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The impact of key processing stages and flock variables on the prevalence and levels of \textit{Campylobacter} on broiler carcasses

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\textbf{ABSTRACT}

This study examined the impact of key processing stages and flock variables on the prevalence of \textit{Campylobacter} on broiler carcasses. Overall, the prevalence of \textit{Campylobacter} was 62% in caeca, and 68%, 65% and 62% in neck skin samples collected after evisceration, final wash and carcass chilling, respectively. \textit{Campylobacter} were found in 32% of caeca, and 52%, 40% and 32% of neck skin samples collected after evisceration, final wash and carcass chilling, respectively from first thin broiler batches. Final thin broiler batches were more frequently contaminated with prevalences of 83% found in caeca, 80% in neck skin samples collected after evisceration and 83% found in neck skin samples collected after both final wash and carcass chilling stages ($p < 0.05$). Thinning status had a significant effect on \textit{Campylobacter} counts with significantly higher counts observed in samples from final thin batches ($p < 0.05$). Highest \textit{Campylobacter} concentrations in neck skin samples were observed at the evisceration stage in both first and final thin samples, with counts ranging from 2.0 to 3.8 $\log_{10}$ CFU/g and 2.3 to 4.8 $\log_{10}$ CFU/g in first and final thin batches, respectively. All first thin samples had counts below the European Union (EU) Process Hygiene Criterion threshold level of 3 $\log_{10}$ CFU/g after chilling while 52% of final thin batches had counts above this limit.

\section{1. Introduction}

\textit{Campylobacter} is the main cause of bacterial foodborne gastroenteritis in the European Union with over 246,000 cases reported in 2018 (EFSA and ECDC, 2019) and the cost associated with it is in the European Union with over 246,000 cases reported in 2018 (EFSA, 2010a). In Ireland approximately 70 million chickens are produced each year (Enterprise Ireland, 2019) and both production and consumption of poultry meat is expected to increase by 2025 (Meat Industry Ireland, IBEC, 2016). The risk of foodborne disease, frequently caused by \textit{Campylobacter}, poses a significant challenge for the poultry industry (Sofos, 2008).

High \textit{Campylobacter} counts of up to $10^9$ CFU/g can be present in broiler caeca (Ijaz et al., 2018). During evisceration rupture or leakage of viscera can occur resulting in caecal contents contaminating carcasses and the processing environment (EFSA, 2011). Such contamination on carcasses can result in survival of \textit{Campylobacter} on raw poultry products during their shelf-life, potentially infecting humans. During broiler processing \textit{Campylobacter} may be exposed to a range of stresses, including high and low temperatures and oxidative stress which may affect survival. However, campylobacters are known to be well adapted to survive in food processing environments (Yahara et al., 2017).

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Adaptation to persist through the food chain is facilitated by high genotypic diversity (Hanson et al., 2018) and numerous virulence factors (Cantero et al., 2018). *Campylobacter* is able to survive moderate heat and exposure to high concentrations of oxygen and can survive for long periods during refrigerated storage (Humphrey et al., 2007). In addition, under unfavourable conditions it can also survive in a viable but non-cultural (VBNC) state (Bolton, 2015).

In 2018 the European Commission (EC) introduced a Process Hygiene Criteria (PHC) for *Campylobacter* on broilers (EC, 2017) requiring intervention if a threshold level of 1000 CFU/g for neck skin samples after chilling of carcasses in the processing plant is exceeded. The PHC limit applies to 50 samples from 10 consecutive sampling sessions (EFSA and ECDC, 2019) and initially a maximum of 20 samples were permitted to exceed 1000 CFU/g. The number of samples permitted to exceed the PHC limit will be reduced to 15 and 10 samples in 2020 and 2025, respectively. Based on an EFSA risk assessment, compliance with this PHC should reduce the public health risk of campylobacteriosis associated with raw chickens by 50% (EFSA, 2011). The objective of this research was to determine the prevalence of *Campylobacter* in caeca and on carcasses during the main stages of broiler processing. Another objective was to determine the relationship between *Campylobacter* counts in caeca and on corresponding carcasses after chilling. Up to date, data on the effect of key processing stages on *Campylobacter* prevalence and the relationship between *Campylobacter* counts in caeca and on carcasses is important to identify high risk stages and to predict which batches are more likely to exceed the PHC threshold level. In addition, the effect of a range of flock variables, including flock age, flock weight and thinning status on *Campylobacter* counts were also examined.

