Animal &
Plant Health
Agency

Descriptive analysis of the results of the monitoring programme for *Campylobacter* in broiler flocks and broiler carcases in the UK

For the period

January 2016 to March 2017

(FS101126)

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Introduction

In response to the joint Government and Industry target to reduce the percentage of chickens with more than 1,000 colony forming units (cfu) per gram (g) of *Campylobacter* on carcases from 27% in 2008 to 10% by end of 2015. APHA have been independently monitoring the progress towards achievement of the target, which was subsequently rolled into 2016.

The monitoring programme aims to identify differences in prevalence and/or levels of *Campylobacter* contamination and production practices within the UK broiler population which could potentially be used to target further and more intensive investigations aimed at identifying 'protective' factors in controlling *Campylobacter* in the slaughterhouse.

This report describes the epidemiology of the broiler slaughter batches collected from January 2016 through to March 2017 (inclusive) under project FS101126.

Methods

Survey design and population

The survey design and sampling methods are consistent with the technical specifications annexed in Decision 2007/516/EC and therefore comparable to the EU baseline survey in 2008.

Sample size calculations were carried out in Stata to determine the number of slaughter batches that needed to be sampled to detect a change in the prevalence of highly contaminated batches from an expected prevalence of 27% to the reduction target of 19% (2013 target), as this target has not been achieved the sampling calculation from the previous monitoring (2012-2015) remains valid. A total of 458 samples were needed to detect an 8% reduction in prevalence, with 80% power and 0.05 significance, each year (using a one-sided test). In summary, 504 slaughter batches were scheduled for collection each year (458 plus 10% to account for non-responses and ineligible batches), so that a significant change in prevalence of the target contamination threshold could be detected.

The slaughter batches originated from 19 abattoirs representing more than 80% of the broiler production throughput in the UK (based on previous data). Samples were scheduled to be collected by trained staff in the Food Standards Agency in GB and by the Veterinary Public Health Unit of DARD in NI.

The schedule for sampling was randomised and weighted according to throughput to ensure that the number of slaughter batches to be sampled per abattoir was proportional to the broiler throughput processed by the abattoir. To avoid seasonal bias, sampling was distributed throughout the year with 1/12th of the total samples taken each month. The random selection was generated from a database in Microsoft© Access. The sampling day and batch to sample was randomly chosen based on the opening hours of the abattoir and maximum numbers of batches that the abattoir processed per day. One carcase per slaughter batch was sampled after chilling and before further processing. In addition to the carcase sample, ten birds were

sampled at the evisceration point and caecal samples collected for *Campylobacter* quantification.

Microbiological methods

Both, caecal and carcase (neck and breast skin) samples were tested for detection and quantification of *Campylobacter* following ISO10272:2006 part 2 and ISO 7218:2007, respectively. The quantity of neck skin available to be sampled from each carcase was recorded and breast skin was used to supplement the sample when there was less than 27g of neck skin available. Confirmation and speciation of *Campylobacter* was undertaken either as described in ISO 10272:2006 or by matrix assisted laser desorption ionisation (MALDI). One isolate from positive caeca and carcase samples was fully identified to species level and stored for further typing. The limit of detection was 5 cfu/g of broiler neck-skin or caecal content. Counts between 5 and 45 were considered estimated results.

Data collection

A standardised data collection form was completed by trained personnel after sampling the slaughter batch. Information relating to the flock of origin was collected for each slaughter batch including:

- Parent company
- Abattoir identifier
- Farm name and address
- Time of collection of birds from farm
- Time of arrival of the birds at the abattoir
- Time of unloading birds
- Time at which processing began
- Time at which processing ended
- Production type (conventional, free range or organic)
- Number of birds in the slaughter batch
- Shed number
- Age of birds
- Average weight of birds
- Type of crate used to transport birds to abattoir (open floor, solid of both)
- Flock mortality at 14 days of age (% of birds)

- Flock mortality at 72 hours before slaughter (% of birds)
- Rejects from slaughter batch (% of birds)
- Reasons for condemnation (conditions: ascites, skin lesions, joint lesions, septicaemic carcase, perihepatitis/peritonitis, pericarditis, emaciated, over scalded carcase, bruised carcase, badly bled carcase, cellulitis, culls, dead on arrival, dermatitis and other)
- Line speed (birds slaughtered per hour)
- Approval scheme
- Supplier (company or independent)

All of the data and laboratory results from the slaughter batches sampled were entered onto a bespoke Microsoft© Access database and collated and analysed.

Eligibility criteria

Samples were required to be tested within 80 hours of collection and therefore any batches tested outside of this deadline were excluded from the analysis. A slaughter batch was defined as a quantity of broilers raised in the same house/shed/range and delivered to the abattoir in the same vehicle. Only slaughter batches consisting of birds from the same flock were eligible for inclusion in the analysis.

Analysis

Data were analysed using Stata v. 12 (StataCorp, USA).

The outcome in the descriptive univariable analysis was a highly contaminated *Campylobacter*-positive slaughter batch (> 1,000 cfu/g). The baseline group included all slaughter batches that were either negative for *Campylobacter* or had counts of 1,000 cfu/g or less. Continuous variables were recoded as categorical variables as per previous analysis so that comparisons could be made to previous reports. The exposure ‘recent mortality (%)’ was calculated by subtracting ‘mortality at 14 days (%)’ from ‘mortality at 72 hours before slaughter (%)’. Univariate analysis, with calculation of odds ratios, was used to estimate the statistical significance (P value) of crude associations between exposure variables and *Campylobacter* status χ^2 test.

