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1	Investigation of the concurrent colonization with Campylobacter and Salmonella in
2	poultry flocks and assessment of the sampling site for status determination at slaughter
3	
4	G. Rasschaert, K. Houf, J. Van Hende, L. De Zutter*
5	
6	Department of Veterinary Public Health and Food Safety, Faculty of Veterinary Medicine,
7	Ghent University, Salisburylaan 133, 9820 Merelbeke, Belgium
8	

^{*} Corresponding author. Tel.: +32 2647455; fax: +32 2647491 E-mail address: lieven.dezutter@ugent.be

1 Abstract

Fifty six broiler flocks and 20 laying hen and breeder flocks were sampled in six slaughterhouses for the presence of *Campylobacter* and *Salmonella*. Samples were taken from three different sites of the gastrointestinal tract, namely from the crop, the duodenum and the ceca. The prevalence of flocks colonized with *Campylobacter* and *Salmonella* was determined and an association between the concurrent colonization with these two pathogens was investigated. Furthermore, the best sampling site for status determination at the slaughterhouse level was evaluated.

9 Of the broiler flocks, 73% were colonized with Campylobacter, whereas 13% were 10 Salmonella positive at slaughter. Concerning the laying hen and breeder flocks, all flocks 11 were colonized with Campylobacter and 65% of the flocks were Salmonella positive. No 12 association was found between Campylobacter and Salmonella occurrence in broiler flocks. 13 Since all laying hen and breeder flocks were colonized with *Campylobacter*, no association 14 between the concurrent colonization with the two pathogens could be determined. At the 15 slaughterhouse level, sampling only the duodena was sufficient to determine the 16 Campylobacter status of poultry flocks, whereas the three sampling sites had to be analyzed 17 to detect all flocks colonized with Salmonella.

18

19

20 Key words: *Campylobacter*; *Salmonella*; broiler flocks; laying hen and breeder flocks;

21 concurrent colonization

1 1. Introduction

2

3 *Camp vlobacter* and *Salmonella* are two major causes of human bacterial gastroenteritis in the 4 industrialized world. Contaminated poultry meat is an important source of infection for both 5 zoonoses. Many studies have determined the prevalence of broiler flocks colonized with 6 *Campylobacter*, *Salmonella*, or both, at slaughter age. The reported prevalence ranges from 7 3% in Finland to more than 90% in the UK for *Campylobacter*, and from 4% in Canada to 8 67% in Japan for Salmonella (Chambers et al., 1998; Limawongpranee et al., 1998; Evans and 9 Sayers, 2000; Perko-Mäkelä et al., 2002). Only few studies have investigated the possible 10 association between the occurrence of *Campylobacter* and *Salmonella* in poultry flocks. 11 Though no association was found in a Danish study (Wedderkopp et al., 2001), a positive 12 correlation was reported in Dutch poultry flocks (Jacobs-Reitsma et al., 1994; Jacobs-13 Reitsma, 1995).

14 The intestines, especially the ceca are the primary sites of colonization for both 15 Campylobacter and Salmonella (Fanelli et al., 1970; Beery et al., 1988; Achen et al., 1998). 16 Birds are subjected to feed withdrawal during transport to the slaughterhouse, resting time, 17 and sometimes even a few hours before transport. Some studies have demonstrated that 18 following feed withdrawal more crops than ceca were contaminated with Campylobacter and 19 Salmonella (Hargis et al., 1995; Byrd et al., 1998). Therefore, it is possible that the ceca are 20 not the best sampling site for determining the *Campylobacter* and *Salmonella* prevalence in 21 flocks at the slaughterhouse level. However, the studies above are performed on individual 22 birds and it is not clear if the results reported can be extrapolated to the flock level.