2. Materials and methods

2.1. Study design and samples collection

Samples were collected from a large broiler processing plant in Ireland over a 12 month period (October 2018 to September 2019). The factory processed approximately 12,000 broilers per hour. Samples were collected monthly and a total of 60 batches were sampled during the study, including 25 first thin batches and 35 final thin batches. Caeca (5 per batch) and neck skin samples (5 per batch) from the same batch were randomly collected under aseptic conditions and placed in sterile bags and containers. Neck skin samples (5 per batch) were collected at each of the following processing stages: (i) after evisceration, (ii) after final wash and (iii) after carcass chilling. Data collected for each batch included flock information such as date and time of sampling, flock age, mean live weight, flock size, first/final thin status, grower code and thinning status on *Campylobacter* and *Escherichia coli*. flock ages ranged from 33 to 41 days.

3 Results

3.1. Flock variables

A number of flock variables were recorded for each sampled batch, including flock age, flock live weight, flock size and first/final thin status and are summarized in Table 1. Flock ages ranged from 33 to 41 days while mean weights ranged from 1.7 to 2.8 kg. Flock sizes ranged from 4,504 to 45,459 birds. The results were divided into first and final thin batches.

Correlation coefficient values (r) above 0 indicated a positive relationship between a flock variable and *Campylobacter* counts at the different sampling stages. Significance of correlation was tested using regression analysis with the level of significance defined at p < 0.05. A
significant positive relationship between flock age and Campylobacter counts was observed ($r = 0.65$ for Campylobacter counts in caeca, $r = 0.60$, 0.55 and 0.65 for counts in neck skin samples collected after evisceration, after final wash and after carcass chilling, respectively). Also, a significant positive relationship between flock weight and Campylobacter counts was observed, which reflected the correlation between weight and age of broilers. There was no positive correlation observed between flock size and Campylobacter counts. Most of the broiler batches slaughtered at 33 and 34 days were Campylobacter negative, while older birds, particularly between 38 and 41 days were mostly Campylobacter positive (Fig. 1).

### Table 1
Mean flock variables in broiler batches sampled during the study ($n = 60$).

| First/final thin status | Number of sampled batches | Average flock age (days) ± SD | Mean live weight (kg) ± SD | Average flock size ± SD |
|-------------------------|---------------------------|------------------------------|----------------------------|-------------------------|
| First                   | 25                        | 34.2 ± 1.3                  | 1.9 ± 0.1                  | 15,859 ± 8,157          |
| Final                   | 35                        | 38.9 ± 1.8                  | 2.5 ± 0.3                  | 16,006 ± 9,140          |
| All samples             | 60                        | 36.9 ± 2.8                  | 2.2 ± 0.4                  | 15,944 ± 8,673          |

SD - standard deviation, n-number of sampled batches.

3.2. Prevalence and levels of Campylobacter in broiler caecal and neck skin samples at key processing stages

Fig. 2 summarizes the prevalence of Campylobacter observed in caeca and neck skin samples at key processing stages. Data for first and final thin samples and the overall prevalence for all batches are presented. The prevalence of Campylobacter was significantly higher in final thin batches compared with first thin batches ($p < 0.05$). In 46 of 60 batches Campylobacter was detected either in caeca or on neck skin sample. Neck skins from most of these batches were Campylobacter positive at all 3 processing steps (33/46). 29 out of 33 neck skin positive batches, including 3 first and 26 final thin batches, also had Campylobacter positive caeca. In these batches counts in caeca ranged between 6.1 and 9.3 log$_{10}$ CFU/g, Campylobacter counts in neck skin samples after evisceration, after final wash and after carcass chilling ranged from 2.0 to 4.8 log$_{10}$ CFU/g, 2.0 and 4.3 log$_{10}$ CFU/g and 2.5 to 3.7 log$_{10}$ CFU/g, respectively. A single first thin and 2 final thin batches had positive caeca with counts ranging from 5.0 to 8.8 log$_{10}$ CFU/g but the carcasses were not contaminated or were below the limit of detection of the enumeration method used in our study ($<2$ log$_{10}$ CFU/g for neck skin samples and $<4$ log$_{10}$ CFU/g for caeca samples). A single first thin batch had positive caeca with count of 4.5 log$_{10}$ CFU/g and neck skin contamination was detected at the evisceration step only with count of 3.7 log$_{10}$ CFU/g. One first thin batch had caeca and neck skin samples collected after evisceration and carcass washing that were Campylobacter positive with counts of 8.8, 3.6 and 2.8 log$_{10}$ CFU/g, respectively. One final thin batch had positive caeca and neck skin samples collected after final wash and after carcass chilling with counts of 5.1, 3.1 and 2.5 log$_{10}$ CFU/g, respectively. A further 2 batches had positive caeca and neck skin samples collected after evisceration and after the final wash with counts ranging from 6.8–5.5, 3.3–3.6 and 2–3 log$_{10}$ CFU/g, respectively. One first thin batch had only positive neck skin samples collected after the final wash with counts of 2.5 log$_{10}$ CFU/g. In total, 4 first thin batches had positive neck skin samples collected after evisceration and after the final carcass wash with counts ranging from 2.0 to 3.3 log$_{10}$ CFU/g and 2.0–4.0 log$_{10}$ CFU/g, respectively.