Results and discussion

Prevalence and quantification of *Campylobacter* on carcases

A total of 622 carcases were sampled and enumerated for *Campylobacter*. Of these, 618 (99.4%) were eligible for inclusion in the survey. Four batches were excluded from the analysis due to either technical issues in the laboratory (n=3) or the batch exceeding 80 hours between sample collection and arriving for processing in the laboratory (n=1).

Nineteen abattoirs, associated with eleven parent companies, participated in the survey. The number of slaughter batches sampled at each abattoir varied from 10 to 77 slaughter batches over the fifteen months.

Slaughter batches originated from 431 individual farms and approximately a third of the farms (31.6%) were sampled more than once. The number of batches sampled from a farm ranged from one to six and 8.6% of farms had three or more slaughter batches sampled. The majority of eligible slaughter batches originated from conventionally reared broilers (93.9%) with the remainder coming from free-range (5.8%) and organic farms (0.3%). Only five abattoirs processed birds that came from free-range or organic farms and these abattoirs also processed conventional broilers.

Overall, 410 (66.3%) of the carcases were positive for *Campylobacter. C. jejuni* was identified on 56.5% (n=349) of the carcases and a smaller proportion had *C. coli* (9.9%; n=61). Table 1 shows the enumeration results and compares the data to the 2008 baseline survey and the monitoring survey 2012/15 (Project FS241051). A small decrease between 2008 and 2016-17 can be seen in the band 3 prevalence from 26.3% to 25.1%, however this is not statistically significant. In addition, the distribution of the band 1 and band 2 results has shifted significantly, with band 1 increasing (9.8% vs 15.9%; p=0.005) and band 2 decreasing (32.3% vs. 25.4%; p=0.02) when compared with the baseline survey. The median log of the positive batches has not changed significantly over time.

A timeline showing the prevalence of all batches collected since March 2012 through to March 2017 is shown in Figure 1. Historically the highest prevalence of highly contaminated carcases was seen in August 2012 and in the study period for this report (January 16-March 17) the highest prevalence of highly contaminated carcases was seen in December 2016 (35.1%). The 2015 target of 10% was not reached in any month but in both January 2016 and March 2016 it reached the lowest prevalence of 16.7%. Similarly, in the last fifteen months the 2013 target was not reached and only on two occasions (January 2016 and March 2016) did it fall below the 2013 target.

All abattoirs were found to have carcases that were considered to be highly-contaminated (>1,000 cfu/g). Eighteen of the nineteen abattoirs, processed negative batches and three abattoirs only had one negative batch. All abattoirs processed some positive batches that had counts≥100 cfu/g (bands 2 and 3).

The age of the birds in the slaughter batch ranged from 27 days to 70 days (average age 38 days). The mean age of *Campylobacter*-positive birds was 39 days ($CI_{95\%}$ 38.5 – 39.7 days) compared to 36 days ($CI_{95\%}$ 35.8 – 37.6 days) for *Campylobacter*-negative birds.

Univariable analysis

Thirty-eight variables were tested in the univariable analysis and 14 showed an association ($p<0.05$) with highly *Campylobacter*-contaminated carcases (Table 2). The statistically significant variables include abattoir, parent company, age category, chiller method, neck skin weight, number of birds in the slaughter batch, recent mortality, crate type, line speed and several reasons for condemnation. The variables which have consistently shown to have an association in both this analyses and previous analyses are shown below and conversely those that have not shown an association in any analyses are also detailed below. These variables will be investigated further in the multivariate risk factor analyses when the full dataset of monitoring data is analysed.

Summary of variables used in the univariable analysis for association with highly contaminated carcases

Variables that were significant in this analysis and full four year analysis	Abattoir	Dermatitis
	Parent Company	Ascites
	Chilling method	Cellulitis
	Neck skin weight (g)	Line Speed
	Age category	Processing damage
	Recent mortality	Dead on arrivals
	No. of birds in slaughter	Culls/runts
Variables that were not significant in either analysis	Month	Perihepatitis/peritonitis
	Season	Septicaemic carcase
	Stress	Pericarditis
	Other reasons for	Bruised/fractures
	Rejects	Contaminated carcase
	Sampled slaughter batch	Supplier
	Hepatitis	Emaciated

The analyses of fifteen months of data mirrored what has been seen before with respect to season. A summer seasonal increase in odds ratio is observed when analysing presence/absence of *Campylobacter* (data not shown), however there is no statistical significant seasonal pattern when the outcome variable is highly contaminated carcases.

The weight of the neck skin used for the carcase sample was recorded and analysed in this survey. Six abattoirs left less than 10g of neck skin on the carcase in 50% or more of the slaughter batches. At one abattoir (AQ), thirteen of the fourteen batches sampled had less than 10g of neck skin. Conversely another abattoir (AN) had only trimmed one of their batches as 94.7% of the batches had over 20g of neck skin available. Both of these abattoirs had less than 25 batches sampled. The mean neck skin weight (g) available per slaughter batch had shown a declining trend in previous analyses, however, in the past fifteen months this trend has reversed (Figure 2). Interestingly, the box plot in Figure 3 shows a higher mean amount of neck skin on highly contaminated carcases (band 3) adding further evidence that trimming the neck skin may result in reduced prevalence of highly contaminated carcases.

