Prevalence of *Salmonella* and *Campylobacter* on Broiler Chickens from Farm to Slaughter and Efficiency of Methods To Remove Visible Fecal Contamination

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ABSTRACT

A study was conducted to investigate the prevalence of *Salmonella* and *Campylobacter* from farm to slaughter. The efficiency of trimming and water spray (490 to 588 kPa pressure) on the removal of visible fecal contamination from broiler carcasses before chilling was also investigated. Drag swabs were used to sample litter from the farm houses. Samples of ceca and carcasses without and with visible fecal contamination before and after trimming or spray washing of fecal contamination were taken during slaughter of the flocks previously visited at the farms. There was a low prevalence of *Salmonella* on the litter from the farms (5%) and cecum and carcasses (0%). However, *Campylobacter jejuni* and *Campylobacter coli* were present in farms’ litter (100 and 58.8%, respectively), cecum samples (100 and 70.6%, respectively), and carcasses with (58.8 and 11.6%, respectively) and without (17.6 and 9.8%, respectively) visible fecal contamination. There was high prevalence of *C. jejuni* but at low counts and low prevalence and high counts of *C. coli*. *Campylobacter lari* was not detected in any sample. Trimming the visible fecal contamination decreased the prevalence of *C. jejuni* but increased occurrence of *C. coli*. Trimming did not reduce the counts of *Campylobacter* and of hygiene indicator microorganisms on the carcasses. Water shower reduced the counts of hygiene indicator microorganisms by 20%. Therefore, control measures for preventing introduction of *Campylobacter* and the use of good hygienic conditions are needed to warrant the microbiological quality and safety of broiler carcasses.

The global poultry industry has faced challenges concerning the microbiological safety of poultry carcass and meat, with several reports indicating that broiler meat is contaminated with *Campylobacter* and *Salmonella*. Therefore, poultry meat and products have been considered a significant source and reservoir of these pathogens (12, 30, 47). Contamination of carcasses with these pathogens remains a problem worldwide: *Salmonella* is still prevalent in retail chicken meat (up to 34%) and in broiler carcasses (up to 7.5%), and *Campylobacter* has an even higher prevalence in broiler ceca (77.2%) and in broiler carcasses (87.5%) (1, 19, 25). Furthermore, *Salmonella* and *Campylobacter* caused most of the foodborne diseases in the European Union recently (19, 25). In Brazil, *Salmonella* is also the pathogen involved in most of the foodborne disease outbreaks, but there is no information about *Campylobacter* (50). Therefore, the presence of these pathogens in poultry meat is still an important concern, and the control of these microorganisms in poultry has great impact on public health and international trade.

For this reason, many countries are working to decrease foodborne pathogens through the implementation and use of programs based on hazard control linked to public health objectives. In the last 10 years, poultry industries have developed food safety quality programs throughout the production chain. These programs have improved the quality and reduced the presence of some indicator microorganisms on chicken carcasses and meat, but *Salmonella* and *Campylobacter* are still the bacteria with high impact in poultry industries and public health (30).

The critical control points to prevent poultry contamination with *Salmonella* are well known, and when correctly applied from farm to slaughter, they are effective in the control of the prevalence of this bacterium. However, there is limited information regarding the *Campylobacter* status of conventional broiler slaughterhouses in Brazil, as in many producing countries.

In the United States, mandated inspection procedures, based on the implementation of hazard analysis and critical control point (HACCP), included the monitoring of *Salmonella*, *Campylobacter* (53), and of *Escherichia coli* to check hygiene during slaughter and “zero fecal tolerance” for visible fecal contamination before chilling (51). Additionally, in the United States, chemical decontaminants during chicken slaughtering are allowed, and chlorine is widely used (30). In the European Union (EU), *Salmonella* and *Campylobacter* are evaluated in chicken carcasses by all member states (19), and food business operators shall not use any substance other than potable water to remove surface contamination from...
products of animal origin (16). In Brazil, the pathogen reduction program was introduced in 2003 to control *Salmonella* in the poultry slaughter plant, and chemical decontaminants during chicken slaughtering are not allowed (33). Additionally, zero fecal tolerance for visible fecal contamination on carcasses before chilling is, since 2006, an obligatory critical control point for all broiler slaughtering establishments (34). From that time until 2011, fecal contamination on carcass surface was removed by trimming before the last wash step. However, trimming of fecal contamination is time-consuming and laborious (21). Recently, a new regulation allowed the use of potable water to remove fecal contamination, and each establishment must validate the process before using water (37, 39).

