



## The impact of primary and secondary processing steps on *Campylobacter* concentrations on chicken carcasses and portions

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### ABSTRACT

*Campylobacteriosis* is the most commonly notified foodborne disease in New Zealand and poultry meat is the major source for human infection. Carcasses and portions were sampled from key points along primary and secondary processing chains of three New Zealand poultry processors to determine the impact of processing steps on *Campylobacter* concentrations. Primary processing reduced *Campylobacter* concentrations on carcasses by almost 6-log; the biggest reduction was achieved by the spinchill, followed by the scald step. Significant plant differences in the degree of *Campylobacter* reduction were also observed at these steps. The spinchill and final acidified sodium chlorite wash resulted in carcasses with low-to-no levels of *Campylobacter* regardless of concentrations at prior steps. A similar study was conducted at primary processing for one plant in 2013; significant improvements in *Campylobacter* mitigation since 2013 were noted. *Campylobacter* concentrations from final product from secondary processing were higher than concentrations at the end of primary processing. Drumsticks had lower *Campylobacter* concentrations than other portion types. Skin removal from product did not consistently result in product with lower *Campylobacter* concentrations. Results identify key areas to target for further reduction of *Campylobacter* on poultry meat, and provide a benchmark to compare the efficacy of future interventions.

### 1. Introduction

*Campylobacteriosis*, primarily caused by the species *Campylobacter jejuni* and *Campylobacter coli*, is the most commonly notified foodborne disease in New Zealand (Horn et al., 2021). Following the implication of poultry meat as the most common foodborne source, voluntary biosecurity interventions by the poultry industry and changes to slaughter and processing, together with the implementation of Ministry for Primary Industries' *Campylobacter* Risk Management Strategy, led to a ~50% reduction in incidence from 2006 to 2008 (Sears et al., 2011).

*Campylobacteriosis* incidence has continued to decline (albeit more gradually) since 2008 (Horn et al., 2021), despite an increase in poultry consumption per capita (Poultry Industry Association of New Zealand, 2021). *Campylobacter* concentrations and prevalence on carcasses have also declined since 2008, as monitored by the National Microbiological Database (NMD) Programme which documents *Campylobacter* concentrations on carcasses at the end of primary processing (Table 1, step 23) (Ministry for Primary Industries, 2022). Nevertheless, poultry remains the most important vehicle for human infection in New Zealand, and a recent study estimated that 84% of *campylobacteriosis* cases could be

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**Table 1**

Process steps for primary and secondary processing, indicating sample collection points and designations.

NO.	PROCESSING STEP	DESCRIPTION	SAMPLING SITE/ SAMPLE NAME <sup>b</sup>
<b>Primary processing</b>			
1	Bird receipt	Receipt of birds from farm in crates.	
2	Shackles	Birds removed from cages, hung by feet from shackles.	
3	Stun	Electrical stunning to render bird unconscious. Defecation may occur.	
4	Slaughter	Ventral cut severs carotid arteries before bird regains consciousness. Death occurs quickly (<40 s). Defecation may occur. Larger processing plants use machines to make cut; smaller plants cut manually.	
5	Bleed-out	Bleed-out tunnel is ~3 min long. First sample taken at end of tunnel before the next scald. Carcasses complete with feathers, feet, heads.	Pre-scald
6	Scalder	Carcasses immersed in hot water (56–59 °C) to soften skin and facilitate feather removal. Carcasses sampled at end of this process, complete with feathers, feet, heads.	Post-scald
7	Plucker	Carcasses massaged by rubber fingers to remove feathers. Defecation may occur.	
8	Spray	Water spray with or without antimicrobial to wash carcass and remove free organic matter. Sampled after spray.	Post-plucker
9	Head puller	Head removed.	
10	Feet removal and transfer	Feet removed at hock and carcasses transferred from slaughter line to evisceration line.	
11	Vent drill	Probe inserted into cloaca, hole is drilled around vent, and cloaca draped over back of carcass.	
12	Vent cutter	Blade widens vent opening to allow evisceration spoons to enter body cavity.	
13	Manual evisceration	Viscera removed from carcass. In most plants, viscera separated from carcass on hooks or trays. In some smaller plants, viscera laid over back of carcasses.	
14	Spray	Water spray, usually with antimicrobial, to remove organic matter from surface of carcass.	
15	Manual inspection	Residual parts of viscera removed from carcass manually.	
16	Spray	Spray, usually with antimicrobial, to remove any organic matter from carcass surface. Carcass sampled after spray.	Post-manual evisceration
17	Cropper	Probe creates hole between body cavity and neck. It removes neck contents; thymus gland etc. Carcass sampled.	Post-cropper
18	Neck breaker	Breaks and removes neck.	
19	Neck skin cutter	Cuts neck skin to pre-determined length. Not all plants have this fitted.	
20	Final inspection machine	Vacuum removes remaining cavity contents; air sacs etc. Not all plants have vacuum fitted.	
21	Inside/outside bird wash (IOBW)/spray	Final wash before carcass enters spinchill system. Carcass sampled after IOBW or spray.	Post-IOBW
22	Immersion chilling (spinchill)	Chilled water, ice and an antimicrobial. In New Zealand, chlorine (either as a gas or sodium hypochlorite liquid), with pH correction used in most plants. Carcass sampled.	Post-spinchill
23 <sup>a</sup>	Post-chill dip	All plants currently use acidified sodium chlorite (ASC) as a dip or spray. Carcass drained and sampled. At some plants, sampled carcasses rehung onto the secondary line before entering ASC.	Post-ASC
24	Rehang	Carcasses placed on overhead line leading to secondary processing.	
<b>Secondary processing</b>			
25	Transfer to bins or cut-up line	Carcasses graded, weighed and delivered to secondary processing. May be delivered on-line to cut-up machine (in some plants) or to bins where they may be manually hung on a line to a cut-up machine, packed as whole birds, injected (and/or stuffed) or placed directly into cut-up machine.	
26	Whole birds bagged	Whole birds removed from bin, placed in bag and heat sealed or clipped and sent for freezing.	Whole bird
27a	Cut up machine	Machines are automated. Outputs are: •Wings •Front half: breasts on frame •Back half: cut into legs (backbone in or removed) •Legs usually cut into drumsticks and thighs All sampled after trimming, immediately before packing.	Wings Drumsticks Thighs, skin-on
27b	Further cut up	Breasts removed from frames by machine or manually, then trimmed. Sampled after trimming, immediately before packing.	Breasts, skin-on
27c		Breasts skinned and trimmed. Sampled after trimming, immediately before packing.	Breasts, skin-off
28	Deboned thighs or whole legs	Deboning may be by machine or manual. Products are trimmed and may be skin-on or skin-off. Samples may be thighs or whole legs. May be ready for retail sale or used for value added or further processed products. Sampled immediately before packing.	Thigh fillets, skin-off

<sup>a</sup> Carcasses for the National Microbiological Database Programme monitoring are sampled at this point (see Introduction).

<sup>b</sup> Note that sample types are capitalized to differentiate sample type from processing step, and to discriminate sample types from individual portions (e.g. Drumstick samples comprise multiple drumstick portions).

assigned to poultry (Lake et al., 2020).

Primary poultry processing encompasses slaughter and dressing, whilst secondary processing may include portioning (cutting up/partitioning), deboning, marinating, forming, cooking and packaging ready-to-eat products (Table 1). Current primary processing antimicrobial intervention steps implemented by New Zealand processors include high scald temperatures, chlorine spray steps, carcass immersion in chlorine solution (spinchill step) followed by an acidified sodium chlorite (ASC) dip. Processing improvements since 2006–2008 have included new evisceration machines, new spray washes, and better control of pH and chlorine levels in the spray washes and spinchillers (Lake et al., 2013). There are no antimicrobial processes implemented during secondary processing. However, processes such as portioning, deboning and deskinning may influence *Campylobacter* prevalence and concentrations on product via cross-contamination or reduction of hospitable niches

(such as the cavity or feather follicles) during de-skinning (Davis and Conner, 2007; Habib et al., 2019; Stella et al., 2017).

The current study sampled broiler whole carcasses and carcass portions (pieces or parts) at key points along the primary and secondary processing chain of plants owned by the three major poultry processors in New Zealand (anonymized as Plants A, D and F). These companies produce >90% of broilers for the New Zealand retail market, and the three plants in the study produce ~56%. The objective was to assess the impact of current broiler poultry processing steps and interventions in primary and secondary processing on *Campylobacter* concentrations on final product. Findings were also compared against data from an earlier study to ascertain the impacts of recent processing improvements on the degree of mitigation of *Campylobacter* on carcasses. Results will identify areas for future focus toward a further reduction of *Campylobacter* prevalence and concentrations on broiler carcasses and portions.

## 2. Materials and methods

### 2.1. Sampling event logistics and capture of flock and processing variables

The longitudinal study consisted of six sampling events conducted at each of the three processing plants. These were conducted within the first quarter of the year (January and February 2021) because historical NMD data typically shows a higher prevalence of *Campylobacter* at this time. To ensure consistency between sampling at the different processing plants, an industry expert from the study team attended and supervised the first sampling event at each site. The same staff members collected all samples at each sampling event, although some processing plants had separate sampling teams for primary and secondary sampling (with at least one of the core samplers involved at both primary and secondary sampling). An industry-developed *Campylobacter* primary processing control checklist (Table S1) was completed at each facility at each sampling event to assess the performance of the equipment at the time of processing.