23 The study aimed to determine the prevalence of *Campylobacter* and *Salmonella* colonized 24 broiler flocks and laying hen and breeder flocks at slaughter age; to investigate an association 25 between colonization with *Campylobacter* and *Salmonella* in poultry flocks; and to evaluate

- the best sampling site for determining the *Campylobacter* and *Salmonella* prevalence in flocks
 at the slaughterhouse level.
- 3

4 **2. Materials and methods**

5

6 2.1. Sampling

7 During the period from January 2002 to March 2004, 76 flocks were examined for the 8 presence of Campylobacter and Salmonella. A flock was defined as all birds reared in the 9 same poultry house on a farm. The sampled flocks consisted of 56 broiler flocks and 20 spent 10 laying hen and breeder flocks. Flock size ranged from 1,100 to 18,000 chickens. Broiler 11 flocks were between 35 and 42 days old when slaughtered, whereas the laying hen and 12 breeder flocks were between 10 and 26 months old. The broiler flocks were slaughtered in 13 four Belgian slaughterhouses, and the laying hen and breeder flocks were slaughtered in three 14 other Belgian slaughterhouses. The flocks were sampled just before slaughter and during 15 processing. From each flock, 30 live birds were randomly chosen from 15 crates from 16 different transport containers. Of each bird, a swab sample of the crop was taken. In addition, 17 30 gastrointestinal tracts per flock (95% CI to detect a prevalence of 10% for more than 1,000 18 birds) were randomly collected from the slaughter line just after mechanical evisceration. All 19 samples were packed in sterile plastic bags, transported to the laboratory under cooled 20 conditions, and processed the same day.

21

22 2.2. Bacterial culture for Salmonella

From each of the 30 gastrointestinal tracts, 1 g of duodenal content and 1 g of one cecum were aseptically collected. These samples were pooled resulting in three subsamples of 10 g ceca content and three subsamples of 10 g duodenal content. The pooled samples were

1 homogenized for 1 min. with 90 ml of buffered peptone water (BPW, Oxoid, Basingstoke, 2 UK) in a stomacher blender at normal speed. The 30 crop swabs were pooled to three 3 subsamples and homogenized with 25 ml of BPW each. The homogenates were incubated at 4 37° C for 16 to 20 h. One portion of 100 µl of each of the homogenates was plated in the 5 middle of Diagnostic Semi-Solid Salmonella Agar plates (Diassalm, LabM 537, Lancashire, 6 UK). Furthermore, 100 µl of each homogenate was added to 10 ml Rappaport-Vassiliadis 7 broth (RV, Oxoid CM669, Basingstoke, UK). After incubation for 24 h at 42°C, a loopful of 8 the discolored Diassalm plates and 10 µl of all RV tubes were plated onto Xylose Lysine 9 Deoxycholate plates (XLD, Oxoid CM469, Basingstoke, UK) and incubated at 37°C for 24h. 10 Presumptive Salmonella colonies were confirmed at genus level by PCR using the primers 11 described by Aabo et al. (1993). The reaction mixture and amplification protocol were as 12 described by Botteldoorn et al. (2003). Per flock, one Salmonella isolate per pooled sample 13 was further characterized, which resulted in a maximum of nine isolates per flock if all plates 14 showed Salmonella growth. The Salmonella isolates were serotyped by the Belgian reference 15 laboratory for Salmonella according to the Kauffman-White scheme (Popoff and Le Minor, 16 1997).

17

18 2.2. Bacterial culture for Campylobacter

19 Of each of the BPW homogenates, 1 ml was added to 9 ml selective Preston broth (Nutrient 20 Broth n°2 CM 67, Oxoid, Basingstoke UK, enriched with 5% (v/v) lysed defibrinated horse 21 blood and 1% Preston Supplement (5000 IU polymixin B, 0.010 g rifampicin, 0.0076 g 22 trimethroprim and 0.010 g amphotericin dissolved in 10 ml ethanol)). The enrichment broths 23 were incubated for 24 to 48 h at 42°C under microaerobic conditions (6% CO₂, 6% H₂, 4% O₂ 24 and 84% N₂). After 24 h, 10 μ l of each enrichment broth was plated onto modified 25 Cefoperazone Charcoal Deoxycholate Agar (mCCDA; CM 739 plus SR155, Oxoid,