The objective of this study was to determine the prevalence of *Salmonella* and *Campylobacter* on broilers from farm to slaughter and also to investigate the efficiency of carcass trimming and/or washing visible fecal contamination on the prevalence of hygiene indicator bacteria. Therefore, litters from farm houses were collected, and the respective broilers (cecum and carcass) were analyzed during slaughter for *Salmonella* and *Campylobacter*. *E. coli*, total coliforms, and *Enterobacteriaceae* were also analyzed in the samples. These hygiene indicator microorganisms were also used to investigate the efficiency of different procedures on the removal of fecal contamination from carcass.

**MATERIALS AND METHODS**

**The farms.** Visits, from March until May of 2010, were made to 40 contracted broiler farms, 10 to 15 days prior to slaughter. The farms were located in the western region of the state of Santa Catarina, Brazil. The houses had concrete or dirt floors, and wood shavings were commonly used as litter.

**Slaughterhouse and flocks.** The flocks (group of broiler chickens kept in a farm during the same period of time) corresponding to the previously sampled farms were slaughtered from May until July. The slaughter of the chickens was conducted in a commercial plant located in the western region of Santa Catarina, Brazil. The plant processed 6-week-old chickens under typical industry conditions (Fig. 1). After unloading the birds into the holding areas, they were attached by their feet to a conveyor belt and transported to the slaughter area, where the following actions took place: stunning, bleeding, scalding, defeathering, evisceration, immersion chilling, packing, freezing, and distribution.

**Sampling of farm litter.** Ten to 15 days before slaughter, a drag swab of the litter was taken from each of the 40 farm houses (17, 35). The drag swab consisted of a cotton gauze swab attached to a cord and moistened with buffered peptone water (BPW; Oxoid CM 509, Basingstoke, Hampshire, UK). It was dragged across the surface of the litter as the sampler walked through the house. The swab was placed in a sterile plastic bag and transported to the laboratory. In a laminar flow chamber, 100 ml of BPW was placed into the bag containing the swab, and it was homogenized for 60 s in a stomacher (Logen, Diadema, São Paulo, Brazil). Aliquots were taken and analyzed for *Salmonella* and *Campylobacter*.

**Sampling of intestinal content.** Flocks from the 40 previously sampled farm litters were taken to the processing plant. During evisceration, samples of the gastrointestinal tract were taken from three individual broilers from each flock and pooled together. The ceca were removed from each gastrointestinal tract and placed in sterile plastic bags. In the laboratory, approximately 3.3 g of each cecal content was mixed, and 90 ml of 1.0% BPW was added. The samples were homogenized for 60 s in a stomacher (Logen), and aliquots were taken and analyzed for *Salmonella* and *Campylobacter*.

**Sampling of carcasses with and without fecal contamination.** The same previously taken flocks were also sampled for carcasses evaluation. During slaughter, after complete evisceration and review (Fig. 1, step 8), the carcasses were randomly taken. The carcasses were separated into three different groups (n = 120 each): carcasses without visible fecal contamination, carcasses with visible fecal contamination, and carcasses with visible fecal contamination after its removal by trimming.

Visible fecal contamination was defined as the macroscopic evidence of feces on the external and/or the internal surfaces of the carcasses. The employees on the production line in the carcass review step (Fig. 1), according to Brazilian legislation (34), used a knife for trimming, cutting the parts with fecal contamination.

![FIGURE 1. Flow diagram of broiler slaughtering process indicating the Brazilian compulsory critical control points (34).](image-url)
Usually, only the skin with the fecal contamination was cut to remove the contamination. However, in some instances, depending on the extent of the contamination, skin and muscle were also removed. Every sampled carcass was placed in individual sterile plastic bags and transported to the laboratory for analysis of Salmonella and Campylobacter.

In a laminar flow chamber, 400 ml of 0.1% BPW was added to each plastic bag containing the carcass. The broth was used to rinse the carcass inside and outside for 60 s. The carcass was removed from the BPW, which was homogenized for 60 s more in a stomacher. Aliquots were taken for the analysis of Campylobacter. To analyze for Salmonella, 30 ml of the broth was incorporated to 30 ml of BPW, and the sample was homogenized for 60 s prior to analysis (22, 54).