Flocks were selected based on having *Campylobacter*-positive caecal samples from the first shed cut (harvest or depopulation). Due to the number of samples required, the chosen flock needed to be large enough to be in the primary processing area for at least 60 min, preferably 90 min. Flock variables captured included shed cut number, flock age, sample weights, housing system, and flock sex.

### 2.2. Sample numbers and procedures

The target sample size was informed by an earlier industry study performed in 2013 (the data of which is also included in this study). Sample sizes of 30 samples per processing plant/processing point allowed a detection of a difference of at least  $0.4 \log_{10}$  CFU/carcass in the mean concentration between two processing plant/processing points (power 0.8, confidence 0.95).

A total of 1350 samples were tested (six sampling events at each processing plant, each comprising eight primary and seven secondary sample types, five samples of each sample type per sampling event, and a total of 30 of each sample type per processing plant; Table 1). Samples per sampling event were collected from the same flock where possible. However, breast samples came from an earlier flock slaughtered on the same day (Plant D and F), or previous day (Plant A), as these required aging for several hours before processing.

Sampling of carcasses was performed by the NMD method (Ministry for Primary Industries, 2022) with modifications for some sample types (Table S2). Portions were sampled by a modification of the United States Department of Agriculture Food Safety and Inspection Service (FSIS) method (United States Department of Agriculture Food Safety and Inspection Service, 2013). Briefly, samples were collected from the processing line and added to a rinse bag (1 carcass or  $1.8 \text{ kg} \pm 200 \text{ g}$  portions), to which 400 ml buffered peptone water (BPW) containing sodium thiosulphate (0.003% w/v; which neutralizes any carry-over chlorine or ACS) was added. Carcass samples were rinsed for 2 min, involving complete coverage of the external and internal carcass surfaces with the rinsate, and simultaneously massaging of the carcass surface, particularly around the wings and the legs. Modifications to the FSIS method for portions included a) the inclusion of sodium thiosulphate to BPW for consistency with carcass samples, b) intensively massaging rather than rinsing portions to maximize bacterial recovery, and c) carrying out the procedure for 2 min rather than 1 min for consistency with carcass rinsing. A 120 ml aliquot of the rinsate was captured by snipping off a bag corner, and the aliquots were transported on ice packs to the testing laboratory and stored under refrigeration until testing.

### 2.3. Sample processing and *Campylobacter* enumeration

The following morning (within 30 h following sample collection),

rinsates were plated onto modified Charcoal-Cefoperazone-Deoxycholate Agar (mCCDA; Fort Richard Laboratories, Auckland, New Zealand). Rinsate samples from pre-scald up to and including the inside-outside bird wash/spray (IOBW) were plated onto nine plates per sample: 1 ml of undiluted ( $10^0$ ) rinsate plated over three plates (i.e., method detection limit of 400 colony forming units (CFU)/sample), and 0.1 ml of the  $10^0$ ,  $10^{-1}$  and  $10^{-2}$  dilutions each plated on each of two plates. All rinsate samples following the pinchill, including all secondary processing samples, were processed by a modification of the NMD method as follows. Samples were poured through a micro-perforated filter bag (filter porosity 280  $\mu\text{m}$ ) to remove large particulate matter. A 50 ml volume of filtered rinsate was centrifuged at 4430 relative centrifugal force for 30 min without refrigeration. The supernatant was carefully poured off, retaining a 5 ml volume of supernatant and pellet. Two ml of resuspended pellet was plated onto six plates (0.33  $\mu\text{l}$  per plate; method detection limit of 29 CFU/sample based on a ten-fold concentration of the rinsate and loss of 30% of *Campylobacter* in the discarded supernatant, determined by a validation study of the method external to this study (unpublished results)). Two aliquots each of 0.1 ml concentrated rinsate and 0.1 ml uncentrifuged rinsate were plated. The mCCDA plates were incubated in sealed boxes with a microaerobic atmosphere provided using CampyGen sachets (Oxoid, Hampshire, UK) at  $42 \text{ }^\circ\text{C}$  for  $48 \pm 2 \text{ h}$ . After incubation, suspect *Campylobacter* colonies were enumerated. Where colonies were present, two to four colonies per sample of suspected *Campylobacter* spp. were purified and stored at  $-80 \text{ }^\circ\text{C}$  for future analysis. The species of up to two isolates per sample was identified using Matrix-Assisted Laser Desorption Ionization-Time Of Flight Mass Spectrometry (MALDI-TOF MS) with the extended direct transfer method in a Bruker Biotype (Nisa et al., 2019).

### 2.4. Statistical analysis of *Campylobacter* concentrations

The CFU/400 ml of samples was estimated based on the colony counts, with scaling factors based on the dilution plated and method detection limit. All samples for which no *Campylobacter* colonies were recovered (below the method detection limit) were entered as half of the method detection limit. For primary processing, *Campylobacter* concentrations were presented as CFU/carcass. For secondary processing samples, *Campylobacter* concentrations were standardized for the sample weight (CFU/kg) because portions arose from multiple carcasses and to control for any weight differences between samples.

Data analysis was conducted using the R statistical computing software (R Core Team, 2018). There was a large variability in *Campylobacter* concentrations, carcasses and portions were only sampled each once throughout processing, and the between-flock variability had to be taken into account. The resulting data could not be described by commonly used distributions and this consequently dictated the selected analysis approaches.

Comparisons of processing plant specific step-to-step differences in *Campylobacter* concentrations stratified the results by sampling event. For each sampling event and plant, the five data points were ranked and comparisons made between the same ranked concentrations before and after a processing step. The differences for the six sampling events were then combined to produce the violin plots and summary statistics. Stratification by sampling event was important to assess whether the processing step was reducing *Campylobacter* relative to starting concentrations which might differ between flocks, and processing plant performance might differ between sampling events. Differences of  $\log_{10}(\text{CFU}) < 1$  were recorded as “no change”.

To assess the between-plant differences in changes between sequential samples, the ranked-to-ranked comparisons were resampled with replacement to obtain 50 bootstrap sample mean differences for each processing plant. ANOVA or t-tests tested the difference between the means of plants within processing steps where appropriate. Bonferroni corrections were made to adjust for multiple comparisons.

Bootstrap t-tests were used to assess differences in CFU/rinsate between 2013 and 2021 sample types without ranking.

Counts of *Campylobacter* species types isolated between plants, and before and after antimicrobial steps (Post-manual evisceration with Post-ASC and Whole bird isolates combined to meet the requirements for Chi-square testing), were compared using Pearson's Chi-squared test.

### 3. Results

#### 3.1 Overview of flock and processing variables

The general processing steps involved in primary and secondary processing were common among all three processing plants and are described in Table 1. An overview of the primary processing variables by processing plant is provided in Table 2. Key differences between plants at primary processing included the use of equipment from three different manufacturers, the immersion time and process around the spinchillers, and the application of ASC. Within-plant variability in equipment performance was captured at each event using the *Campylobacter* primary processing control checklist; scores are listed in Table 3.

Plants A and D secondary processing facilities were at the same location as primary processing, while secondary processing for Plant F occurred at a separate facility. While carcasses from Plants A and D transit by conveyor from primary to secondary processing, Plant F carcasses are placed in a bin and transported to a different facility. There are approximately 4 h until secondary processing commences for Plant F, compared with 4 min or less for Plants A and D. Some plant-specific

secondary processing procedures were considered proprietary and were not captured by this study. The secondary processing plants have similar equipment, but from different manufacturers. Plants also used different procedures for aging of breast meat; Plant D used electrical stimulation immediately after slaughter to reduce the time taken for rigor mortis to occur while Plants A and F use a longer hold time.

Sampled flock variables are listed in Table 3. The 18 sampled flocks were from 15 different farms; where more than one flock was from the same farm, flocks were from different sheds. The majority of flocks sampled were from the second cut, three were from the third cut, and one had a combination of first and second cuts (although the first-cut flock would not have been verified to be *Campylobacter*-positive, >95% of free range flocks sampled at the time of year were historically found to be colonized by that stage). Eleven of the 18 flocks were from free range housing systems, including all six from Plant F. Plants A and D had a mix of free range and barn flocks. The lowest average live weight was from Plant F (2.21 kg), compared with 2.98 kg and 2.97 kg for Plants D and A, respectively.