Basingstoke, UK) and incubated at 42°C under microaerobic conditions. If there was no 1 2 Campylobacter growth on mCCDA after 24 h of incubation, 10 µl of the 48-h incubated 3 enrichment broth was plated on a new mCCDA plate. Morphologically typical colonies were 4 picked, examined by Gram staining, subcultured on a blood agar plate (CM 965 and L13, 5 Oxoid, Basingstoke, UK and 5% (v/v) defibrinated horse blood) and stored in whole horse blood at -80°C for further examination. Per flock, one *Campylobacter* isolate per pooled 6 7 sample was stored, which resulted in a maximum of nine isolates per flock if all plates 8 showed *Campylobacter* growth. Identification on species level was performed according to 9 the PCR assay of Vandamme et al. (1997) for C. jejuni and C. coli, and according to the PCR 10 assay of Linton et al. (1996) for C. lari.

A flock was considered *Salmonella* or *Campylobacter* colonized, when *Salmonella* or
 Campylobacter, respectively, was detected in at least one of the pooled samples of the crop,
 the duodenum or the ceca.

14

15 2.3. Statistical analysis

16 The chi square (χ^2) test was used to investigate an association between *Campylobacter* and 17 *Salmonella* occurrence in poultry flocks, and to determine the differences in *Salmonella* and 18 *Campylobacter* colonization of the crops, the duodena and the ceca. Differences were 19 considered to be nonsignificant at p \ge 0.05. If the data contained frequencies lower than 5, the 20 Cramers' V test was used. The outcome of Cramers' V ranges from -1 (negative association) 21 to 1 (positive association), with 0 indicating no association.

22

3. Results

24

25 3.1. Broiler flocks

Forty one (73%) broiler flocks were colonized with *Campylobacter*, whereas *Salmonella* was 1 2 isolated from seven flocks (13%). Three flocks were positive for both *Campylobacter* and 3 Salmonella, and 11 flocks were negative for the two species (Table 1). There was little to no 4 association between Campylobacter and Salmonella occurrence in broiler flocks 5 (Cramers'V=0.26). Of the 41 Campylobacter positive flocks, 32 flocks were colonized with only one Campylobacter species: 29 flocks with C. jejuni, two flocks with C. coli and one 6 7 flock with C. lari. Six flocks carried two species in the gastrointestinal tract: four flocks 8 harboured C. jejuni and C. coli in the intestines, whereas the other two were colonized with C. jejuni and C. lari. The isolates of the three remaining flocks were not identified on species 9 10 level. The seven Salmonella positive flocks were each colonized with only one Salmonella 11 serotype: two flocks were colonized with serotype Typhimurium O5+, two flocks with 12 serotype Infantis, whereas the other three flocks were colonized with serotype London, 13 serotype Hadar and an isolate which was not typeable by serotyping, respectively.

14 The site of colonization for the *Campylobacter* and *Salmonella* positive flocks is shown in 15 Table 2. Concerning the Campylobacter colonized broiler flocks, there was a significant difference between the presence of Campylobacter in the three sampling sites (χ^2 test, 16 17 p=0.038). More flocks were colonized in the duodena and ceca than in the crops. On the other 18 hand, there was no association between the prevalence of Salmonella in the three sampling 19 sites (Cramers'V=0.040). Sampling only the duodena was sufficient to detect all 20 *Campylobacter* positive flocks, whereas the three sampling sites had to be analyzed to 21 determine the Salmonella status of flocks at the slaughterhouse level (Table 2).