Quantification of *Campylobacter* in caecal samples

Of the 622 caecal samples collected during the fifteen month survey, 613 were eligible for inclusion in the analysis. Batches were deemed ineligible due to a number of reasons including incomplete sample (n=5), over 80 hours between sample collection and testing at the laboratory (n=2) and technical errors in the laboratory (n=2). The overall prevalence of *Campylobacter* in caecal samples was 70.6% (n=433), which was similar to that found in the previous years of monitoring (Table 3), and continues a subtle downward trend. There was a statistically significant difference (p=0.01) between 2013/14 (81.8%) and 2016/17 (70.6%). However, it is worth noting that the 2013/14 period ran from March 2013 to February 2014, whilst the 2016/17 period ran from January 2016 to March 2017. Therefore the 2016/17 group contains more

batches from the winter period than the 2013/14 group, and *Campylobacter* prevalence is lowest in winter months. *C. jejuni* was isolated from 54.3% (333 batches) and *C. coli* from 16.3% (100 batches).

The median log of both the positive batches and all the batches included in the analysis was 8 logs cfu/g or more indicating a high load of *Campylobacter* entering the abattoir (Table 3). There has been no significant reduction in the median or mean caecal enumeration results since monitoring began in 2012. Caecal samples originating from 14 of 19 abattoirs had counts greater than 9 log cfu/g.

The mean and median *Campylobacter* count of positive samples was very similar across the three production types. In conventional flocks the mean and median was 8.24 log cfu/g and 8.43 log cfu/g respectively, compared to the mean and median for free-range and organic flocks, of 8.21 log cfu/g and 8.34 log cfu/g.

In this survey 50.4% of all slaughter batches were colonised with 8 log cfu/g and above in caecal contents, which was similar to findings in previous years; 2012/13 (45.5%), 2013-14 (52.9%), 2014-15 (52.9%) and March 2015-December 15 (44.8%) (Table 3).

Comparison of batches with eligible carcase and caecal samples

In total, 611 slaughter batches were eligible for inclusion in the analyses when both sample types (carcase and caeca) were considered. The results are shown in Table 4 and indicate that 378 (61.9%) slaughter batches were positive for *Campylobacter* spp. using results from both sample types and 153 (25.0%) were negative by both methods.

Campylobacter spp. were cultured from the carcase of 27 batches from which *Campylobacter* was not detected in the caeca. Conversely, in 53 batches *Campylobacter* was detected in the caeca but not from the carcase in the same slaughter batch.

For all abattoirs, *Campylobacter* counts obtained by caecal sampling and those obtained by carcase sampling were positively correlated; indicating that if high levels were found in the caeca, high levels were also found on the carcase. It is interesting to note that some abattoirs had high caecal counts but negative carcases, indicating that contamination of some carcases from the supply flock was prevented in the abattoir. However, abattoirs may also have batches that had negative caeca but positive carcases; suggesting that these batches were cross-contaminated by *Campylobacter* from the slaughter line. In addition, the overall prevalence of *Campylobacter* in caecal samples taken at each abattoir was broadly similar to the carcase prevalence (Figure 4).

A comparison of the monthly mean carcase and caecal contents counts is shown in Figure 5. A seasonal peak in the mean counts is seen in July and August for the caeca and carcase, respectively. The mean carcase cfu/g for August is particularly high due to two samples from two separate abattoirs that had counts in excess of 400,000 cfu/g.

Concluding summary

- There is no evidence of any significant reduction in the production of highly contaminated carcases since 2008. However, there has been a slight decline in production of highly contaminated carcases since a peak in 2012.
- No new risk factors associated with production of contaminated carcases have been identified in the univariable analysis beyond those found in the 2012-15 analysis. A multivariable analysis of risk factors is to follow at the end of this project.
- The trend of declining neck-skin due to trimming at plants appears to have halted, but an increasing quantity of neck skin available to sample appears to increase the odds of the carcase being designated as highly contaminated.
- The prevalence of *Campylobacter* in flocks entering abattoirs is showing a downward trend and when comparing the proportion of slaughter batches that were positive in 2013/14 (March 2013 - February 2014) with 2016/17 (January 2016 - March 2017) there was a statistically significant difference. However the level of colonisation in positive flocks appears unchanged.
- A positive correlation was noted in samples from all abattoirs between *Campylobacter* levels in flocks (cfu/g. caecal contents) and levels in the carcases from these flocks.