#### 3.2. *Campylobacter* concentrations through primary processing

At each of the six sampling events per processing plant, five replicates were collected following eight primary processing steps, totalling 720 enumerated samples. The *Campylobacter* CFU per carcass rinsate stratified by sampling event and primary processing plant, distributions of the *Campylobacter* concentrations per primary processing sample type are presented in Fig. 1 and summary statistics in Table S3. There were

**Table 2**  
Summary of primary processing operations at the three plants at the time of the study.<sup>a</sup>

PROCESSING STEP	VARIABLE	PLANT A	PLANT D	PLANT F
Scald	Scalder temperature	55–59 °C; target 56 °C	58–59 °C	Tank 1: 45–50 °C Tank 2: 50–57 °C Tank 3: 55–60 °C
	Scald duration (seconds)	120–210 (2 lines)	91–132	191
	pH adjustment; target	Adjusted; pH 9	Not adjusted (actual pH 7.4)	Not adjusted
Plucker	Stage at which anti-microbial used during plucking	Post-pluck spray	Last bank (2 × 0.5) of pluckers, post-pluck spray	Post-pluck spray
	Antimicrobial type, concentration	Chlorine, 50–100 ppm	Chlorine, 80–100 ppm	Chlorine, 50–200 ppm
	All sprays on the processing lines	Chlorine, 100 ppm	Chlorine, 80–100 ppm	Chlorine, 50–200 ppm
Manual evisceration	Year of vent opener manufacture, brand	2014 and 2003 (2 lines), Meyn	2010, Stork	1996, Meyn
	Year of eviscerator manufacture, brand	1993 and 2000, Meyn	2010, Stork	1996, Meyn
	Line speed of evisceration line (carcasses per minute)	80–130 for both lines	100–145	92–102
Cropper	Removal of neck flap from all carcasses	Yes	No	Yes
	IOBW in place	Present	Absent	Present
	Final spray just before carcasses enter spinchill	Absent	Present	Present
Inside outside bird wash (IOBW)	Anti-microbial used, concentration	Chlorine, 50–100 ppm	Chlorine, 50–200 ppm	Chlorine, 80–100 ppm
	Additional pre-spinchill treatments	No	No	No
	Retention time of carcasses in spinchill	110 min and 140 min	67 min	90 min
Spinchill	Type of anti-microbial, incoming concentration	Chlorine, 40–50 ppm	Chlorine, 80–100 ppm	Chlorine, 50–200 ppm
	Hourly volume of make-up water	11–94 m <sup>3</sup> and 11.4 m <sup>3</sup>	24–27 m <sup>3</sup>	15 m <sup>3</sup>
	pH of water in spinchill	pH 5.5–6.5 (target pH 5.5–6.0)	pH ~8.0 No pH correction	pH 6.0–7.0 Citric acid used
Acidified sodium chlorite (ASC)	Citric acid used	Citric acid used	60 m <sup>3</sup>	79.9 m <sup>3</sup>
	Water capacity of spinchill	65 m <sup>3</sup> and 80 m <sup>3</sup>	60 m <sup>3</sup>	79.9 m <sup>3</sup>
	Type of ASC equipment	Continuous Online Pathogen Eliminator	Grayson dip tank	Combined dip and spray
	Duration of ASC treatment	15–25 s	22–24 s	22 s
	Hourly make-up rate	Up to 3000 L	2300 L	800 L
	Target chlorite level (during normal operation; during <i>Campylobacter</i> response, maximum is 1200 ppm)	700–850 ppm	700–764 ppm	720–860 ppm
	Target pH range (limits pH 2.3–2.9)	pH 2.5–2.7	pH 2.4–2.6	pH 2.4–2.6
Treatment on/off weigh line	Carcasses treated and rehung onto weigh line	Carcasses treated and rehung onto weigh line	Carcasses treated on weigh line	
Time from end of ASC to arrival in secondary processing	68 s & 10 s	4 min	2.5 min drip time then 4 h (processed in separate facility)	

outliers in *Campylobacter* concentrations for some samples; however, all data were retained because they reflect the inherent variability of *Campylobacter* abundance within different flocks and across processing events and steps.

Carcasses at the first sampled location (Pre-scald, when carcasses were still complete with feathers, feet and heads) had a wide distribution in *Campylobacter* concentrations (5.3->8.5 log<sub>10</sub> CFU/carcass) reflecting the varying degree of contamination of birds entering into primary processing. Median concentrations were similar between processing plants (6.8–7.1 log<sub>10</sub> CFU/carcass). Depending on the plant, the primary processing steps resulted in >5.3 to >5.6-log reduction in median *Campylobacter* concentrations from Pre-scald to Post-ASC samples (final step in primary processing). Furthermore, *Campylobacter* was below the limit of detection (<29 CFU/carcass) in 76% of samples at the end of primary processing.

The violin plots (Fig. 1B) and summary statistics (Table S3) provide an indication of *Campylobacter* reduction between steps. To further explore the efficacy of each step in reducing *Campylobacter* concentrations on carcasses, or conversely which result in increased concentrations, differences were calculated between sequential sample types for ranked carcass concentrations in each processing plant within sampling events. Step-to-step changes in *Campylobacter* concentrations for individual sampling events are shown in Fig. S1 and the overall changes relative to the *Campylobacter* concentrations following each step are summarised in Fig. 2A and Table S4. The biggest reductions in *Campylobacter* concentrations were between the Post-IOBW and Post-spinchill samples (median 3.0–4.0 CFU/carcass log reduction). Decreases in *Campylobacter* concentrations were seen between these processing steps for all processing plants and sampling events. The scald step resulted in the second highest reduction in *Campylobacter* concentrations on carcasses of any of the steps at primary processing (median 0.5–2.3 log-reduction in CFU/carcass). The mean change between these two sample types had the widest range, which reflects the high interquartile range present for both sample types.

Between-plant differences in the efficacy of certain primary processing steps were also apparent (Table S4). To further assess between-plant differences, ranked-to-ranked comparisons were resampled with replacement to obtain 50 bootstrap sample mean differences for each processing plant (Fig. 2B). There were significant differences (p < 0.001)

between plants for *Campylobacter* concentration changes between all samples except between the Post-manual evisceration and Post-cropper samples. The biggest between-plant difference was from Pre-scald to Post-scald samples, with Plant D showing the greatest mean and median reduction. Plant D had a higher average scald temperature at this step compared with the other two plants, although the scald duration time was shorter (Table 2). Plant A had the second highest decrease in *Campylobacter* concentrations and the lowest interquartile range between Post-scald *Campylobacter* concentrations, suggesting greater consistency at the Scald step than the other plants. Plant A differs from the other two plants by the use of pH adjustment to an alkaline pH at this step (target of pH 9).

Plant differences were also observed in the spinchill efficacy. The greatest decrease in concentrations was from Plant F. Median *Campylobacter* concentrations from Post-spinchill samples were the highest from Plant D, and there was less reduction in the bootstrap mean *Campylobacter* concentrations from Post-IOBW samples compared with the other two processing plants (which partially reflects that Plant D had lower median concentrations from Post-IOBW samples). Plant D also had the fewest samples where *Campylobacter* was below the limit of detection (40% compared with 70% for Plant A and 53% for Plant F). Relative to the other two plants, the Plant D spinchill system has no pH correction, no water recirculation and the shortest retention time (Table 2).

The ASC dip and/or spray step comprises the final antimicrobial step during primary processing, the administration of which differs between processing plants. The ASC step resulted in minimal-to-no detectable reduction in median *Campylobacter* concentrations at all plants because concentrations from Post-spinchill samples were already at, or near, the method detection limit (29 CFU/carcass). The smallest interquartile range and median of concentrations across all processing plants and sampling events were at Post-ASC. The lowest maximum *Campylobacter* concentration from Post-ASC was from Plant D. Plant A had the highest percentage of samples (86.7%) below the limit of detection for *Campylobacter* at this step, followed by Plant D (80.0%) and Plant F (63.3%). Despite between-plant differences at earlier sample points, plants had the same median *Campylobacter* concentrations on carcasses at the end of primary processing.