**Influence of washing the visible fecal contamination on E. coli, coliforms, and Enterobacteriaceae counts in the carcasses.**

From May until June 2010, carcasses from flocks were randomly separated into three different groups described previously and sampled in duplicate: carcasses without visible fecal contamination, carcasses with visible fecal contamination, and carcasses with visible fecal contamination after removal of the fecal contamination by trimming. One carcass of each group was removed from the processing line and placed immediately in individual sterile plastic bags. The other carcasses from each group were removed from the primary line and placed in a secondary line. After the carcasses were washed in a shower with 490 to 588 kPa of pressure, they returned to the primary line. The water used to wash the carcasses, 1.5 liters per carcass (32), contained less than 2.0 ppm of chlorine, as determined by the Brazilian legislation (38), and no visible fecal material was observed on the carcasses after washing. To warrant HACCP requirements at the plant, the washing of the carcasses was always performed at the end of the slaughter line, and after which, there was a complete slaughterhouse cleaning and sanitization. Each washed carcass was placed in a plastic bag and transported to the laboratory for analysis of E. coli, total coliforms, and Enterobacteriaceae.

**Microbiological analysis.** The methods of analysis were standardized using laboratory guidelines, based on procedures established by the International Organization for Standardization 17025 (26).

**Detection of Salmonella.** The BAX System PCR assay (DuPont Qualicon, Wilmington, DE) was used for Salmonella detection. Prior to analysis, the samples were enriched. For DNA extraction, aliquots of the enriched samples (drag swabs, ceca, and carcasses) were added to cluster tubes containing the lysis reagent (DuPont Qualicon). The mixture was heated and then chilled. PCR tablets in PCR tubes were hydrated with aliquots of the cooled lysate and loaded into the BAX System Q7 Cycler-Detector for a full process run. The presence or absence of C. jejuni, C. coli, and C. lari was displayed in ca. 1.5 h (14, 15).

When the results were positive and the concentrations of C. jejuni, C. coli, and C. lari were higher than 10^5 CFU/ml or 10^5 Enterobacteriaceae. Salmonella, C. jejuni isolates was determined using polyvalent O antiserum (Probac, São Paulo, Brazil). Positive samples were sent to the Enterobacteriaceae Laboratory at Fundação Oswaldo Cruz (Fiocruz, Rio de Janeiro, Brazil) for serotype identification.

**Detection of Campylobacter jejuni, Campylobacter coli, and Campylobacter lari.** Aliquots (5 μl) of the prepared sample (drag swabs, ceca, and carcasses) were added to cluster tubes containing 200 μl of lysis reagent (DuPont Qualicon). The mixture was heated at 37°C for 20 min, at 95°C for 10 min, and then chilled to 4°C for 5 min. PCR tablets in PCR tubes were hydrated with 30-μl aliquots of the cooled lysate and loaded into the BAX System Q7 Cycler-Detector for a full process run. The presence or absence of C. jejuni, C. coli, and C. lari was displayed in ca. 1.5 h (14, 15).

When the results were positive and the concentrations of C. jejuni, C. coli, and C. lari were higher than 10^5 CFU/ml or 10^5 CFU/g, the counts were obtained directly from the BAX System Q7 program. All the positive samples in the BAX System were confirmed by the traditional culture method (27, 54). Aliquots of the prepared samples (1 ml) were added to tubes containing 9.0 ml of Bolton SR 183E supplement (Oxoid). The tubes were incubated at 41.5°C for 24 h under microaerobic atmosphere. The plates were streak plated on modified charcoal cefoperazone deoxycholate agar with SR 155 selective supplement (Oxoid). The plates were incubated at 41.5°C for 48 h under microaerobic atmosphere. Typical colonies were confirmed as Campylobacter spp. by morphology, motility, microaerobic growth at 25°C, and oxidase test (27).