3.3. Campylobacter speciation

In total 554 isolates were speciated, 80 of which were from first thin broilers samples and 474 from final thin broiler samples. Fig. 3 presents results for each sampling point in first and final thin samples and in all batches tested. Table 2 presents the number of batches positive for C. jejuni, C. coli and other Campylobacter in the caeca and at different processing stages. C. jejuni was the most prevalent species and C. coli was the second most frequently confirmed species. Higher prevalences of C. coli (33%) were observed in isolates from first thin samples compared with final thin samples (8%).

3.4. Mean values of Campylobacter counts in caeca and at key processing stages in Campylobacter positive batches

Campylobacter counts in caeca and neck skin samples of positive batches at the various processing stages are presented in Table 3. Mean Campylobacter counts in caeca and neck skin samples at all processing stages in positive batches were significantly different when first and final thin batches were compared ($p < 0.05$). When reductions in Campylobacter counts in neck skin samples between processing stages were compared, statistically significant reductions in Campylobacter counts were observed in samples taken following final carcass washing compared to those taken after evisceration stage ($p < 0.05$).
Campylobacter counts found in caeca and in neck skin samples are summarized in Figs. 4 and 5, respectively. Most of the final thin samples had concentrations in caeca of over 8 log\(_{10}\) CFU/g. Highest Campylobacter counts were observed in samples immediately after evisceration, for both first and final thin batches. The majority of final thin samples had counts of Campylobacter in neck skin samples collected after evisceration of over 3 log\(_{10}\) CFU/g. After final wash most first thin samples had Campylobacter concentrations between 2 and 3 log\(_{10}\) CFU/g and most of the final thin samples had counts of over 3 log\(_{10}\) CFU/g. After carcass chilling all first thin samples had Campylobacter counts between 2 and 3 log\(_{10}\) CFU/g and 52% of final thin samples had Campylobacter counts of over 3 log\(_{10}\) CFU/g.

### 3.5. Campylobacter counts in caeca and on corresponding carcasses after chilling

A positive correlation (r\(^2\) = 0.54) was observed between Campylobacter counts in caeca and corresponding neck skin samples collected after chilling of carcasses (Fig. 6). A total of 18 caeca and corresponding neck skin samples were Campylobacter negative, while 32 were both positive. Five paired caecal samples were found to be Campylobacter positive while corresponding neck skin samples were negative. Conversely, 5 paired neck skin samples were Campylobacter positive even though corresponding caecal samples were negative (Table 4).

### Table 2

|                | C. jejuni | C. coli | Other Campylobacter |
|----------------|-----------|---------|---------------------|
| (n - nr of batches) |           |         |                     |
| Caeca          | 27        | 7       | 3                   |
| Neck skin after evisceration | 29        | 7       | 5                   |
| Neck skin after final wash   | 28        | 6       | 5                   |
| Neck skin after chill       | 25        | 6       | 6                   |

Campylobacter counts found in caeca and in neck skin samples are summarized in Figs. 4 and 5, respectively. Most of the final thin samples had concentrations in caeca of over 8 log\(_{10}\) CFU/g. Highest Campylobacter counts were observed in samples immediately after evisceration, for both first and final thin batches. The majority of final thin samples had counts of Campylobacter in neck skin samples collected after evisceration of over 3 log\(_{10}\) CFU/g. After final wash most first thin samples had Campylobacter concentrations between 2 and 3 log\(_{10}\) CFU/g and most of the final thin samples had counts of over 3 log\(_{10}\) CFU/g. After carcass chilling all first thin samples had Campylobacter counts between 2 and 3 log\(_{10}\) CFU/g and 52% of final thin samples had Campylobacter counts of over 3 log\(_{10}\) CFU/g.
4. Discussion