The *Campylobacter* reduction efficacy of primary processing at each

Table 3

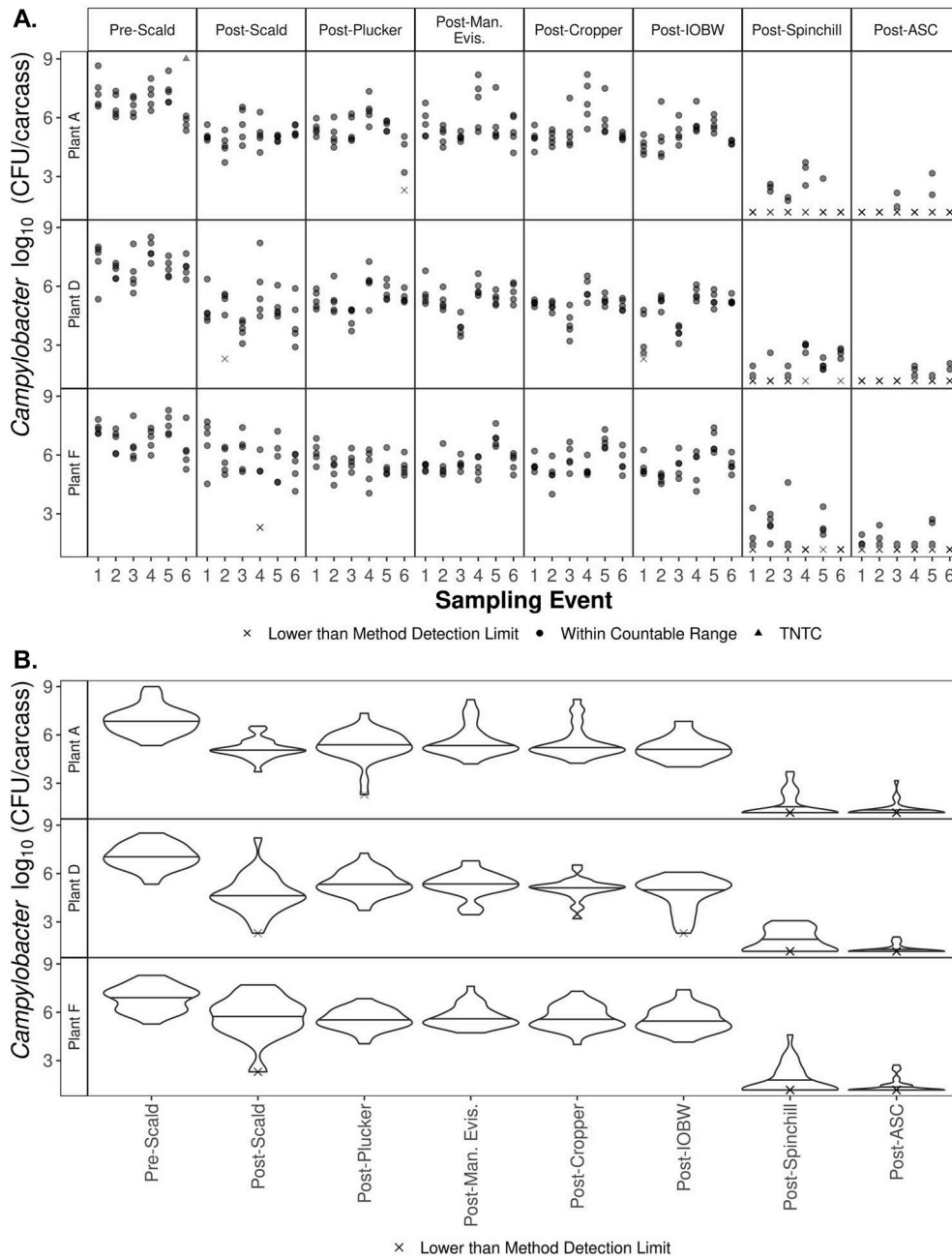
Flock and processing variables and *Campylobacter* primary processing control checklist for each processing week for which there was data available.

PLANT	SAMPLING EVENT	FARM	SHED	CUT NUMBER <sup>a</sup>	AGE (DAYS)	BIRD AVE LIVE WEIGHT (KG)	FARM TYPE <sup>a</sup>	LINE SPEED (CARCASSES/MINUTE)	CAMPYLOBACTER CHECKLIST (%) <sup>c</sup>
A	1	1	95	2F	34	3.09	FR	90	No data
	2	2	194	2F	43	3.10	B	90	81.5
	3	3	260	2F	43	3.19	B	103	81.5
	4	4	285	2F	46	3.45	B	90	81.5
	5	5	248	2F	36	2.45	FR	No data	81.5
	6	6	6	2F	36	2.60	FR	No data	81.5
	Ave (std dev)					39.7 (4.9)	2.98 (0.38)		94.3 (7.5)
D	1	7	3	2M	39	3.1	FR	115	73.0
	2	8	8	2M	40	2.9	FR	115	75.2
	3	9	3	3M	40	3.28	B	100	75.7
	4	10	6	3M	41	3.41	B	100	70.0
	5	11	5	2F	36	2.24	B	130	79.1
	6	12	2	3M	40	2.86	B	115	73.9
	Ave (std dev)					39.3 (1.8)	2.97 (0.41)		112.5 (11.3)
F	1	13	3	2AH	35	2.2	FR	100	71.5
	2	14	9	2AH	35	2.2	FR	100	66.7*
	3	14	10	2AH	35	2.2	FR	100	65.2*
	4	15	4 + 5	2+1AH	36 + 32	2.35 + 1.95 <sup>b</sup>	FR	100	69.6
	5	15	6	2AH	35	2.25	FR	100	71.5
	6	15	7	2AH	35	2.3	FR	100	70.0
	Ave (std dev)					34.8 (0.4)	2.21 (0.17)		100 (0.0)

<sup>a</sup> F female, M male, AH as hatched, FR free range, B barn. Number refers to cut number (e.g. “2” refers to second cut).

<sup>b</sup> The average of the two flock ages and weights were used to calculate the average and standard deviation for Plant F ages and weights.

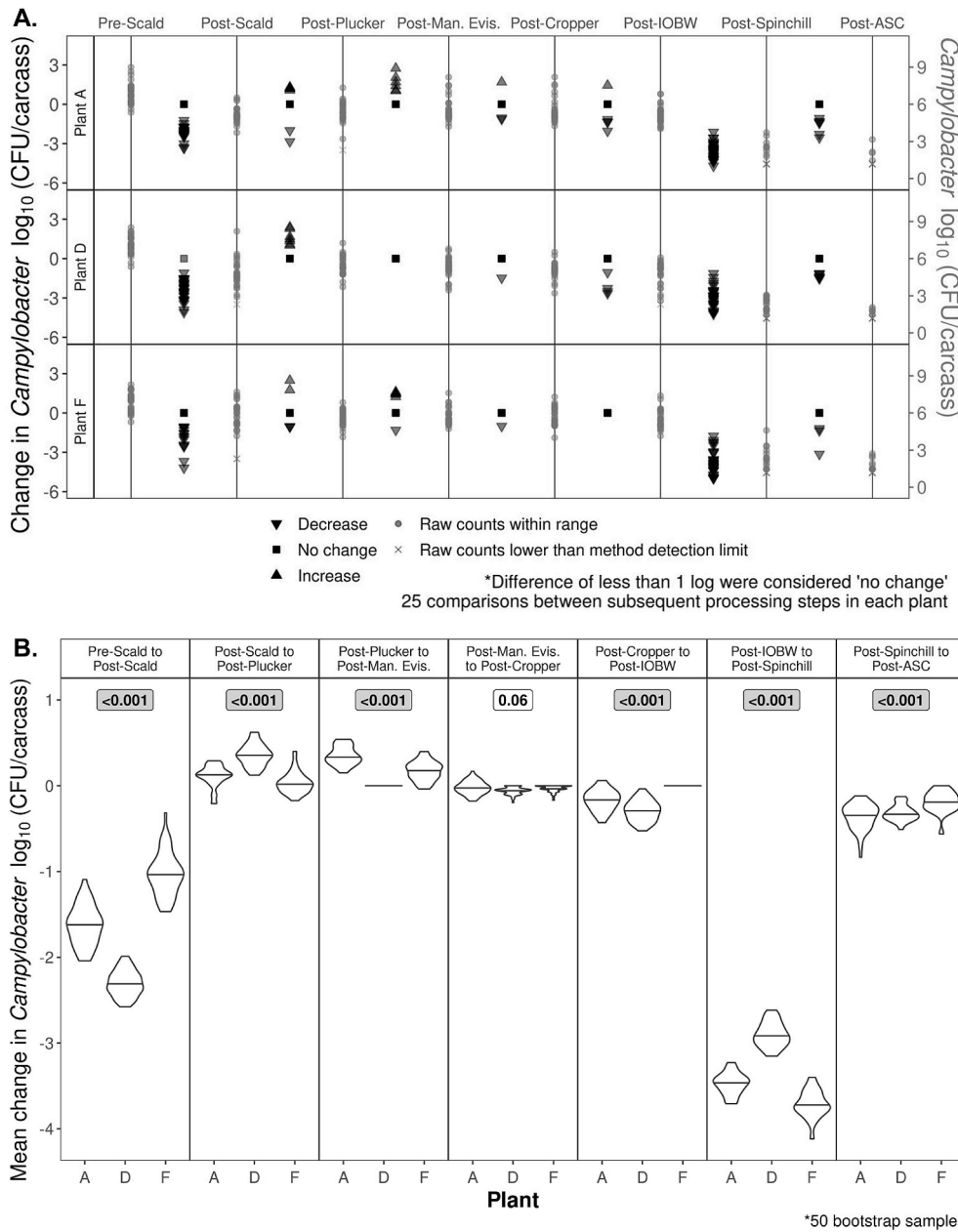
<sup>c</sup> Successful score ≥70%, marginal score 60–69% (indicated by \*); <60% requires action plan; for scoring criteria, see Table S1. Because the scoring criteria is defined in whole numbers, the rounded numbers were used for defining whether scores were successful or marginal.



