Journal of Food Protection, Vol. 68, No. 6, 2005, Pages 1147–1153

A Study of the Prevalence and Enumeration of *Salmonella enterica* in Cattle and on Carcasses during Processing

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MS 04-571: Received 15 December 2004/Accepted 5 February 2005

ABSTRACT

Salmonella prevalence and counts were estimated for samples from the oral cavity, hide, rumen, and feces of 100 cattle at slaughter and from the pre- and postchill carcasses of these cattle. Samples were collected from 25 consecutively slaughtered cattle from each of four unrelated groups slaughtered at a single abattoir on different days. Ten additional fecal samples from each group were collected from their respective abattoir holding pens prior to slaughter. The prevalence of *Salmonella* was estimated using automated immunomagnetic separation, and the counts were estimated using a combination of most probable number (MPN) and automated immunomagnetic separation. A total of 606 samples were collected with *Salmonella* isolated from 157 (26%), including 29% of oral cavities, 68% of hides, 16% of feces collected after evisceration, 25% of rumen samples, 2% of prechill carcasses, 3% of postchill carcasses, and 48% of feces collected from holding pens. The prevalence and count of *Salmonella* varied between the different groups of animals tested. The highest count obtained was from a rumen sample (1.1×10^4 MPN/g). Other counts were generally low, with a maximum count in feces collected after evisceration and in the abattoir holding pens of 93 and 23 MPN/g, respectively. The highest count on hides, in oral cavities, and on carcasses was 4.8 MPN/cm^2, 23 MPN/g, and 0.31 MPN/cm^2, respectively. Even though *Salmonella* was present on the hides and in the rumen and feces of at least one animal from each group of cattle, the processing of animals at this abattoir resulted in few contaminated carcasses, and when contamination occurred, *Salmonella* was detected at low numbers.

Salmonella is an important cause of human gastroenteritis and is second only to *Campylobacter* as the leading cause of bacterial gastroenteritis in Australia and other countries *(19, 22).* Infections with *Salmonella* can be serious and may result in hospitalization and possibly death *(15, 19). Salmonella* is present in the gastrointestinal tract of many animals and can cause disease in these animals, although most colonized animals do not show signs of illness *(15).* Foods originating from domestic animals, such as poultry, pork, beef, eggs, and unpasteurized dairy products, are frequently responsible for foodborne outbreaks of salmonellosis. *Salmonella* can be carried by healthy cattle at slaughter *(18, 27)* and can therefore serve as a reservoir and source of contamination of carcasses during processing, providing an opportunity for entry of the pathogen into the human food chain. The consumption of beef has been associated with outbreaks of salmonellosis *(8, 9, 25, 29).* To develop science-based controls, it is necessary to understand the relationship between the carriage of *Salmonella* by cattle and the dynamics of transfer during transformation to carcasses *(8, 25, 29).*

Salmonella has been found on the hides, in the rumen, and in the feces of cattle at slaughter *(1, 18).* However, little is known about the numbers of *Salmonella* at these sites of cattle and the impact of these levels on the risk of carcass contamination. This study was designed to test different sites on cattle during the slaughter process for the presence of *Salmonella* and to determine the numbers of *Salmonella* at these sites to provide data to fill these knowledge gaps. The quantitative and qualitative data generated will lead to a further understanding of the dynamics of carcass contamination during the slaughter process that is essential for quantitative modeling of the risk of salmonellosis via the beef production pathway.

MATERIALS AND METHODS

Sampling. The cattle sampled were from four unrelated groups of 30 cattle each; two groups of cattle had been finished on grain diets in feedlots, one group consisted of grain-assisted grass-fed cattle, and the other group consisted of all grass-fed animals as previously described *(13).* All animals were slaughtered at the same abattoir under usual slaughter conditions, and each group was sampled in a different week during March and April 2003. Samples from hides, oral cavities, rumen, feces, and pre- and postchill carcasses were collected from the first 25 animals slaughtered from each group as described previously *(13).* Each animal tested was given a number between 1 and 100 in the order that it was slaughtered (e.g., group 1 contained animal numbers 1 to 25, and group 2 contained animal numbers 26 to 50), so that each sample collected could be related back to a particular animal. A total of 100 cattle were sampled at each sampling site; however, one oral cavity (animal 92) and one rumen sample (animal 26) were not collected, and fecal samples after evisceration were obtained for only 68 cattle, as there were not enough feces present in the lower intestine of the remaining cattle for testing. A further 10 samples were collected from freshly dropped feces 1 to 2 h prior to slaughter from the floors of the pens in which the animals were housed at the abattoir. These samples were not