**Enumeration of E. coli, total coliforms, and Enterobacteriaceae.** An additional aliquot (1 ml) from the original 400 ml of the carcass rinsate was removed from each sample for analysis. Serial dilutions (10^-2 to 10^-5) were performed, and for each dilution, a 1.0-ml aliquot was plated onto Petrifilm 6414 (E. coli and total coliforms) and 6421 (Enterobacteriaceae; 3M, St. Paul, MN), according to manufacturer’s instructions. The plates were incubated at 36 ± 1°C for 24 ± 2 h, and the characteristic colonies of each microorganism were enumerated: E. coli and total coliforms, according to the U.S. Department of Agriculture Food Safety and Inspection Service methods (52), and Enterobacteriaceae following Association of Analytical Chemists International methods (3). The counts of these bacteria were expressed as CFU per gram of sample. In the analysis of the carcasses, the CFU per gram was calculated using the formula CFU/g = (CFU × V × D)/W, where V is the volume of BPW used to rinse the carcass (400 ml), D is the dilution used on the plate, and W is the carcass weight (22).

**Statistical analysis.** Descriptive statistical analysis including Salmonella and Campylobacter prevalence at 95% confidence intervals (CI) for farm litter, cecum, and carcass samples were calculated. Counts in CFU per milliliter of C. jejuni and C. coli on cecum and carcass samples were used to determine the mean, standard deviation (SD), and maximum value. Counts of C. jejuni and C. coli on the carcass were submitted to analysis of variance. The Tukey test was used to compare means. When C. jejuni and C. coli were not detected, the results were expressed as <4.0 CFU/g, and the mean and SD results were calculated using 4.0 CFU/g. The counts of E. coli, total coliforms, and Enterobacteriaceae were transformed into log CFU per gram and submitted to analysis of variance. The Tukey test was used to compare the means. All
statistical analysis was conducted using XLSTAT 2009.5.01 (Addinsoft, New York, NY) at a significance level of 95% (7).

RESULTS

Prevalence of Salmonella and Campylobacter on the broiler farm litter. The presence of Salmonella was only detected in 5.0% (2 in 40) of the litter samples collected at the farms. Further studies indicated that the Salmonella serovars were Salmonella Agona and Salmonella Lexington.

The presence of Campylobacter was observed in every farm litter sample analyzed. C. jejuni was isolated from the litter of every farm, whereas C. coli was detected in 58.8% (95% CI, 45.3 to 72.3%) of the samples (Fig. 2). C. lari was not detected in any of the litter samples analyzed.

Prevalence and counts of Salmonella and Campylobacter in the broiler ceca. Salmonella and C. lari were not detected in any of the cecum samples examined. However, C. jejuni was present in 100% of the samples and C. coli in 70.6% (95% CI, 58.1 to 83.1%) of the samples (Fig. 2).

C. jejuni was present in the ceca at counts ranging from <4.00 to 7.20 log CFU/g, with a mean of 5.43 log CFU/g and a coefficient of variation of 18%. The counts of C. coli in the positive cecum samples (70.6%) ranged from 5.70 to 8.98 log CFU/g, with a mean count of 7.95 log CFU/g (coefficient of variation = 12%). Based on these results, a larger number of samples of broiler ceca contained C. jejuni at low counts, whereas C. coli was present in a smaller number of samples but at high counts.

Counts of E. coli, total coliforms, and Enterobacteriaceae on broiler carcasses without and with visible fecal contamination before and after trimming. E. coli, total coliforms, and Enterobacteriaceae were detected in every broiler carcass analyzed. The counts of these bacteria are indicated on Table 2. The carcasses without fecal contamination showed mean counts of 4.73 log CFU/g for E. coli, 5.18 log CFU/g for total coliforms, and 5.27 log CFU/g for Enterobacteriaceae. Similar counts were observed on the carcasses with fecal contamination either

Prevalence and counts of Salmonella and Campylobacter in broiler carcasses without and with visible fecal contamination before and after trimming. Salmonella was not detected on any of the broiler carcasses analyzed independently of the presence or not of visible fecal contamination. C. lari was also not detected on any of the carcasses.

According to Figure 2, the carcasses without visible fecal contamination had a low prevalence of C. jejuni and C. coli, 17.6% (95% CI, 7.2 to 28.0%) and 9.8% (95% CI, 1.7 to 17.9%), respectively. However, high Campylobacter prevalence was observed in the carcasses with visible fecal contamination: C. jejuni was present in 58.8% (95% CI, 45.3 to 72.3%) of the carcasses and C. coli was detected in 11.6% (95% CI, 2.8 to 20.4%). After the removal of the visible fecal contamination by trimming, 19.6% (95% CI, 8.8 to 30.4%) of the carcasses were contaminated with C. jejuni and 17.6% (95% CI, 7.2 to 28.0%) were contaminated with C. coli. These results indicate that the removal of the visible fecal contamination by trimming reduced the occurrence of C. jejuni by 66.6% but increased C. coli prevalence by 52%.

