey of *Campylobacter* in the natural residences of ducks and wild birds in London which found 23-430 colony forming unit of *Campylobacter* spp. per 100 ml of water. Moreover, fecal examination of those birds revealed that the prevalence of *Campylobacter* spp. in mallard was 30%; 82 samples of them were *C. jejuni* (90%), *C. coli* (7%), and other *Campylobacter* spp. (3%) (Jones, 2011).

Prevalence data of *Salmonella* from several countries from a survey during 1997-2012 reported that an average prevalence was 19.9% (range 3.3-56.9%) in ducks and 32.5% (range 10.5-82.6%) in rearing and processing environment. In addition, the prevalence of *Salmonella* in ducks was highest in Brazil (56.9%) and lowest in the USA (3.3%), while the prevalence of *Salmonella* in rearing and processing environment was highest in Brazil (82.6%) and lowest in China (10.5%) (Adzitey et al., 2012a). In the present study, the survey of *Salmonella* spp. demonstrated that serovars from environmental and fecal samples were the same. In the 1-day-old ducklings of flock 1, *S*. Mbandaka, *S*. Montevideo, and *S*. Amsterdam were found in the feces, as well as in the incubator, egg shell, and floor after sexing. This indicated the poor sanitation of the hatchery section, putting the ducklings at risk of oral infection and dispersion to the rest of the flock. Likewise, the 1-day-old ducklings of both flocks, in the present study, possessed the same serovars: *S*. Mbandaka and *S*. Montevideo, even though they hatched in different periods. This could be synopsized that the sanitary regulations of the hatchery should be improved according to the standards of the Department of Livestock Development of Thailand to reduce the environment-contaminated pathogens. Moreover, the same serovar (*S*. Thomspon) from environmental samples such as the water in field (flock1), soil in field (flock2), watercourse (flock2) and fecal samples was detected in 30-day-old ducklings. Even though the ducks from the two flocks were reared in different places and times, the existence of same serovar from the examined samples signified that it might be endemic serovar in this region of Thailand. Although the current study identified credible association between pathogens from cloacal swabbing and pathogens from environmental contamination, future studies using molecular subtyping techniques including MLST and PFGE could be employed with better accuracy than bacterial species identification and serotyping.

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บทคัดย่อ

การศึกษาระยะยาวของ *Salmonella* spp. และ *Campylobacter* spp. จากลูกเป็ดไข่สองฝูงในภาคกลางของประเทศไทย

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สำรวจหา *Campylobacter* spp. และ *Salmonella* spp. ด้วยวิธีการศึกษาระยะยาวจากลูกเป็ดไข่สองฝูงที่มีพ่อแม่พันธุ์เป็ดชุดเดียวกัน โดยเก็บตัวอย่างรวมทั้งหมด 477 ตัวอย่าง จากเป็ดไข่พ่อแม่พันธุ์ (n=100) ลูกเป็ดเพศเมียอายุ 1 วัน (n=160) และ 30 วัน (n=178) และตัวอย่างจากสิ่งแวดล้อมที่เป็ดอาศัย ได้แก่ ตู้ฟัก ดิน น้ำ และอาหาร (n=39) จากตัวอย่างทั้งหมดพบ *Campylobacter* spp. 27.0% (129/477) ซึ่งตัวอย่างที่ให้ผลบวก 129 ตัวอย่างแยกได้เป็น *C. coli* 43.4% และ *C. jejuni* 56.6% และพบ *Salmonella* spp. 31.0% (148/477) โดยแยกได้เป็น *Salmonella enterica* 8 ซีโรวาร์ดังนี้ *S.* Amsterdam, *S.* Chester, *S.* Dublin, *S.* Enteritidis, *S.* Hvittingfoss, *S.* Mbandaka, *S.* Montevideo และ *S.* Thompson โดยซีโรวาร์ที่พบมาก 3 อันดับแรก ได้แก่ *S.* Montevideo 42.6%, *S.* Mbandaka 36.5%, *S.* Amsterdam 12.8% ความชุกของ *Campylobacter* spp. และ *Salmonella* spp. ในลูกเป็ดทั้งสองฝูงมีแนวโน้มในการพบที่อายุ 1 วัน และ 30 วันในลักษณะเดียวกัน คือ เมื่อลูกเป็ดอายุ 1 วัน ความชุกของ *Salmonella* spp. มากกว่า *Campylobacter* spp. แต่เมื่อลูกเป็ดอายุ 30 วัน มีความชุกของ *Campylobacter* spp. มากกว่า *Salmonella* spp. พบการปนเปื้อนเชื้อแบคทีเรียในระดับสปีชีส์ของ *Campylobacter* และซีโรไทป์ของ *Salmonella* ที่สอดคล้องกันในมูลเป็ดและสิ่งแวดล้อมที่เป็ดอาศัยอยู่ ดังนั้นจากผลการสำรวจสรุปได้ว่าสิ่งแวดล้อมของเป็ดอาจเป็นแหล่งที่มาของการปนเปื้อนทั้ง *Campylobacter* spp. และ *Salmonella* spp. สู่ลูกเป็ด

คำสำคัญ: แคมไพโลแบคเตอร์ เป็ดไข่ ความชุก ซัลโมแนลลา

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