This study provides up to date data on Campylobacter prevalence in broilers at key processing stages. The information presented is likely to be useful for risk managers within the poultry industry and regulatory bodies enforcing relevant food hygiene legislation at a national level. In this study the average concentration of Campylobacter found in caeca was 7.9 log_{10} CFU/g for all positive samples investigated. Mean concentrations in positive samples from first and final thin batches was 6.8 and 8.2 log_{10} CFU/g, respectively. In comparison, Rosenquist et al. (2006) reported average counts of Campylobacter in caeca from four different flocks of 6.96, 6.65, 8.20 and 7.72 log_{10} CFU/g. In the current study a positive relationship between Campylobacter counts in caeca and on corresponding carcasses was observed ($r^2 = 0.54$, Fig. 6). Malher et al. (2011) reported that in some studies no correlation between Campylobacter counts in caeca and on carcasses was found, while in other studies higher correlation rates with $r$ values of 0.59 and 0.81 were reported.

Intestinal contents can be a source of contamination when viscera are ruptured during processing (EFSA, 2011). In this study highest counts of Campylobacter were observed after the evisceration stage of processing and similar observations have also been previously reported (Pacholewicz et al., 2016; Rosenquist et al., 2006). Another high risk processing stage is plucking (defeathering) due to potential contamination by leakage of faecal material (Hutchison et al., 2017; Pacholewicz et al., 2016). Furthermore, cross-contamination between carcasses can occur during processing, for example during carcass chilling (Humphrey et al., 2007; Allen et al., 2007; Wang et al., 2019). In the current study caeca from some batches were Campylobacter negative while corresponding neck skin samples were positive, which could indicate that Campylobacter counts in caecal contents were below the limit of detection or that cross-contamination during processing might have occurred. Sources of cross-contamination during processing include leakage or breakage of viscera during evisceration, machinery used during the defeathering step and processing of negative batches after positive batches (FSAI, 2011). Furthermore, sources of cross-contamination in the processing plant include contact between carcasses, equipment, water used during processing, for example from scalding tanks or chilling water, plant workers and air (Rasschaert et al., 2020). Campylobacter was detected in some slaughterhouses after cleaning and disinfection processes and corresponding neck skin samples was statistically significant ($p < 0.05$).

### Table 3

| Sample type                  | First/final thin status | Mean Campylobacter level (log_{10} CFU/g ± SD) |
|------------------------------|-------------------------|-----------------------------------------------|
| **Caeca**                    |                         |                                               |
| First (n = 8)                | 6.8 ± 1.6^a             |                                               |
| Final (n = 29)               | 8.2 ± 1.1^b             |                                               |
| All samples (n = 37)         | 7.9 ± 1.3               |                                               |
| **Neck skin after evisceration** |                         |                                               |
| First (n = 13)               | 2.9 ± 0.6^a             |                                               |
| Final (n = 28)               | 4.1 ± 0.5^b             |                                               |
| All samples (n = 41)         | 3.7 ± 0.8               |                                               |
| **Neck skin after final wash** |                         |                                               |
| First (n = 10)               | 2.4 ± 0.7^a             |                                               |
| Final (n = 29)               | 3.3 ± 0.5^b             |                                               |
| All samples (n = 39)         | 3.0 ± 0.7^c             |                                               |
| **Neck skin after chill**    |                         |                                               |
| First (n = 8)                | 2.5 ± 0.5^a             |                                               |
| Final (n = 29)               | 3.0 ± 0.4^b             |                                               |
| All samples (n = 37)         | 2.9 ± 0.5^c             |                                               |

SD = standard deviation, mean counts with superscripts a and b are significantly different (based on t-test, $p < 0.05$). ^c significant reduction of Campylobacter counts compared to previous stage based on t-test ($p < 0.05$).