Table 1 shows the counts of C. jejuni and C. coli in the broiler carcasses. The mean counts of C. jejuni varied from <4.00 to 4.66 log CFU/g, whereas mean C. coli counts ranged from 4.96 to 5.07 log CFU/g. There was no significant difference on Campylobacter counts among carcasses without fecal contamination and with fecal contamination before and after trimming. Therefore, the counts of C. jejuni and C. coli in broiler carcasses were not affected by the absence or presence of visible fecal contamination and also by the removal of the contamination by trimming.

Counts of E. coli, total coliforms, and Enterobacteriaceae on broiler carcasses without and with visible fecal contamination before and after trimming. E. coli, total coliforms, and Enterobacteriaceae were detected in every broiler carcass analyzed. The counts of these bacteria are indicated on Table 2. The carcasses without fecal contamination showed mean counts of 4.73 log CFU/g for E. coli, 5.18 log CFU/g for total coliforms, and 5.27 log CFU/g for Enterobacteriaceae. Similar counts were observed on the carcasses with fecal contamination either

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**TABLE 1. Counts of C. jejuni and C. coli on broiler carcasses without visible fecal contamination and with fecal contamination before and after trimming**

<table>
<thead>
<tr>
<th>Counts of Campylobacter (log CFU/ml)</th>
<th>C. jejuni</th>
<th>C. coli</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. jejuni</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Without fecal contamination</td>
<td>&lt;4.00</td>
<td></td>
</tr>
<tr>
<td>Mean ± SD</td>
<td>4.67 ± 0.57</td>
<td>5.46 ± 0.92</td>
</tr>
<tr>
<td>Maximum</td>
<td>4.86</td>
<td>6.49</td>
</tr>
<tr>
<td>With fecal contamination</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Before trimming</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean ± SD</td>
<td>4.67 ± 0.57</td>
<td>5.07 ± 0.67</td>
</tr>
<tr>
<td>Maximum</td>
<td>5.63</td>
<td>5.90</td>
</tr>
<tr>
<td>After trimming</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean ± SD</td>
<td>&lt;4.00</td>
<td>4.96 ± 0.76</td>
</tr>
<tr>
<td>Maximum</td>
<td>&lt;4.00</td>
<td>6.30</td>
</tr>
</tbody>
</table>

* n = 17 per treatment. Mean values in the same column are not significantly different (Tukey test, P > 0.05). Limit of detection = 10⁴ CFU/ml.
before or after trimming (Tukey test, \( P > 0.05 \)). Based on these results, the presence of visible fecal contamination on the carcasses, as well as its removal by trimming, did not significantly affect the counts of \( E. \) coli, total coliforms, and \( \text{Enterobacteriaceae} \) compared with broiler carcasses without visible fecal contamination. These results are similar to those observed for \( C. \) jejuni and \( C. \) coli.

### DISCUSSION

#### Prevalence of \( \text{Salmonella} \) from farm to slaughter.

The prevalence of \( \text{Salmonella} \) in the farm litter was low: it was isolated from only 5.0% of the 40 investigated farms. Data on the occurrence of \( \text{Salmonella} \) on farm litter in Brazil is scarce. Similar \( \text{Salmonella} \) prevalence on farm litter has been described by European Food Safety Authority (18) for the member states of the EU in 2007 to 2009. However, these values are lower compared with positive drag swabs of litter from grow-out houses in the United Kingdom and Canada (56). In Colombia, Donado-Godoy et al. (13) found a higher prevalence of \( \text{Salmonella} \) (65%) in drag swabs of farm litter. The low prevalence of \( \text{Salmonella} \) observed in this study is probably associated with the efforts implemented by the industry to control \( \text{Salmonella} \) in the broiler chain, taking into account biosecurity measurements at the integrated farms.