**Fig. 1.** *Campylobacter* concentrations (CFU/carcass rinsate) from primary processing samples tested from each processing plant. (A) *Campylobacter* concentrations of each sample. (B) Violin plot showing distribution of *Campylobacter* concentrations for different sample types. Lines across the middle of each violin indicate the median. The width of each plot displays the relative frequency of samples recording a specific concentration.

plant was considered against primary processing control checklist scores (Table 3). Plant A consistently scored the highest average score (81.5%), followed by Plant D (74.5%) and Plant F (69.1%). Most sampling events recorded a successful score ( $\geq 70\%$ ), and there were only two marginal scores (60–69%; Plant F, events 2 and 3). The *Campylobacter* checklist scores were considered relative to the efficacy of *Campylobacter* control on carcasses during primary processing. Statistical analyses were not conducted to relate *Campylobacter* concentrations by sample type and plant to the checklist scores due to insufficient samples per type to meet traditional method assumptions or generate sufficient variation using re-sampling methods. Instead, simple observational comparisons were made between the checklist scores and *Campylobacter* concentrations. The highest median *Campylobacter* concentrations from any processing step was typically from Plant F (except at Post-spinchill), consistent with

this processing plant having the lowest checklist scores. Although checklist scores differed between processing plants and sampling events, median *Campylobacter* concentrations on carcasses at the end of primary processing were the same for each processing plant, and were similar between sampling events. While *Campylobacter* concentrations were higher on average for some earlier samples in the processing chain for certain sampling events, these did not correspond to lower *Campylobacter* checklist scores. For example, although Plant F sampling event 5 had the highest equal checklist score recorded for this processing plant (71.5%), higher *Campylobacter* concentrations than all other sampling events from this processing plant were recorded from Post-manual evisceration to Post-IOBW samples at this event. Conversely, of the two sampling events recorded as marginal for this processing plant (events 2 and 3), there were no unusually high *Campylobacter*



concentrations following any processing step (except a single sample from Post-spinchill; event 3). Therefore, no obvious association was found between the *Campylobacter* checklist score and *Campylobacter* concentrations on carcasses at primary processing.

### 3.3. Plant D primary processing

#### 3.3.1. A comparison of 2013 and 2021 data

A similar study was carried out in 2013, which assessed *Campylobacter* concentrations on carcasses at the equivalent primary processing sites from ten sampling events at Plant D (poultry industry data). Fig. 3 depicts Plant D 2013 data for the individual *Campylobacter* concentrations per carcass rinsate, stratified by sampling event and sample type, and violin plots comparing the distributions of the data between the two years. Summary statistics comparing *Campylobacter* concentrations for 2013 and 2021, and bootstrap *t*-test results of *Campylobacter* CFU/carcass are shown in Tables S5 and S6, respectively.

The median *Campylobacter* concentrations at the start of processing

did not differ significantly between studies ( $p = 0.340$ ). Following each subsequent processing step, *Campylobacter* concentrations were lower in the 2021 study compared with the 2013 study, although differences were not significant from the Pre-scald to Post-cropper samples ( $p = 0.029-0.429$ ). There were significant differences ( $p = 0.002$ ) in *Campylobacter* concentrations between 2013 and 2021 Post-IOBW, Post-spinchill and Post-ASC samples. Furthermore, there were >1.5-log lower median concentrations at the end of primary processing in 2021 (>5.6-log reduction in 2021, 4.0-log reduction in 2013). Concentrations partly reflect different method detection limits between studies for the final two sample types. However, 18% of the 2013 Post-ASC samples were below the limit of detection of *Campylobacter* (<400 CFU/sample), while all 2021 Post-ASC Plant D samples had <400 CFU/sample and 77% were below the limit of detection (<29 CFU/sample).

#### 3.4 *Campylobacter* concentrations on whole birds and portions during secondary processing

The six sampling events undertaken at each secondary processing

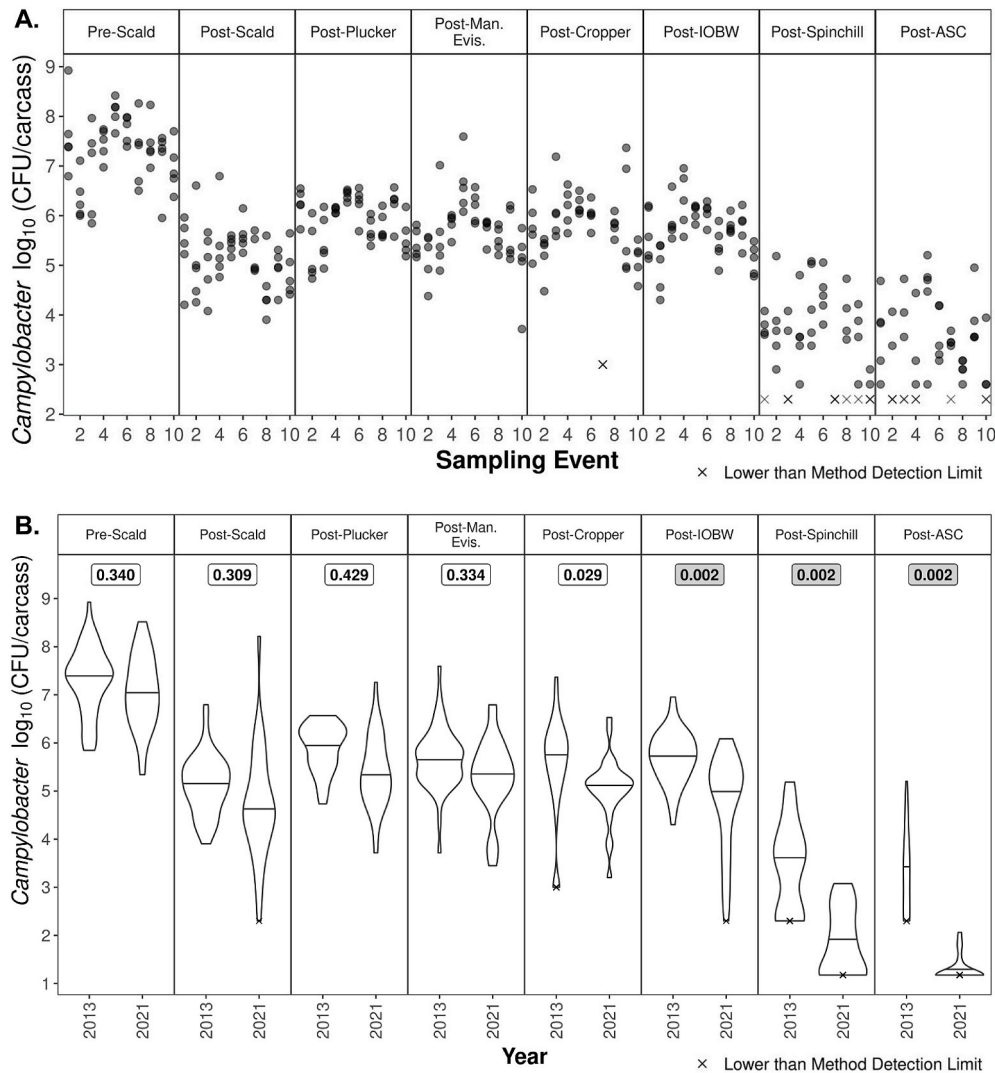
plant collected five replicates from seven different product types, totalling 630 samples enumerated from secondary processing. The number of portions in each sample depended on the portion type and carcass weight; portions arising from multiple carcasses were present in a single sample. The number of portions per sample was not recorded for each event, but for one event (Plant D, sampling event 6), there were 12–13 drumsticks, 16–17 wings, 7–8 thighs skin-on, 8 thigh fillets skin-off, 4 breast skin-on and 4–5 breast skin-off portions per  $1.8 \pm 0.2$  kg sample. The *Campylobacter* concentrations for all secondary processing samples are presented stratified by sampling event and processing plant, and violin plots of the distributions of *Campylobacter* concentrations standardized to sample weight are provided in Fig. 4. Summary statistics are provided in Table S7.

*Campylobacter* concentrations for Whole birds sampled at secondary processing were similar for Plants A and D ( $<1.3 \log_{10}$  CFU/kg), but were more than one-log higher from Plant F ( $2.5 \log_{10}$  CFU/kg). While no *Campylobacter* were detected ( $<29$  CFU/sample) from 73.3% samples from Plant A and 63.3% samples from Plant D, *Campylobacter* was enumerated for all samples from Plant F Whole birds. *Campylobacter* concentrations were also compared with those from carcasses at the end of primary processing (Post-ASC; Fig. 5, Tables S8 and S9). The median *Campylobacter* concentrations from Plant F Whole birds were  $>1.2 \log_{10}$

CFU higher than observed for Plant F Post-ASC samples, but there were no differences in concentrations between the sample types for Plants A and D.

The pH of BPW rinsate aliquots from Post-ASC and Whole bird samples from a subset of sampling events was ascertained to test whether excess carry-over of ASC might lower the rinsate pH and thereby reduce *Campylobacter* concentrations. However, all pH results were within, or very close to, the designated pH of the control BPW medium;  $7.0 \pm 0.2$  (Table S11).