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TABLE 1. *The prevalence of* Salmonella *in samples from different groups of cattle*[a]

Group		Oral	Hide	Rumen	Feces	Prechill carcass	Chilled carcass	Pen feces
1	No. tested	25	25	25	15	25	25	10
	Positive	10 (40) A[b]	25 (100) A	18 (72) A	8 (53) A	0	0	6 (60)
2	No. tested	25	25	24	21	25	25	10
	Positive	1 (4) B	15 (60) B	3 (13) B	1 (5) B	0	3 (12)	4 (40)
3	No. tested	25	25	25	14	25	25	10
	Positive	18 (72) A	23 (92) A	1 (4) B	1 (7) B	2 (8)	0	7 (70)
4	No. tested	24	25	25	18	25	25	10
	Positive	0 B	5 (20) C	3 (12) B	1 (6) B	0	0	2 (20)
Total	No. tested	99	100	99	68	100	100	40
	Positive	29 (29)	68 (68)	25 (25)	11 (16)	2 (2)	3 (3)	19 (48)

[a] Numbers in parentheses are percentages.

[b] Statistical analysis was performed only on oral, hide, rumen, and feces samples; for each sample type, value followed by different letters are significantly different ($P < 0.05$).

linked to specific animals but were representative of the total group.

Detection and isolation of *Salmonella enterica* serovars. All samples were diluted 1/10 with buffered peptone water (Oxoid, Basingstoke, UK) immediately upon return to the laboratory or, if this was not possible, were stored at 2°C for up to 3 h until they were diluted. Diluted samples were enriched at 37°C for 6 h or, when this was not possible, were kept chilled at 2°C for 16 to 18 h before incubation. *Salmonella* was detected in enriched samples using Dynabeads anti-*Salmonella* (Dynal, Oslo, Norway) and automated immunomagnetic separation with a BeadRetriever (Dynal) following the manufacturer's instructions. The beads were placed into 10 ml of Rappaport-Vassiliadis soya peptone broth (Oxoid) and incubated at 42°C for 20 h prior to plating onto brilliant green agar (Oxoid) and xylose lysine desoxycholate (Oxoid) agar. Plates were incubated for 24 h at 37°C. Colonies with typical *Salmonella* morphology on these media were tested with a polyvalent O A-S antiserum (Denka Seiken, Tokyo, Japan). The colonies that agglutinated with the antiserum were subcultured onto nutrient agar (Oxoid), confirmed as *Salmonella* using biochemical tests (Microbact 12E and 24E, Oxoid), and forwarded to John Bates at Queensland Health Scientific Services, Coopers Plains, Queensland, for serotyping. Isolates that required phage typing were sent to Mary Valcanis at the Microbiological Diagnostic Unit, The University of Melbourne, Victoria. Only one *Salmonella* colony per positive sample was stored and analyzed, except for samples from group 2 animals, where five individual colonies were picked per positive sample and stored for further characterization. Pulsed-field gel electrophoresis (PFGE) of *Salmonella* isolates was performed following previously described methods *(11)*.

Enumeration of *Salmonella.* The total amount of *Salmonella* was enumerated in all samples from which *Salmonella* was isolated as described previously *(14)* using a combination of 5- × 3-tube most probable number (MPN), followed by automated immunomagnetic separation. MPN values were calculated using MPN Calculator Build 22 by Mike Curiale (http://members.ync.net/mcuriale/mpn/index.html).

Statistical analyses. The prevalence of *Salmonella*-positive samples from different groups of cattle was compared using the chi-square test for independence (MINITAB, Minitab Inc., State College, Pa.). Unless otherwise stated, significance was assessed at the 95% confidence level.