The serotypes of \( \text{Salmonella} \) detected on the farm litters were \( \text{Salmonella} \) Agona and \( \text{Salmonella} \) Lexington. None of these are among the main serotypes isolated from chicken farms in the EU (18). However, \( \text{Salmonella} \) Agona was the third major serotype detected in turkey carcasses and raw ground meat (49). In Brazil, \( \text{Salmonella} \) Agona was the third most common \( \text{Salmonella} \) serovar isolated in chicken from 2004 to 2010 and the second isolated in southern Brazil (5). According to Hendriksen et al. (23), \( \text{Salmonella} \) serovar Agona is frequently observed in Latin America, ranking among the top three most common nontyphoidal serovars; however, it also ranked 7th in Europe and 13th in North America. \( \text{Salmonella} \) Lexington has not been detected in poultry carcasses in Brazil in recent years (5). However, it has been considered one of the main serovars isolated from pork and cattle (2, 55). In Brazil, the presence of \( \text{Salmonella} \) Enteritidis and \( \text{Salmonella} \) Typhimurium on chickens farms before slaughter is not allowed (35).

### TABLE 2. Counts of \( \text{Escherichia coli} \), total coliforms, and \( \text{Enterobacteriaceae} \) on broiler carcasses without visible fecal contamination and with fecal contamination before and after trimming$^a$

<table>
<thead>
<tr>
<th>Carcasses</th>
<th>( E. ) coli Mean counts ± SD (log CFU/g)</th>
<th>Total coliform Mean counts ± SD (log CFU/g)</th>
<th>( \text{Enterobacteriaceae} ) Mean counts ± SD (log CFU/g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Without fecal contamination</td>
<td>4.73 ± 0.75 A</td>
<td>5.18 ± 0.62 A</td>
<td>5.27 ± 0.59 A</td>
</tr>
<tr>
<td>After washing</td>
<td>3.74 ± 1.08 B</td>
<td>4.34 ± 0.68 B</td>
<td>4.37 ± 0.69 B</td>
</tr>
<tr>
<td>With fecal contamination</td>
<td>5.00 ± 0.63 A</td>
<td>5.24 ± 0.58 A</td>
<td>5.14 ± 0.79 A</td>
</tr>
<tr>
<td>Before washing</td>
<td>3.96 ± 0.83 B</td>
<td>4.32 ± 0.63 B</td>
<td>4.26 ± 0.61 B</td>
</tr>
<tr>
<td>After trimming of fecal contamination</td>
<td>4.82 ± 0.49 A</td>
<td>5.15 ± 0.51 A</td>
<td>5.13 ± 0.55 A</td>
</tr>
<tr>
<td>After washing</td>
<td>4.04 ± 0.67 B</td>
<td>4.45 ± 0.72 B</td>
<td>4.52 ± 0.62 B</td>
</tr>
</tbody>
</table>

$^a n = 56$ per treatment. Mean values followed by different letters in the same column are significantly different (Tukey test, \( P < 0.05 \)).
The ceca and the carcasses of the broilers were free from *Salmonella*, even though this bacterium was found in some litter samples from the farms. Even the flocks from the two farm litters identified as positive for *Salmonella* did not contain the bacterium in the gastrointestinal tract or in carcasses with visible fecal contamination. Based on this result, the *Salmonella* status of the flocks determined by means of the farm litter analyzed a few weeks before slaughter did not correlate with the carcass status at the slaughterhouse. According to Rasschaert et al. (44), a change from *Salmonella* carrier to *Salmonella* shedder and vice versa, becoming apparently clear of colonization, or acquiring a new one, could support this finding.

The prevalence of *Salmonella* in carcasses analyzed after the chiller (Fig. 1, step 10) in Brazil between 2003 and 2008 was 6.06% (36). The Brazilian program for *Salmonella* in poultry carcasses allows the presence of 12 in 51 carcasses examined (33). However, similar to the results reported here broiler carcasses were found to be free of *Salmonella* (46). The absence of *Salmonella* in broiler carcasses indicates that *Salmonella* control programs from the farm to the slaughterhouse undertaken by Brazilian industries are effective in the control of infection level.

Traditionally, it has been thought that contaminated farm litter is a source of flock infection, the pathogens in the intestine of animals are transmitted to the meat during slaughter, and also feces in broiler carcasses during slaughter can result in carcasses contaminated with *Salmonella* (44). Based on that, the presence of feces in carcasses has been used as an indicator of the presence of *Salmonella* in poultry carcass (34). However, in this study, carcasses of broilers from the two flocks that were positive for *Salmonella* in the farm litter and also carcasses contaminated with feces were not positive for *Salmonella*. In a similar way, Reiter et al. (46) found broiler carcasses free of *Salmonella* from flocks with a 6.7% prevalence of intestine contamination. Therefore, the traditional thoughts were not supported by scientific evidence.