Because portions were derived from Whole birds, differences in *Campylobacter* concentrations between weight-standardized Whole birds to skin-on portions were compared for each processing plant and sampling event (skin-off portions were derived from skin-on portions and were instead compared with skin-on portions) (Fig. 6, Table S10). Whole birds had lower *Campylobacter* concentrations than most portion types. Of the portions, Drumsticks had the lowest maximum and median *Campylobacter* concentrations across processing plants and sampling events. In total, there were 32 Drumstick samples (35.6%) from which no *Campylobacter* colonies were detected; these included approximately one half of the samples from Plants A (50.0%) and D (46.7%), but only 10% of Plant F samples. The lowest median concentrations from Drumsticks were also from Plant A and D ( $<1.3 \log_{10}$  CFU/kg compared



**Fig. 3.** Comparison of Plant D primary processing from 2013 to 2021 data. (A) *Campylobacter* concentrations per carcass rinsate during primary processing for Plant D in 2013. (B) Comparison between *Campylobacter* concentrations from carcasses sampled at equivalent sites in Plant D in 2013 and 2021. Labels represent the bootstrap *t*-test *p*-values; shaded boxes indicate that means are significantly different between 2013 and 2021.

with 1.9 log<sub>10</sub> CFU/kg for Plant F).

Relative to all other sample types at secondary processing, Wings had the widest range of *Campylobacter* concentrations. Concentrations from Plant A sampling event 2 Wings were much higher than for other sampling weeks, processing plants and secondary sample types. The lowest median, maximum and range of *Campylobacter* concentrations from Wing samples were from Plant D samples. Despite having the highest *Campylobacter* concentrations on Whole birds, Plant F had the lowest increases from Whole birds to all portion types, including wings (median 0.04-log increase). Median 1.6- and 0.9-log increases from Whole birds to Wings were recorded from Plant A and D, respectively.

The lowest median *Campylobacter* concentration from Thigh skin-on samples was from Plant D (2.5 log<sub>10</sub> CFU/kg) while the highest was from Plant F (3.1 log<sub>10</sub> CFU/kg), which was the highest median concentration for any processing plant and portion type. The lowest median *Campylobacter* concentration from Thigh fillet, skin-off portions was also

from Plant D (2.1 log<sub>10</sub> CFU/kg), while both Plant A and F had 3.0 log<sub>10</sub> CFU/kg. Plant D recorded the lowest maximum concentration, and was the only processing plant where *Campylobacter* was below the limit of detection in some samples. Changes in *Campylobacter* concentrations were calculated relative to Thigh skin-on samples (Fig. 6, Table S10). Overall, there was a 0.5-log decrease for Plant D, no change in concentrations for Plant F, and a 0.3-log increase in *Campylobacter* concentrations for Plant A. For Plant D, decreases occurred on four sampling events while the other two events had no change. For Plant F, there were no changes at any event. Increases for Plant A occurred on two sampling events, which might indicate cross-contamination during skin removal and filleting.

Plant F had the highest Breast skin-on median *Campylobacter* concentrations (2.6 log<sub>10</sub> CFU/kg), while median concentrations were similar from Plants A (2.3 log<sub>10</sub> CFU/kg) and D (2.3 log<sub>10</sub> CFU/kg). Although Breast samples arose from an earlier flock than all other

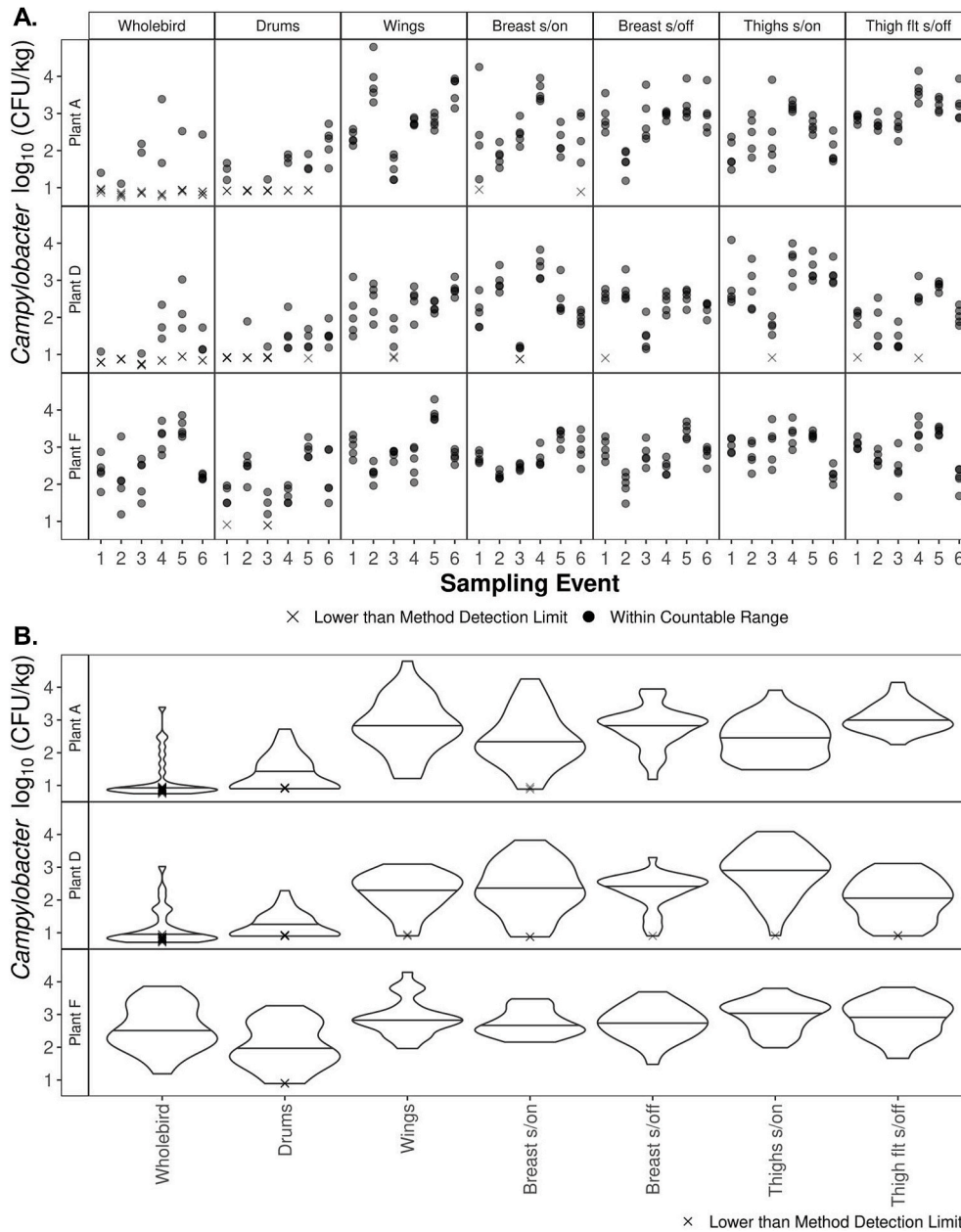
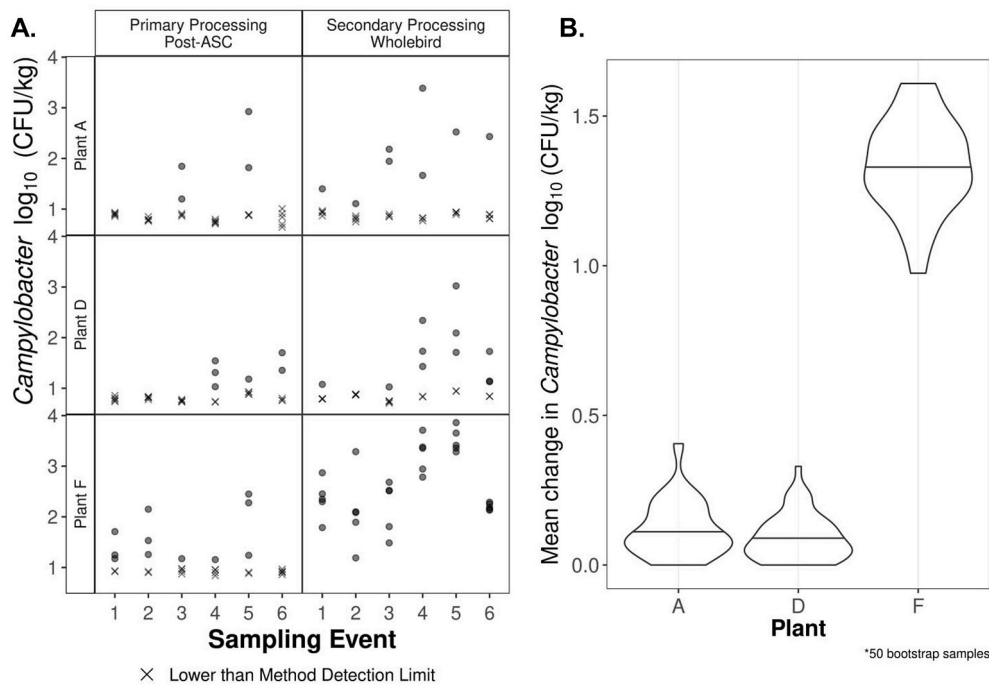


Fig. 4. *Campylobacter* concentrations (CFU/kg of product) from secondary processing product rinsates tested from each processing plant. (A) *Campylobacter* concentrations for each product type. (B) Violin plots of the distributions of *Campylobacter* concentrations from product. Lines across the middle of each violin indicates the median.