Table 1 – *Quantification of Campylobacter on broiler carcases*

	Prevalence % (no. of batches)			Median log cfu/g			Mean log cfu/g		
	2008 survey	2012/15 survey	2016/17 survey	2008 survey	2012/15 survey	2016/17 survey	2008 survey	2012/15 survey	2016/17 survey
Band 1 (≥5 and <100 cfu/g)	9.8 (39)	15.6 (290)	15.9 (98)	1.65	1.54	1.60	1.62	1.47	1.49
Band 2 (100-1,000 cfu/g)	32.3 (129)	32.3 (601)	25.4 (157)	2.59	2.58	2.53	2.64	2.54	2.52
Band 3 (>1,000 cfu/g)	26.3 (105)	28.5 (530)	25.1 (155)	3.57	3.53	3.63	4.03	3.67	3.80
Positive	68.3 (273)	76.4 (1,421)	66.3 (410)	2.83	2.75	2.70	3.63	2.74	2.75
Negative	31.8 (127)	23.6 (440)	33.7(208)						

Figure 1 – *Prevalence of highly contaminated carcases from monitoring results (Mar 2012 – Mar 2017)*

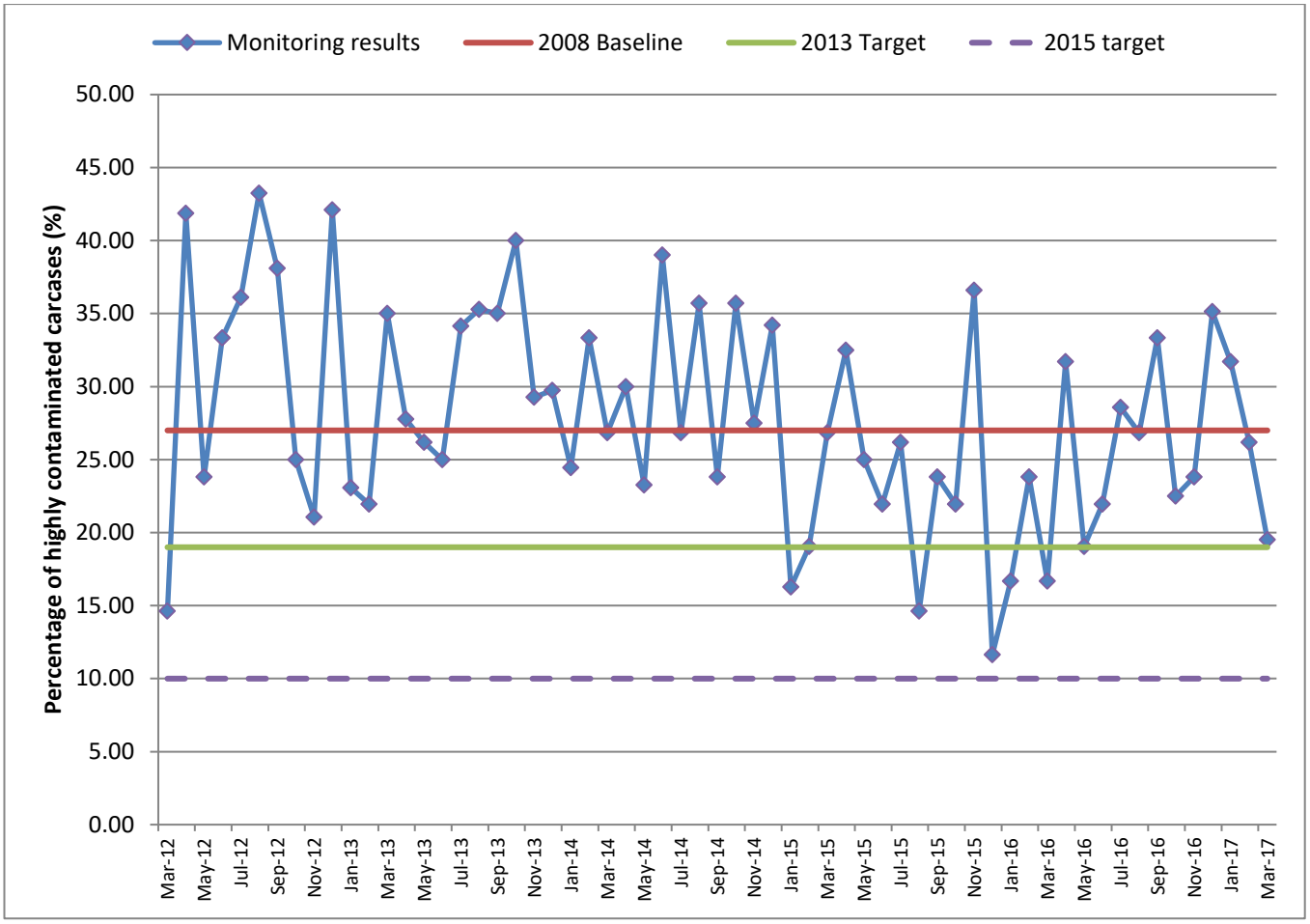

Table 2 – ***Univariable analysis: association between exposure variables and highly Campylobacter-contaminated carcases (>1,000 cfu/g)***