22

23 *3.2. Laying hens and breeder flocks*

Campylobacter was isolated from each of the 20 sampled flocks (100%), whereas *Salmonella*was isolated from 13 (65%) flocks (Table 1). Since all flocks were colonized with

Campylobacter, it was not possible to determine an association between *Campylobacter* and *Salmonella* occurrence in these flocks. Four flocks were colonized with only one *Campylobacter* species (*C. jejuni*), 11 flocks with two species (*C. jejuni* and *C. coli*), and five flocks with three species (*C. jejuni*, *C. coli* and *C. lari*). From 11 of the 13 *Salmonella* positive flocks, serotype Enteritidis was isolated. The two remaining flocks were colonized with serotype Braenderup and a strain which was not typeable by serotyping, respectively.

There was a weak association between the presence of *Campylobacter* in the three sampling sites (Cramers'V=0.51). As for the broiler flocks, the duodena and the ceca were more often colonized than the crops. Sampling the duodena or the ceca was sufficient to determine the *Campylobacter* status. Concerning *Salmonella*, there was no significant difference between the prevalence in the three sampling sites (χ^2 test, p=0.333). As for the broiler flocks, sampling the three sampling sites was necessary to detect all flocks colonized with *Salmonella*.

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- 15

16 4. Discussion

17

18 In the present study, 73% of the broiler flocks and 100% of the laying hen and breeder flocks 19 were colonized with *Campylobacter*. This prevalence of *Campylobacter* colonized broiler 20 flocks is in agreement with another Belgian study (Herman et al., 2003), in which 67% of the 21 broiler flocks were colonized with *Campylobacter* at slaughter. In contrast to broiler flocks, 22 only limited data is available about the *Campylobacter* prevalence in laying hen and breeder 23 flocks. Moreover, the duration of colonization in older birds is not completely clear. It is 24 generally accepted that for broiler flocks, the colonization persists at least until the slaughter 25 age of 6 weeks (Newell and Fearnley, 2003). As the birds get older, the number of infected

birds and the level of campylobacters recoverable may gradually reduce (Newell and Wagenaar, 2000). Self-limitation of colonization and the presence of antibodies against *C*. *jejuni* without colonization have also been reported (Newell and Fearnley, 2003). However, instead of reduced colonization, the present study reveals that colonization in laying hen and breeder flocks is higher than in broiler flocks in terms of the number of flocks colonized and the number of species isolated from the gastrointestinal tract.

7 In the present study, 13% of the broiler flocks were colonized with *Salmonella* at slaughter. 8 This prevalence is comparable to the results of the study of van de Giessen et al. (2006), in 9 which approximately 12% of the broiler flocks at slaughter age were colonized with 10 Salmonella (van de Giessen et al., 2006). This is a decline compared to a previous Belgian 11 study of Heyndrickx et al. (2002) and an earlier Dutch study of Jacobs-Reitsma et al. (1994) 12 in which 33% and 27% of the examined broiler flocks at slaughter age were colonized with 13 Salmonella, respectively. In the present study, 65% of the laying hen and breeder flocks were 14 colonized with Salmonella. In execution of regulation EC/2160/2003 on the control of 15 Salmonella and other specified foodborne zoonotic agents, the E.U. have published a report 16 about the Salmonella prevalence in laying hen flocks during the last nine weeks of their 17 production period in 2004-2005. The prevalence ranged from 0% in Luxembourg and Sweden 18 to 80% in Portugal (EFSA, 2006). The prevalence in Belgium (38%) was almost half of the 19 reported prevalence in the present study. In the EFSA study, the prevalence was determined at 20 the farm by collecting fecal and environmental samples during the last nine weeks of their 21 production period, whereas in the present study three different sites of the gastrointestinal 22 tract of the birds were sampled at slaughter. That way, only flocks shedding Salmonella are 23 detected in the EFSA study, whereas flocks carrying Salmonella without shedding the 24 bacteria are detected by our sampling method. This may be an explanation for the higher 25 prevalence found in the present study. Another possibility is that flocks, Salmonella-free nine

weeks before slaughter, acquire an infection during the last weeks of their production period or even during transport as demonstrated by Rigby and Pettit (1980). A last explanation is that in the time span between the present study and the EFSA study, the *Salmonella* prevalence is reduced due to the increased vaccination of laying hen flocks.