**Fig. 5.** Comparison between *Campylobacter* concentrations from carcass rinsates at the end of primary processing (Post-ASC) and the beginning of secondary processing (Whole bird) from each processing plant. (A) *Campylobacter* concentrations from each sample. (B) Estimated bootstrap mean ranked differences in *Campylobacter* concentrations from the two sample types.

samples, Breast skin-on concentrations were compared relative to Whole birds under the assumption that the median and range of Whole bird concentrations from the six events would be representative of Whole bird samples from that plant as a whole. However, this should be taken into consideration when interpreting ranked-to-ranked changes between Whole bird to Breast skin-on samples presented in Fig. 6A. There was approximately 1 log<sub>10</sub> CFU/kg median increase from both Plants A and D, but no change from Plant F. The highest Breast skin-off median *Campylobacter* concentrations were from Plant A (2.9 log<sub>10</sub> CFU/kg) followed by Plant F (2.8 log<sub>10</sub> CFU/kg) and Plant D (2.5 log<sub>10</sub> CFU/kg). Relative to Breast skin-on samples, Plant F had no estimated changes between Breast skin-on to Breast skin-off, Plant D had one sampling event where there were estimated reductions; and Plant A had three sampling events with estimated increases (Fig. 6, Table S10). The increases in *Campylobacter* concentrations following skin removal from Plant A Breast samples suggest that cross-contamination is also occurring during this process.

### 3.5. Effect of processing steps on the proportions of *Campylobacter* species

The *Campylobacter* species present from each sample type, processing plant and most sampling events, are shown in Fig. 7. Of the 1831 *Campylobacter* isolates for which species was determined, there were two isolates of *C. lari* (0.1%; from two samples prior to spinchill at Plant A, event 2), 319 isolates of *C. coli* (17.4%) and 1510 *C. jejuni* (82.5%). Proportions of *C. jejuni* to *C. coli* differed by processing plant with the highest percentage of *C. coli* from Plant A (45.2%, n = 558) and lowest at Plant F (2.7%, n = 595). Within processing plants, proportions also differed at different sampling events, with the highest proportions of *C. coli* at Plant A sampling events 3 (69.1%, n = 110) and 4 (70.7%, n = 116), but only 1.9% from event 6 (n = 106); all events were from flocks from different farms. For Plant D, two sampling events (1 and 2) had no *C. coli* isolations, while event 4 had 33.8% *C. coli* (n = 139). Three events from Plant F also had no *C. coli* identified (n = 99, 105 and 140). Of the five sampling events that had the highest proportions of *C. coli* (Plant A sampling events 2, 3, 4 and 5, and Plant D sampling event 4), all were from different farms, four of five were from barn-raised flocks, and birds

were aged 36–46 days (average age of 41.8 days compared with an average of 37.9 days for all events).

The effect of antimicrobial processing steps on *C. jejuni* and *C. coli* proportions was investigated by comparing combined data from Post-manual evisceration samples (before antimicrobial processing steps) with Post-spinchill (after main antimicrobial treatment) and Post-ASC samples (after all antimicrobial steps). Relative to Post-manual evisceration isolates (17.5%, n = 177), proportions of *C. coli* were similar from Post-spinchill samples (21.2%, n = 66) but lower from Post-ASC samples (9.1%, n = 22). However, there were only 22 *Campylobacter* isolates from Post-ASC samples which provides insufficient data to determine levels of significance, so results should be interpreted with caution. When data from the Post-ASC and Whole bird samples were combined, there was still a lower proportion of *C. coli* (7.8%, n = 102), and the difference between proportions was significant (p = 0.039).

For Plant F, *C. jejuni* was the only *Campylobacter* species isolated (for which the species was determined) during primary processing (all 273 isolates), while *C. coli* was isolated from secondary processing samples (16 of 322 isolates). *C. coli* was present on various secondary product types from two sampling events. Although the Breast samples arose from a different flock, results suggest that cross-contamination is occurring for the Drumstick and Thigh portion types during secondary processing at this processing plant, involving *Campylobacter* from a flock not sampled in this study.

## 4. Discussion

Current primary processing steps in New Zealand poultry processing plants involve multiple physical and chemical decontamination interventions, including high scald temperatures, chlorine spray steps, chlorine spinchill with or without acidification, and a final ASC dip and/or spray. The biggest reductions in *Campylobacter* concentrations in this study were achieved by the spinchill followed by the scald step. Between-plant differences were also noted at these steps. Despite plant-specific differences from samples arising earlier in the processing chain, primary processing steps in all three plants were highly effective in



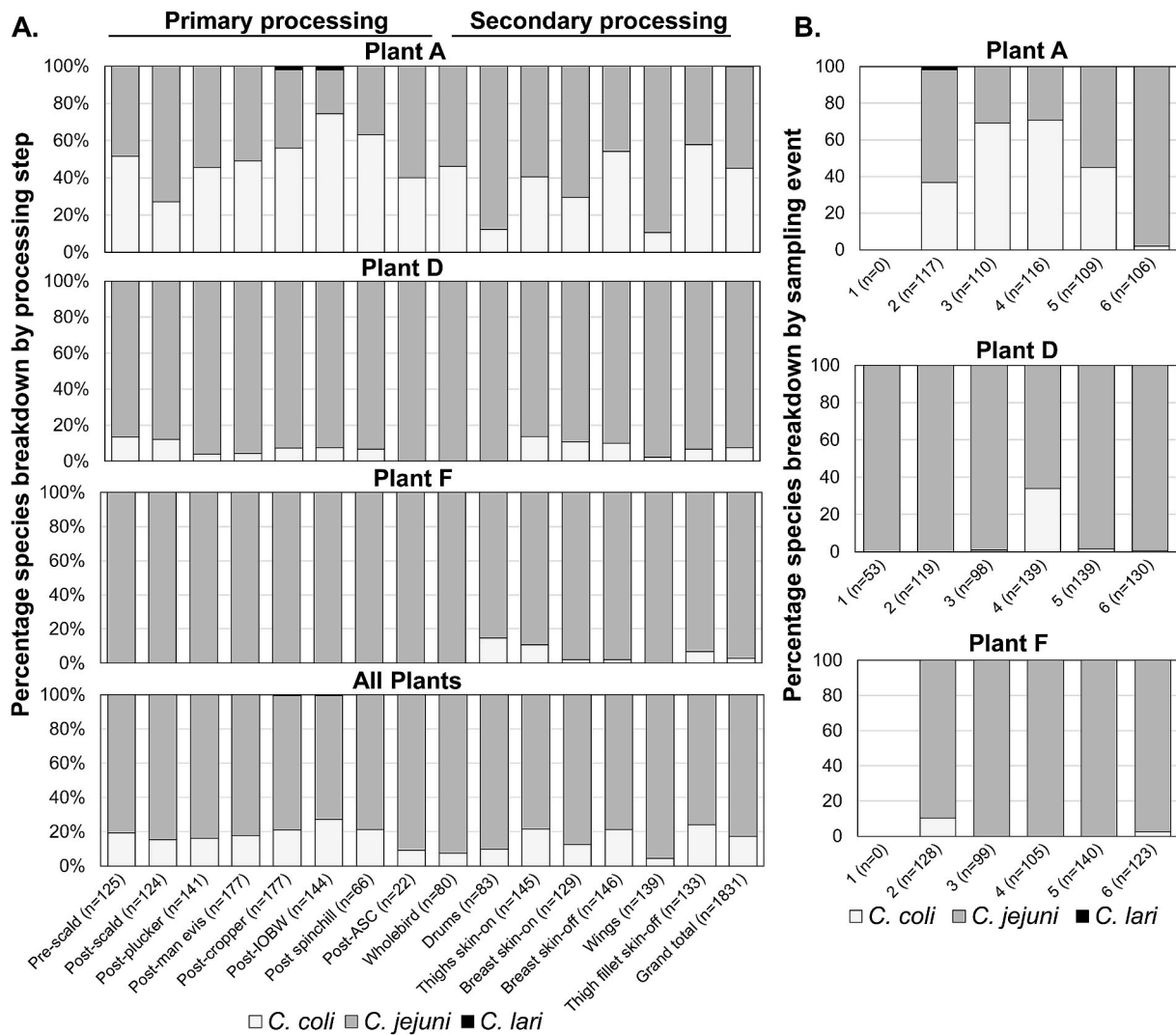


Fig. 7. Proportions of *Campylobacter* species isolated from each processing plant, sample type (A) and sampling event (B). Species identification was not carried out for isolates from the first sampling event from Plants A and F.