Variable (number of batches)		Highly contaminated carcases* (%)	Crude Odds Ratio	$CI_{95\%}$	Chi-squared p-value
Abattoir					**<0.0001**
	AA	10.0	0.67	0.07-6.12	
	AB	27.3	2.25	0.66-7.64	
	AC	14.3	1.00		
	AD	26.5	2.16	0.73-6.40	
	AE	16.1	1.15	0.42-3.18	
	AF	5.3	0.33	0.09-1.19	
	AG	29.2	2.47	0.91-6.68	
	AH	60.0	9.00	1.79-45.34	
	AI	68.8	13.2	2.89-60.37	
	AJ	57.9	8.25	2.21-30.84	
	AK	51.7	6.43	2.04-20.22	
	AL	8.6	0.56	0.14-2.31	
	AM	31.8	2.80	0.84-9.30	
	AN	68.4	13.00	3.06-55.00	
	AO	48.2	5.57	1.70-17.57	
	AP	13.8	0.96	0.26-3.53	
	AQ	35.7	3.33	0.85-13.09	
	AR	11.4	0.77	0.27-2.23	
	AS	35.0	3.23	0.95-11.00	
Parent company					**<0.0001**
	1	31.8	2.87	1.06-7.75	
	2	57.9	8.45	2.94-24.20	
	3	16.1	1.18	0.54-2.60	
	4	10.0	0.68	0.08-5.63	
	5	35.7	3.41	1.05-11.10	
	6	68.8	13.51	3.99-45.81	
	7	60.0	9.21	2.32-36.61	
	8	14.0	1.00	.	
	9	29.2	2.53	1.19-5.36	
	10	12.5	0.88	0.45-1.72	
	11	48.4	5.77	3.14-10.61	
Chilling method					**0.0002**
	Air	28.4	1.00	.	
	Air & Spray (60)	8.3	0.23	0.09-0.59	
	Other/Spray (36)	8.3	0.23	0.07-0.77	
Neck skin weight (g)					**<0.0001**
	<10.0 g (270)	16.7	1.00	.	
	10.0 – 14.9 g (118)	21.2	1.34	0.78-2.32	
	15.0 – 19.9 g (100)	32.0	2.35	1.38-4.02	
	≥ 20.0 g (130)	40.8	3.44	2.10-5.63	

Variable		Highly contaminated carcases* (%)	Crude Odds Ratio	$CI_{95\%}$	Chi-squared p-value
Age category					**0.0009**
	<33 days (138)	20.3	1.00	.	
	34-36 days (142)	14.1	0.64	0.34-1.21	
	37-40 days (187)	32.1	1.86	1.10-3.13	
	41-44 days (78)	30.8	1.75	0.92-3.31	
	≥ 45 days (72)	31.9	1.84	0.96-3.54	
No. of birds in slaughter batch					**<0.0001**
	<5000 (156)	37.8	1.00	.	
	5000 - 5750 (165)	26.7	0.60	0.37-0.96	
	5751 - 6600 (148)	14.9	0.29	0.16-0.51	
	≥ 6601 (149)	20.1	0.41	0.25-0.70	
Processing damage					**0.0157**
(overscalded, badly bled carcase or machine damage)					
	< 0.040 % (147)	34.0	1.00	.	
	0.040 % - 0.150 % (190)	23.2	0.58	0.36-0.95	
	≥ 0.151 % (281)	21.7	0.54	0.34-0.84	
Crate type					**0.0002**
	Open (533)	22.1	1.00	.	
	Solid (46)	37.0	2.06	1.09-3.89	
	Solid and Open (37)	51.4	3.71	1.87-7.38	
	Not known (2)	50.0	3.52	0.22-56.93	
Microbiological testing					**0.0151**
Salmonella	No (112)	16.1	1.00	.	
	Yes (506)	27.1	1.94	1.12-3.34	
Recent mortality					**0.0158**
(mortality at 72 hours before	≤1.00 % (173)	17.9	1.00	.	
slaughter minus mortality at 14 days)	≥ 1.00 % (430)	28.4	1.81	1.16-2.83	
	Not known (15)	13.3	0.70	0.15-3.30	
Dermatitis					**0.0001**
	No (380)	30.5	1.00	.	
	Yes (238)	16.4	0.45	0.29-0.67	
Ascites					**0.0002**
	<0.100 % (188)	18.1	1.00	.	
	0.100 - 0.250 % (188)	20.7	1.18	0.71-1.98	
	≥ 0.250 % (242)	33.9	2.32	1.46-3.69	
Cellulitis					**0.0047**
	<0.016 % (165)	34.6	1.00	.	
	0.016 % - 0.099 % (137)	21.9	0.53	0.32-0.90	
	≥ 0.100 % (316)	21.5	0.52	0.34-0.79	
Dead on arrival					**0.0138**
	< 0.078 % (324)	21.0	1.00	.	
	≥ 0.078 % (294)	29.6	1.58	1.09-2.29	
Cull/runts					**<0.0001**
	No (296)	16.8	1.00	.	
	Yes (322)	34.1	0.39	0.26-0.57	