**Fig. 4.** Campylobacter counts in caecal contents in Campylobacter positive batches.

**Fig. 5.** Campylobacter counts in neck skin samples in Campylobacter positive batches. * 3.0 log_{10} - the threshold of the EU PHC.
some strains were reported to persist in the processing environment even after cleaning (Raschaert et al., 2020), which could also lead to cross-contamination. Neck skin samples which were not positive at all stages of processing could have contained low levels of Campylobacter below the limit of detection. Batches containing negative caeca but with contaminated neck skin samples suggest that the skin samples could have become positive as a result of cross-contamination from positive batches processed earlier in the day in the factory or that levels in the caeca were below the limit of detection. Allen et al. (2007) reported cross-contamination on carcasses from Campylobacter negative broilers. In the study conducted by Allen et al. (2007) some carcasses became cross-contaminated even when a preceding flock was negative and the authors indicated that cross-contamination may occur at various points of processing. Allen et al. (2007) and Duffy et al. (2014) reported variable concentrations of Campylobacter within flocks at various sampling points. Possible reasons for this variability are different concentrations of Campylobacter in caeca, differences in stress response of bacteria and variable levels of contamination occurring during evisceration (Allen et al., 2007).

In the EU baseline survey on Campylobacter in broilers conducted in 2008 the reported prevalence of Campylobacter in broiler batches in Ireland was 83.1% (EFSA, 2010b). In the current study the overall Campylobacter prevalence in broiler batches after chilling was lower, at 62%. However, there was a significant difference in prevalence in first (32%) and final thin batches (83%) (p < 0.05). Thinning or partial depopulation is used by poultry producers to maximise economic yield (Humphrey et al., 2007). Depopulation was previously reported as a risk factor in Campylobacter colonization of birds (Hermans et al., 2011; Sibanda et al., 2018). Thinning may increase the number of positive flocks at slaughter age, which will lead to a higher number of positive carcasses. In this study depopulation also had a significant impact on Campylobacter prevalence and the level of contamination (p < 0.05). In a study conducted by Rosenquist et al. (2006) highest Campylobacter counts in caecal contents were observed in flocks which also had the highest numbers of positive birds while lower counts of Campylobacter were observed in flocks with a low prevalence. In the current study samples from first thin broilers had significantly lower Campylobacter counts compared to final thin broilers (p < 0.05), which could be determined by the stage at which the pathogen is introduced to a production unit on farm. Also, first thin broilers were slaughtered at a younger age, which could also have an impact on colonization. Slaughter age has previously been reported as a risk factor for Campylobacter on broiler carcasses (Hue et al., 2011; Gölz et al., 2014; Hutchison et al., 2017). In the current study first thin broiler batches had a mean age of 34.2 days compared with 38.9 days in final thin broilers. Weight also had a positive correlation with Campylobacter counts. Birds with higher weight had higher Campylobacter counts most likely due to these birds coming from older flocks which had already been thinned. Positive correlation between Campylobacter counts, thinning status and age of broilers was observed in the current study. These variables were previously reported as risk factors for Campylobacter contamination in broilers (Hermans et al., 2011; Hutchison et al., 2017). The impact of variable weight of carcasses on Campylobacter counts was reported by Malher et al. (2011). Pacholewicz et al. (2016) observed that differences in weight of broilers might affect performance of the equipment in the slaughterhouse. It can be difficult to adjust evisceration equipment to variable weight of carcasses (2011) and final thin broilers. Depopulation was previously reported as a risk factor for Campylobacter contamination in broilers (Hermans et al., 2011; Hutchison et al., 2017). The impact of variable weight of carcasses on Campylobacter counts was reported by Malher et al. (2011). Pacholewicz et al. (2016) observed that differences in weight of broilers might affect performance of the equipment in the slaughterhouse. It can be difficult to adjust evisceration equipment to variable size of carcasses and as a result damage to the intestines might occur causing excessive Campylobacter contamination (the PSAI, 2011). C. jejuni was the most prevalent species recovered from caecal and neck skin samples (80%) followed by C. coli (11%). Similar results were reported by Hue et al. (2011). From some neck skin samples both C. coli and C. jejuni were isolated. A higher proportion of C. coli was observed in first thin broilers compared to final thin batches. Higher relative prevalences of C. coli in younger birds and higher prevalence of C. jejuni in older birds was reported previously in a longitudinal study carried out on turkeys (Wright et al., 2008). The higher proportion of C. coli detected in first thin broilers also suggests that there might be differences in the gut microbiome of first and final thin broilers. Poultry microbiome studies have recently been conducted using sequencing methods, however, genetic variation is still not well understood and further studies are required to gain more data on Campylobacter colonization in broilers (Sakaridis et al., 2018). High variation in microbiome profiles has been reported in birds from the same flock, even though the birds were of the same age and were on the same diet (Sakaridis et al., 2018). In a recent study conducted by Babacan et al. (2020) age was found to be a significant factor in colonization of birds