5 In the present study, no positive or negative association was found between the presence of 6 Campylobacter and Salmonella in broiler flocks. This in agreement with the results of 7 Wedderkopp et al. (2001) but in contrast with the outcome of the study of Jacobs-Reitsma et 8 al. (1994). They reported a positive correlation between the colonization with these two 9 organisms in broiler flocks. Campylobacter free flocks were more often also Salmonella free, 10 and Campylobacter positive flocks were more often also positive for Salmonella. The lack of 11 an association in the present study may indicate that the transmission routes for flock 12 colonization with Campylobacter and Salmonella are independent in Belgium. Jacobs-13 Reitsma (1995) also reported a positive correlation between Campylobacter and Salmonella 14 occurrence in breeder flocks. However, since all laying hen and breeder flocks were colonized 15 with *Campylobacter* in the present study, no correlation could be demonstrated.

16 In the present study, the duodenum was most often found positive for Campylobacter or 17 Salmonella, followed by the ceca and finally the crop. This in contrast with the studies of a 18 research group (Hagris et al., 1995; Ramirez et al., 1997; Corrier et al., 1999) which has 19 demonstrated that feed withdrawal in market-age broilers resulted in an increased incidence of 20 Salmonella-positive crops and less pronounced in Salmonella-positive ceca. The number of 21 Salmonella-positive crops may even exceed the number of positive ceca. Byrd et al. (1998) 22 observed the same for *Campylobacter* colonized flocks. However, these studies were 23 performed on individual birds, whereas the present study is performed on flock level, which is 24 a possible explanation for the different outcome. It is remarkable in the present study that for 25 the broiler flocks as well as the laying hen and breeder flocks, sampling only the duodenum

was sufficient to detect all flocks colonized with *Campylobacter*, whereas the three sampling
 sites had to be analyzed to determine the *Salmonella* status of flocks.

3 In conclusion, the present study has shown that there was no association between the 4 concurrent colonization with *Campylobacter* and *Salmonella* in broiler flocks. Sampling only 5 the duodenum has been shown to be sufficient to determine the Campylobacter status in 6 poultry flocks at the slaughterhouse level. However, it is still necessary in epidemiological 7 studies to sample the three sites, as the genotypes of the strains isolated from crop, duodenum 8 and ceca may differ (Rasschaert et al., 2006). For determining the Salmonella prevalence in 9 poultry flocks at the slaughterhouse level, a combination of the three sampling sites is 10 necessary.

11

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- 1 **Table 1.** The distribution in the prevalence of *Campylobacter* and *Salmonella* colonized
- 2 flocks.

Broiler flocks			
	Campylobacter +	Campylobacter -	total
Salmonella +	3	4	7
Salmonella -	38	11	49
otal	41	15	56
Laying hen and			
oreeder flocks			
	Campylobacter +	Campylobacter -	total
Salmonella +	13	0	-13
Salmonella -	7	0	7
to ta l	20	0	-20

3

- 1 **Table 2.** The distribution of *Campylobacter* and *Salmonella* colonized flocks for individual
- 2 and combined sampling sites.

	crop	duodenum	ceca	crop	duodenum	c rop	total
				+duodenum	+ceca	+ceca	
Broiler flocks						N.	
Campylobacter +	28 (68%)	41 (100%)	36 (88%)	41 (100%)	41 (100%)	39 (95%)	41
Salmonella +	3 (43%)	3 (43%)	2 (29%)	6 (86%)	4 (57%)	5 (71%)	7
Laying hen and							
breeder flocks							
Campylobacter +	13 (65%)	20 (100%)	20 (100%)	20 (100%)	20 (100%)	20 (100%)	20
Salmonella +	6 (46%)	10 (77%)	7 (54%)	12 (92%)	12 (92%)	10 (77%)	13

4