**Prevalence of Campylobacter from farm to slaughter.** Contrary to the *Salmonella* results, there was a high prevalence of *Campylobacter*, and PCR analysis indicated the presence of both *C. jejuni* and *C. coli*. *C. lari* was not present. *C. jejuni*, the prevalent *Campylobacter* from farm to slaughter, is, indeed, the most frequently isolated *Campylobacter* species from poultry (31, 40, 43). In the EU, *C. jejuni* was also followed by *C. coli*, and *C. lari* was present at very low percentages (0.2 to 0.3%) in chickens flocks and carcasses in 2008 (20).

The litter from every farm was contaminated with *C. jejuni*, and 58.8% of them were contaminated with *C. coli*. These results are similar to data reported by Kuana et al. (28) who found 81.8% (18 of 22) of *Campylobacter* spp. in chicken flocks analyzed at the farms through cloacal swabs. In the EU during 2008, the prevalence of *C. jejuni* and *C. coli* in farm litter was high: 60.8 and 41.5%, respectively (20). In fact, the within flock prevalence of Campylobacter-positive flocks is very high, and once a broiler is infected with *Campylobacter* spp., bird-to-bird transmission is extremely rapid and is enhanced by the coprophagic behavior of chickens (48).

The prevalence of *C. jejuni* and *C. coli* in the ceca was similar to that found in the farm litter. The high prevalence of *Campylobacter* spp. in broiler ceca has also been described in others studies (4, 24, 28, 45). According to Woldemariam et al. (57), the analysis of cecal material is more sensitive and specific compared with feces during the isolation of *Campylobacter* spp. in poultry, which may explain the high prevalence of *Campylobacter*. However, a low prevalence of *Campylobacter* spp. (6.3%) in chicken ceca was observed in Estonia from 2005 through 2007 (31). The detection of *C. jejuni* in all litter samples and also in every broiler cecum from the respective flocks indicates that usually the contamination of chicken flocks by *Campylobacter* starts at the farms and rapidly colonizes the intestine of the birds (20, 48).

When considering the broiler carcasses, *C. jejuni* and *C. coli* were present in the three experimental groups investigated, however, at lower prevalence compared with the farm litter and ceca. The presence of these bacteria in carcasses without fecal contamination suggests that *Campylobacter* spp. contamination can occur not only by fecal contamination but also by other means, such as cross-contamination in the slaughterhouse (20, 24). Carcasses with visible fecal contamination had a lower prevalence of *Campylobacter* spp. compared with the ceca but a higher prevalence compared with carcasses without fecal contamination. Therefore, the presence of *C. jejuni* and *C. coli* in the farm litter and/or in the cecum does not warrant their presence in the carcass.

According to Figure 2, trimming of the visible fecal contamination from the carcasses, as determined by Brazilian legislation (34), was efficient in reducing the prevalence of *C. jejuni*; however, there was an increase on the prevalence of *C. coli* in broiler carcasses compared with the carcass before trimming. Increased prevalence may be related to the higher levels of *C. coli* and to cross-contamination resulting from the handling to remove fecal contamination from the carcasses. The prevalence of *Campylobacter* in broilers from farm to slaughter varies among studies, as it is affected by the farm, slaughterhouse, country, as well as bird rearing and processing conditions. However, there is a consensus that *Campylobacter* prevalence is high, especially *C. jejuni* (11, 28, 29, 45).

Overall, the mean counts of *Campylobacter* in the ceca were significantly higher compared with the carcasses, and no significant difference was found among carcasses without and with visible fecal contamination before and after trimming. Although there was a higher prevalence of *C. jejuni* compared with *C. coli*, *C. coli* was present at higher counts in broiler ceca and carcasses. These counts are similar to literature values for *Campylobacter* spp.: from 4.2 to 10.6 log CFU/g in cecal contents (24, 48), from 3.39 to 3.60 log CFU/g in broiler carcasses (11, 24), and from <1.0 to <4.0 log CFU/g in various categories of chicken meat (6).