while chemical treatment techniques were more effective after IOBW. In the current study, sampling events where *Campylobacter* concentrations were higher on carcasses sampled prior to the spinchill did not necessarily result in higher concentrations at the end of primary processing. The spinchill consistently reduced *Campylobacter* concentrations on carcasses to very low numbers, while implementation of the final ASC wash further reduced concentrations to low-to-undetectable levels. Chlorine is the most commonly used antimicrobial through the primary processing in many countries (Chousalkar et al., 2019) due to its relatively low cost and low concentration required for efficacy, and is implemented at IOBW, pre-chillers, main chillers and post-chill applications. However, recent studies have shown chlorine to be less effective in spray compared with dip applications (Gichure et al., 2022). The effectiveness of chlorine in spinchill tanks is influenced by temperature, pH, residence time, organic and bacterial loads (McCarthy et al., 2017; Muhandiramlage et al., 2020; Yang et al., 2001). Studies show that ASC is more effective than chlorine at reducing *Campylobacter* concentrations during poultry processing (Bashor et al., 2004; Gichure et al., 2022). Results from the current study emphasize the importance of effective functioning of both the spinchill and final ASC wash for ensuring that *Campylobacter* concentrations remain low on product, despite earlier cross-contamination events or process breakdowns. Although the study results showed that primary processing was highly effective in controlling *Campylobacter* concentrations on

carcasses, concentrations recovered from Plant F carcasses during secondary processing were higher than at the end of primary processing. The increase was not due to growth of *Campylobacter* present on carcasses at the end of primary processing because carcasses and rinsates were transported at refrigeration temperatures. Any excess carry-over of ASC from carcasses was also unlikely to affect the survival of *Campylobacter* present in the collected sample as the rinsate was pH-buffered and contained sodium thiosulphate to neutralize the ASC. Resuscitation following sub-lethal injury to *Campylobacter* cells was also considered; however, a laboratory study, did not detect *Campylobacter* resuscitation following ASC treatment (although laboratory studies do not necessarily reflect the real-life situation, e.g. high organic or microbiota levels) (Weerasooriya et al., 2021). Instead, the higher concentrations of *Campylobacter* at secondary processing likely reflect that *Campylobacter* was present in niches that had been protected from the antimicrobial washes, such as the body cavity or in feather follicles. The removal of the feather rod results in an empty cavity which presents a negative pressure that can absorb liquid and associated bacteria from the skin surface, which then become trapped following chilling when the skin contracts around the follicle opening (Campbell et al., 1987; Thomas and McMeekin, 1981; Zhang et al., 2020). The increased friction between carcasses contained in bins during transport to Plant F secondary processing or during sampling of portions may have facilitated the externalization of those bacteria from the protected niches to locations where

they were more readily available during sample rinsate collection.

Unlike primary processing, there are no antibacterial processes administered at secondary processing, and cross-contamination of poultry meat can occur via contact with contaminated machinery, tools, work surfaces and the hands of processing plant workers. The degree of contamination on portions partially reflects the extent and duration of exposure to the processing environment. *Campylobacter* concentrations differed by portion type and processing plant, and relative to Whole birds there were higher concentrations of *Campylobacter* on portions (except Drumsticks). When data from portions were extrapolated to reconstitute all of the parts of a carcass (i.e. two wings, drumsticks, thighs and breasts, to account for different distributions of *Campylobacter* on different portions), *Campylobacter* concentrations were still higher from the reconstituted carcass than whole carcasses. A likely explanation is because there were multiple portions per sample, sampling resulted in friction between portions resulting in increased *Campylobacter* recovery. Portions in each sample came from multiple carcasses; increasing the probability that one may have arisen from a more highly contaminated carcass. Depending on the portion type, they may also have higher skin or cavity content and surface area for contamination, and additional processing increases the opportunity for cross contamination. All explanations for higher *Campylobacter* concentrations on portions relative to Whole birds, and comparisons between portions, would also apply to Drumsticks. Drumsticks had the second highest portion number per sample (the highest being wings), larger surface area and more skin relative to other portions such as Breasts and Thighs. Yet, Drumsticks consistently had the lowest *Campylobacter* concentrations of all portion types. Carcasses are hung by the legs during processing; thus, any spillage which is a source of contamination, drains below the drumsticks. Potentially, any differences in skin microstructure and topology might also contribute to differences in protected *Campylobacter* niches for different portion types.

Compared with primary processing, there are fewer published studies addressing *Campylobacter* concentrations on product at secondary processing. Indeed, based on the limited data on concentrations and/or prevalence of *Campylobacter* contamination both before and after portioning, one study assumed that contamination on portions was evenly distributed for modelling purposes (Dogan et al., 2019); such models could be enhanced using data from this study. A New Zealand study which looked at concentrations of *Campylobacter* on different portions from the same carcass (wings, drumsticks, breast and thighs) from two processors found higher concentrations on wings (Paulin and Wong, 2008). However, samples were taken prior to antimicrobial primary processing interventions, so did not represent the final retail product. A study from Belgian poultry processing plants found that wings had significantly higher *Campylobacter* counts and prevalence than breast and leg portions (Habib et al., 2008). Another study found similar concentrations of *Campylobacter* from breast, thigh and drumstick samples taken from the same eviscerated prechill carcasses, but lower concentrations from drumstick samples at retail (Berrang et al., 2001). A further study reported higher *Campylobacter* contamination from skin-on legs, thighs and wings compared with drumsticks arising from Italian deboning plants, slaughterhouses and retail; differences were attributed to the position of the carcass at the slaughterhouse (Stella et al., 2017). A study from product at retail in New Zealand found significantly lower *Campylobacter* concentrations on drumsticks compared with whole birds (Nohra et al., 2018). A survey of chicken poultry products (whole carcass, wings, breast fillet, thigh fillet, and leg quarters) from Australian supermarkets found the highest *Campylobacter* concentrations from wings and lowest from thigh fillets (Habib et al., 2019). However, a study of product at Lithuanian retail found no differences between *Campylobacter* concentrations on drumsticks and wings (Kudirkiene et al., 2013).

Chicken skin is considered highly susceptible to bacterial contamination during slaughter, with niches such as feather follicles providing a protective niche from antimicrobial washes, and *Campylobacter* has also

been reported to survive better on inoculated poultry skin than meat (Davis and Conner, 2007). However, in the current study, skinless product did not consistently have lower *Campylobacter* concentrations relative to skin-on product. Although *Campylobacter* concentrations were lower for Plant D skinless products relative to skin-on, there were no differences at Plant F, and increases on skinless products at Plant A. Plant A had a longer aging period for processing breast portions (overnight) than Plants D and F (several hours), which might result in higher cross-contamination from skin to meat. One study where the skin was carefully removed aseptically from product in the laboratory found significantly higher concentrations of *Campylobacter* on paired breasts, thighs, and drumsticks with skin compared with skinless (Berrang et al., 2001). However, that does not reflect what happens in processing plants, where manipulation of carcasses and washing steps can compromise skin integrity and cross-contamination from machinery or personnel may also occur. The influence of skin presence on *Campylobacter* concentrations on poultry product arising from secondary processing or retail varied between studies; some studies reported less *Campylobacter* on skinless product, while others reported no difference (Berrang et al., 2001; Pointon et al., 2008; Stella et al., 2017; Uyttendaele et al., 1999).

The diversity of *Campylobacter* strains present on chicken carcasses at the beginning of processing may result in the presence of strains that are more resistant to antimicrobial treatments during processing and better able to survive processing. Those better able to survive processing may in turn have important implications for public health. Consumers of contaminated product will be exposed to higher numbers of these strains, and strains that better tolerate processing stresses due to, for example a higher acid tolerance, might also be better survive transit through the stomach acid following consumption of contaminated product. In this study, there was a reduction in the proportion of *C. coli* relative to *C. jejuni* species following antimicrobial processing steps, although proportions varied across all steps. Additionally, at one plant, *C. coli* was detected at secondary processing but not primary processing, suggesting that cross-contamination from secondary processing equipment may have occurred. However, the biggest determinant of *Campylobacter* species proportions in this study was the processed flock from which they arose. Others have also reported widely varying proportions of *Campylobacter* species between flocks (Duffy et al., 2014; Hunter et al., 2009). In contrast to the findings of this study, one study reported an increase in *C. coli* proportions across processing and suggested that these strains were better able to survive processing compared with the contaminating *C. jejuni* strains (Duffy et al., 2014). Differences between studies might be due to between-strain phenotypic differences, rather than wider species-specific phenotypic differences.

To conclude, the study has demonstrated that improvements to primary processing implemented since 2013 have had a measurable impact on reducing *Campylobacter* concentrations on product during primary processing. The data also provide a benchmark from which to compare the efficacy of future interventions in the poultry industry. Data were used to construct statistical models so that industry can estimate the effect of improvements at individual primary processing steps on the concentrations of *Campylobacter* present on product (Horn et al., unpublished). The findings also inform areas for the poultry industry to further improve processing procedures to reduce *Campylobacter* prevalence and concentrations on product, toward a reduced risk for consumers.

#### Declaration of competing interest

The study was funded by the New Zealand Food Safety Science and Research Centre (NZFSSRC) through its provision from the New Zealand Ministry of Business, Innovation and Employment, with co-funding by the New Zealand Ministry for Primary Industries (MPI) and the Poultry Industry Association of New Zealand (PIANZ). Authors for the study include three members of PIANZ who contributed to project design, assisted with sampling, and provided feedback on the manuscript. In

addition, an author from MPI also contributed to study design and provided feedback on the manuscript. There are no other competing interests.

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## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.fm.2022.104168>.

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