Table 4
Campylobacter prevalence in neck skin samples and corresponding caeca expressed as numbers positive/negative and percentage positive.

| Caeza contents | Neck samples |  |  |
|----------------|--------------|----------------|----------------|
|                | Negative     | Positive       | Total          |
| Negative       | 18 (78%)     | 5 (22%)        | 23             |
| Positive       | 5 (14%)      | 32 (86%)       | 37             |
| Total          | 23           | 37             | 60             |

Fig. 6. Plot of Campylobacter counts in caeca and corresponding neck skin samples.
slaughtered at 38–41 days, which were more frequently colonized by *C. jejuni* compared with older birds slaughtered at 49–56 days that were more frequently colonized by *C. coli*. First thin batches are typically slaughtered at 33–35 days old, while final thin batches at 38–41 days old and further study to investigate colonization in younger broilers could provide additional information on factors that may influence the species of Campylobacter colonising chickens. In a study conducted by Duffy et al. (2014) either *C. jejuni* or *C. coli* were found to be the prevalent species in individual flocks. These authors also reported an increased proportion of *C. coli* through the stages of processing with the highest proportion present after chilling compared to samples taken before scalding or chilling. In the current study such an increase was not observed in first thin samples, while the number of *C. coli* increased in samples from final thin batches which was present in 7 samples collected after evisceration, in 4 samples collected after carcass washing and 9 after chilling. This could suggest that *C. coli* is better adapted to survive the stresses experienced during processing (Duffy et al., 2014).

In some studies significant reductions in the level of Campylobacter were observed after both washing and chilling stages (Rosenquist et al., 2006; Chen et al., 2020). This demonstrates that these stages are important in reducing *Campylobacter* counts and helping to achieve *Campylobacter* counts that would comply with the European PHC. In the current study significant reductions in counts of *Campylobacter* in neck skin samples were observed after final carcass washing compared to the previous processing stage. Thus, monitoring of these stages and possibly some modifications of chilling parameters could contribute to reduced *Campylobacter* counts. The application of crust freezing (also referred to as rapid surface chilling) has been suggested as it was found to significantly reduce *Campylobacter* counts on raw chicken by 0.5–1.5 log_{10} (Haughton et al., 2012). While crust freezing does not achieve as low a reduction in counts as freezing it has the advantage of allowing the birds to be marketed as fresh chilled birds (Regulation (EC) No. 543/2008). *Campylobacter* remains the main bacterial cause of gastroenteritis worldwide. It has been estimated that quantitative reductions in *Campylobacter* concentrations on poultry carcasses would result in fewer human cases of campylobacteriosis compared to reductions in the numbers of *Campylobacter* positive carcasses (Gölz et al., 2014). Our study shows that more than half of chilled carcasses from final thin batches were above the PHC limit with average *Campylobacter* counts of 3.0 log_{10} CFU/g which may pose a risk for consumers. In the EU baseline survey (EFSA, 2010b) 33% of broiler carcasses in Ireland had *Campylobacter* counts of 3–4 log_{10} CFU/g and 8.9% of carcasses had counts of over 4 log_{10} CFU/g. Updating monitoring systems and some interventions during processing, for example adjusting evisceration equipment, temperatures of rinse water and introduction of crust freezing might be expected to reduce *Campylobacter* counts on carcasses. However, the scope of interventions to reduce *Campylobacter* concentrations on carcasses can be limited due to unacceptable changes in sensory characteristics, consumer acceptance of possible interventions (for example irradiation) (Hansson et al., 2018) and regulatory barriers (Humphrey et al., 2007). The monitoring of *Campylobacter* in broilers is of great importance to assess risk and limit contamination. In addition, it has been previously reported that risks associated with *Campylobacter* contamination might vary between slaughterhouses and monitoring of bacterial counts at different processing stages is important to allow critical control points to be adjusted as necessary (Pacholewicz et al., 2016; Rosenquist et al., 2006).

This study will further inform broiler processors and regulators about the influence of key processing stages on the relationship between *Campylobacter* counts in caeca and on carcasses at various stages during processing. It can also be used to update food safety management systems by identifying where additional controls or monitoring procedures could be applied in the process to reduce contamination and lower the risk for consumers associated with the handling and consumption of poultry products. This study also contributes important data that can be used to inform processors about contamination risks and compliance with the Process Hygiene Criteria.

**Declaration of competing interest**

None.

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