Variable		Highly contaminated carcases* (%)	Crude Odds Ratio	$CI_{95\%}$	Chi-squared p-value
Line Speed					**<0.0001**
(birds slaughtered per hour)	<8,501 (90)	50.0	1.00	.	
	8,501-9,999 (124)	31.5	0.46	0.26-0.81	
	10,000-10,500 (140)	24.3	0.32	0.18-0.58	
	≥ 10,501 (264)	14.0	0.16	0.09-0.29	
Mortality at 14 days					**0.1537**
	≤ 2.00 % (282)	28.7	1.00	.	
	>2.00 % (325)	22.2	0.71	0.49-1.02	
	Not known (11)	18.2	0.55	0.12-2.62	
Skin Lesions					**0.6451**
	No (470)	25.5	1.00	.	
	Yes (148)	23.7	0.90	0.59-1.39	
Time in transit					**0.9091**
	≤4 hours (585)	25.1	1.00	.	
	>4 hours (33)	24.2	0.95	0.43-2.16	
Quality assurance scheme					**0.1813**
	No (7)	14.3	1.00	.	
	Yes (610)	25.1	2.01	0.24-16.88	
	Not known (1)	100.0	-		
Sampled slaughter batch					**0.6077**
	First half of processing day (326)	24.2	1.00	.	
	Last half of processing day (292)	26.0	1.10	0.76-1.58	
Microbiological testing					**0.6332**
Campylobacter	No (91)	23.1	1.00	.	
	Yes (527)	25.4	1.14	0.67-1.92	
Month					**0.6940**
	January (83)	24.1	1.00	.	
	February (84)	25.0	1.05	0.52-2.13	
	March (83)	18.1	0.69	0.33-1.48	
	April (41)	31.7	1.46	0.64-3.37	
	May (42)	19.1	0.74	0.29-1.87	
	June (41)	22.0	0.89	0.36-2.18	
	July (42)	28.6	1.26	0.54-2.92	
	August (41)	26.8	1.16	0.49-2.73	
	September (42)	33.3	1.58	0.69-3.58	
	October (40)	22.5	0.91	0.37-2.25	
	November (42)	23.8	0.98	0.41-2.36	
	December (37)	35.1	1.71	0.73-4.00	
Season					**0.7021**
	Winter (204)	26.58	1.00	.	
	Spring (166)	21.7	0.77	0.47-1.25	
	Summer (124)	25.8	0.97	0.58-1.61	
	Autumn (124)	26.6	1.00	0.61-1.67	
Hepatitis					**0.7821**
	No (297)	24.6	1.00		
	Yes (321)	25.6	1.05	0.73-1.52	

Variable		Highly contaminated carcases* (%)	Crude Odds Ratio	$CI_{95\%}$	Chi-squared p-value
Stress (Time from collection at farm to slaughter)					**0.7668**
	<2.51 hours (161)	23.0	1.00	.	
	2.51 - 3.50 hours (174)	24.1	1.07	0.64-1.77	
	3.51 - 4.50 hours (139)	28.1	1.31	0.75-2.21	
	≥ 4.51 hours (144)	25.7	1.16	0.69-1.96	
Rejects					**0.7323**
	≤1.22% (222)	24.3	1.00	.	
	>1.22% (395)	25.6	1.07	0.73-1.56	
Perihepatitis/peritonitis					**0.1595**
	<0.021% (200)	25.0	1.00	.	
	0.021 % - 0.075 % (201)	20.9	0.79	0.50-1.27	
	≥0.0.76 % (217)	29.3	1.23	0.79-1.90	
Septicaemic carcase					**0.2873**
	<0.071 % (202)	28.7	1.00	.	
	0.071 % - 0.200 % (160)	25.0	0.83	0.52-1.33	
	>0.200 % (256)	22.3	0.71	0.46-1.09	
Pericarditis					**0.2057**
	No (511)	24.1	1.00	.	
	Yes (107)	29.9	1.34	0.84-2.14	
Bruised/fractures					**0.8544**
	No (323)	25.4	1.00	.	
	Yes (295)	24.8	0.97	0.67-1.39	
Contaminated carcase					**0.1203**
	No (200)	23.2	1.00	.	
	Yes (418)	29.0	0.74	0.51-1.08	
Joint lesions					**0.1200**
	No (374)	27.3	1.00	.	
	Yes (244)	21.7	0.74	0.51-1.08	
Production type					**0.0803**
	Conventional (580)	25.9	1.00	.	
	Free range and Organic (38)	13.2	0.43	0.17-1.14	
Other reasons for condemnation					**0.4071**
	No (155)	22.6	1.00	.	
	Yes (463)	25.9	1.20	0.78-1.85	
Supplier					**0.8342**
	Company (360)	25.6	1.00	.	
	Independent Grower (252)	24.2	0.93	0.64-1.35	
	Not known (6)	33.3	1.46	0.26-8.10	
Emaciated					**0.3253**
	No (434)	24.0	1.00		
	Yes (184)	27.7	1.22	0.82-1.80	
Mortality at 72 hours before slaughter					**0.2239**
	≤3.00 % (204)	22.1	1.00	.	
	> 3.00 % (410)	26.8	1.30	0.87-1.93	
	Not known (4)	0.00	0		