According to European Food Safety Authority (20), flocks of chickens infected with *Campylobacter* are 30 times more likely to produce carcasses contaminated with
high prevalence and counts of Campylobacter. Therefore, Campylobacter control programs should be based on an integrated approach addressing both the farms and the slaughter process. Risk management approaches to reduce contamination can include logistic slaughter and maintenance of an adequate concentration of free available chlorine in chilled water tanks (48).

Occurrence of E. coli, total coliforms, and Enterobacteriaceae in broiler carcasses and influence of trimming fecal contamination. E. coli, total coliforms, and Enterobacteriaceae counts were similar among the carcasses without visible fecal contamination, with fecal contamination, and after removal of fecal contamination by trimming (Table 2). Therefore, the presence of visible fecal contamination of the carcasses before chilling did not affect significantly the counts of E. coli, total coliforms, and Enterobacteriaceae. This result is similar to what was observed for Campylobacter (Table 1) and indicates that both microorganisms behave in a similar way to the trimming process.

Based on these results, the presence of visible fecal contamination did not affect enterobacteria, coliforms, and Campylobacter counts in the broiler carcass, which is in agreement with Cason et al. (10). Furthermore, trimming of visible fecal contamination was not efficient in reducing the counts of both bacteria.

Influence of washing on the removal visible fecal contamination on the carcasses. Because of the similarity of the counts and of the behavior upon trimming fecal contamination of enterobacteria and Campylobacter and because the quantification of enterobacteria provides a wider range of counts compared with Campylobacter analysis, it could be assumed that the influence of the washing procedure would provide similar results. Therefore, the influence of washing the carcasses on the removal of fecal contamination was investigated using enterobacteria as the indicator microorganism.

As indicated on Table 3, washing the contaminated carcasses prior to the chilling step was effective in reducing contamination of E. coli, total coliforms, and Enterobacteriaceae compared with carcasses in the same condition of contamination but that were not washed. The reduction was of about 1 log, which corresponded to ~20% decrease on counts. These results demonstrate that washing the fecal contamination from the carcasses can be more efficient in improving the microbial quality than removing fecal contamination by trimming. Additionally, the trimming process increases the handling of carcasses and exposes the meat to cross-contamination.

Several studies have reported the efficacy of carcass washing on the removal of visible fecal contamination and reduction of microbial contamination (8, 41). In fact, the use of water to remove fecal contamination on poultry carcasses is already allowed in many countries, such as the United States, EU, and Canada (9, 16, 53). The recent change in the Brazilian legislation (37, 39), allowing the removal of fecal contamination by washing, will certainly improve the microbial quality and safety of the broiler meat.

It is well known that prevention of carcass contamination with intestinal contents should be an important goal during slaughtering (8). However, in case it does happen, washing sprays should be placed where contamination is most likely to occur during the slaughtering process, because the immediate washing of carcasses with fecal contamination is more efficient than late removal (42). According to Berrang and Bailey (7), spray washers after defeathering and brush washers following inside and outside washing can be effective in lowering E. coli and coliforms counts on broiler carcasses. Similar results were reported by Sasaki et al. (48) for Campylobacter when using spray wash twice, with slightly acidified chlorinated water after evisceration; however, this process is not able to make carcasses free of Campylobacter. Therefore, the combination of washing carcasses with other control measures enables an efficient and reliable microbiological control (21).

In summary, Salmonella showed low prevalence in farm litter and was not present in the intestine and carcass of broiler. C. jejuni and C. coli (but not C. lari) were prevalent in farm litter, intestine contents, and in carcasses. Based on these findings, the applied Salmonella control measures are effective in the control of Salmonella along the broiler chain, but it is not effective in the control of Campylobacter. Therefore, additional controls during the slaughter process should be considered to reduce bacterial counts in broiler carcasses. Trimming visible fecal contamination reduced the prevalence of C. jejuni (70% decrease) but increased the prevalence of C. coli (52% increase). Furthermore, it did not affect the counts of Campylobacter or hygiene indicator microorganisms. The removal of visible fecal contamination using water wash reduced, by 20%, the counts of hygiene indicator microorganisms. Therefore, a systematic spray washing procedure can be used to reduce Campylobacter numbers on the carcass surface; however, the best approach would be to effectively use control measures for Campylobacter prevention throughout the production chain in addition to good hygienic practices.

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