Figure 2 – *Mean neck skin weight (g) on sampled slaughter batch by month*

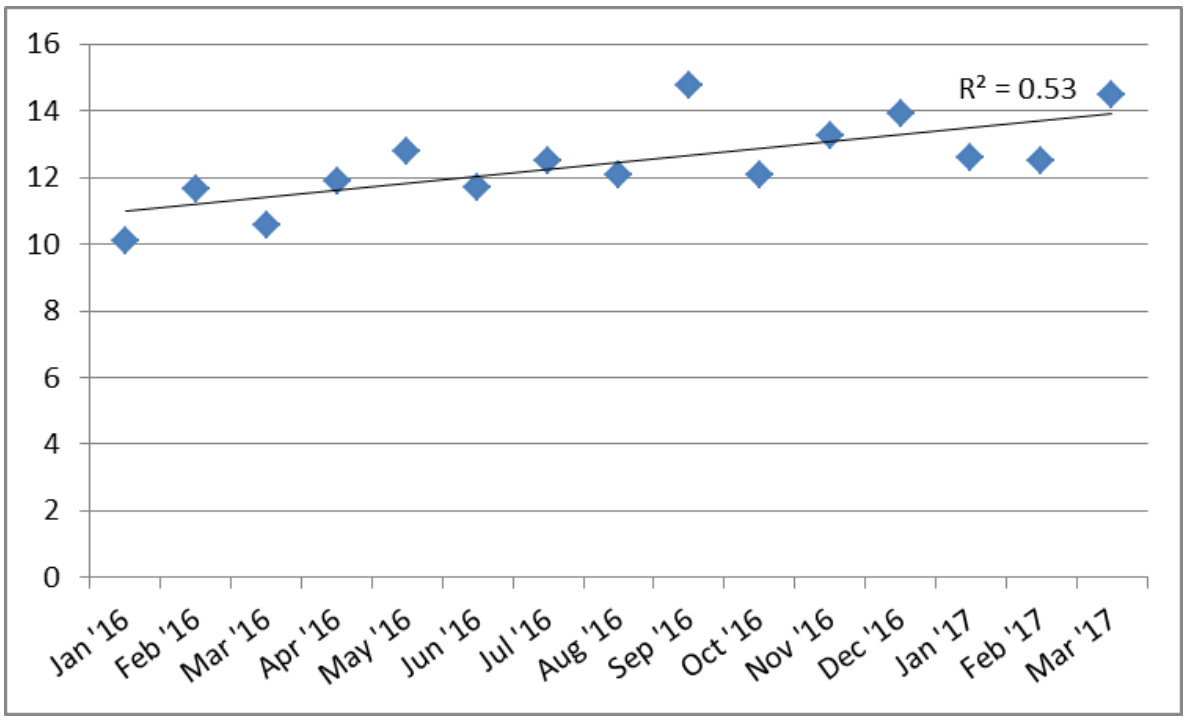

Figure 3 – *Box plot of neck skin (g) stratified by carcase result for Campylobacter contamination*

Band 0 = Negative
Band 1= >0 and <100 cfu/g
Band 2 = 100-1,000 cfu/g
Band 3 = >1,000 cfu/g

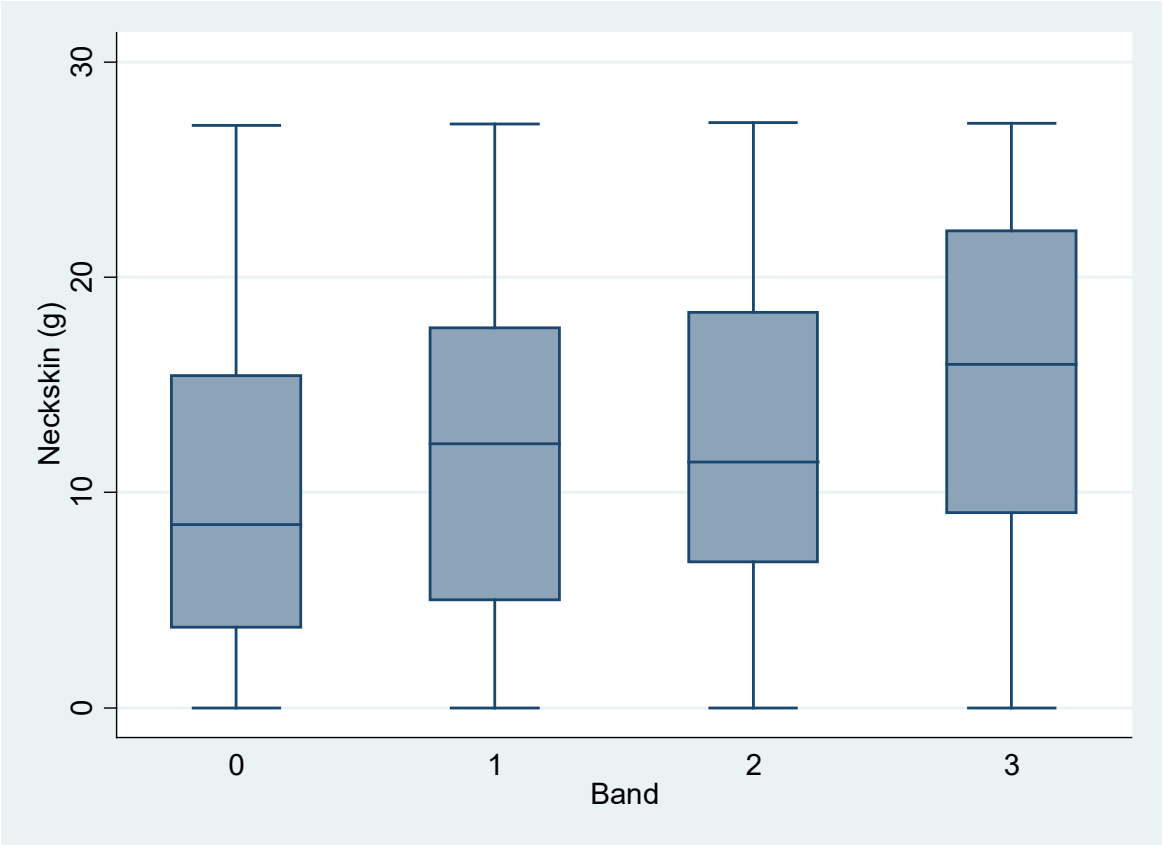

Table 3 – *Prevalence and enumeration results of Campylobacter* in caecal samples

		2012/13	2013/14	2014/15	2015/16*	2016/17**
Prevalence in caeca % (number of batches)	**Positive**	76.0 (92)	81.8 (99)	74.5 (363)	72.5 (301)	70.6 (433)
	Negative	24.0 (29)	18.2 (22)	25.5 (124)	27.5 (114)	29.4 (180)
Median log cfu/g of positive batches		8.23	8.37	8.30	8.16	8.42
Median log cfu/g of all batches		7.93	8.10	8.02	7.88	8.00
Mean log cfu/g (95% CI) of positive batches		8.05 (7.78 – 8.33)	7.94 (7.65 – 8.23)	8.14 (8.04 – 8.24)	7.97 (7.83 – 8.12)	8.24 (8.15 - 8.32)
Mean log cfu/g (95% CI) of all batches		6.12 (5.46-6.77)	6.50 (5.89-7.10)	6.07 (5.74-6.39)	5.78 (5.46-6.11)	5.82 (5.51–6.12)
Proportion of caecal samples with 8 log cfu/g and above (number of batches)		45.5 (55)	52.9 (64)	52.9 (253)	44.8 (186)	50.4 (309)

*= March 2015 – December 2015 **January 2016 - March 2017

Table 4 – *Agreement of Campylobacter detection in caeca and carcase from the same slaughter batch*

	Caeca result		
Carcase result	**Negative**	**Positive**	**Total batches**
Negative	153	53	206
Positive	27	378	405
Total batches	180	431	**611**

* Negative batches are where less than 5 cfu/g or no *Campylobacter* was detected.

Figure 4 – *Prevalence of Campylobacter in carcases and caeca by abattoir*

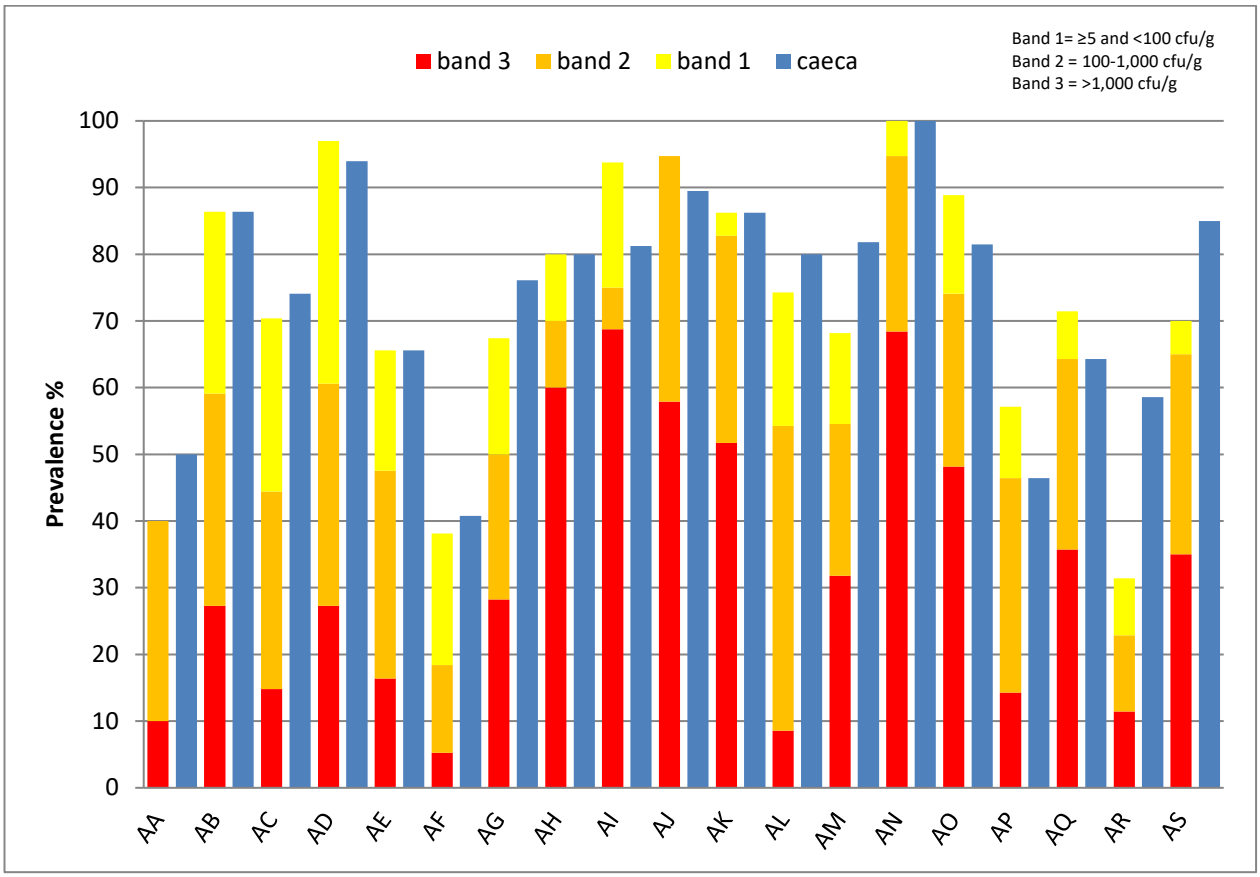

Figure 5 – ***Mean carcase and caeca Campylobacter counts (cfu/g), stratified by month***