RESULTS

Detection of *Salmonella enterica* serovars. A total of 606 samples were collected from 100 cattle during this study, and *Salmonella* was isolated from 26% of these samples. The highest prevalence was found on hides (68%), followed by feces from holding pens (48%), oral cavity material (29%), rumen (25%), and intestinal feces (16%) (Table 1). The lowest prevalence of *Salmonella* was found on pre- and postchill carcasses (2 and 3%, respectively). *Salmonella* was present in at least one sample from each group of cattle. The presence of *Salmonella* varied between the different groups of cattle; 7% of the samples from group 4 cattle tested positive for *Salmonella*, while 45% of the samples from group 1 tested positive. There was variation in the prevalence of *Salmonella* between sample types for each group of cattle (Table 1). The prevalence of *Salmonella* was significantly higher on the hides and in the oral cavities of cattle in groups 1 and 3, but only group 1 had a significantly higher prevalence of *Salmonella* in fecal and rumen samples (Table 1). *Salmonella* contamination of oral cavities varied, with the prevalence in different groups ranging from 0 to 72%. Hide contamination ranged from 20 to 100% between the different groups, while the prevalence in rumen samples ranged from 4 to 72%.

Salmonella was isolated from five carcasses, which included two prechill carcasses from group 3 cattle and three postchill carcasses from group 2 animals. The chilled carcasses contaminated with *Salmonella* were from animals in which *Salmonella* was not isolated from any other site on that animal (animals 39, 42, and 45). For the contaminated prechill carcasses, one came from an animal that had *Salmonella* on its hide (animal 53), while the other was derived from an animal that had *Salmonella* in both the oral cavity and on the hide (animal 63).

Samples from which *Salmonella* was isolated were more frequently found in clusters (at least two adjacent animals had a positive sample from the same site) than as isolated samples when no adjacent animals had positive samples from the same site (Tables 2 through 5). This occurred most frequently on hides in which 94% of all pos-

TABLE 2. *Counts of* Salmonella *in positive samples collected between stunning and carcass chilling from cattle in group 1*

Animal no.	Oral (MPN/g)	Hide (MPN/cm^2)	Rumen (MPN/g)	Feces (MPN/g)
1	—[a]	0.29	<3	—
2	—	<0.06	3.6	NT[b]
3	—	<0.06	9.2	<3
4	—	<0.06	—	23
5	—	<0.06	3.6	—
6	—	<0.06	9.2	NT
7	—	0.07	3.6	23
8	—	<0.06	<3	<3
9	—	0.18	<3	—
10	—	<0.06	43	NT
11	<3	0.46	—	—
12	—	<0.06	<3	NT
13	<3	0.07	—	NT
14	—	<0.06	<3	NT
15	—	<0.06	3.6	NT
16	—	<0.06	<3	3.6
17	3.6	0.07	3.6	9.2
18	—	0.18	—	—
19	<3	0.18	—	<3
20	<3	<0.06	—	NT
21	<3	0.07	—	—
22	<3	<0.06	<3	—
23	<3	0.07	3.6	NT
24	<3	<0.06	9.2	93
25	<3	<0.06	<3	NT

[a] *Salmonella* was not detected in the sample.
[b] NT, sample was not tested, as these animals did not have sufficient fecal material for testing.

TABLE 3. *Counts of* Salmonella *in positive samples tested between stunning and chilling of carcasses in group 2 cattle*

Animal no.	Oral (MPN/g)	Hide (MPN/cm^2)	Rumen (MPN/g)	Feces (MPN/g)	Chilled carcass (MPN/cm^2)
27	—[a]	—	<3	—	—
28	—	<0.06	—	—	—
29	—	<0.06	—	—	—
32	—	<0.06	—	—	—
33	—	<0.06	—	—	—
34	—	<0.06	—	—	—
35	—	<0.06	—	—	—
36	—	—	<3	—	—
37	—	<0.06	—	—	—
38	—	<0.06	—	—	—
39	—	—	—	—	<0.1
40	—	<0.06	—	NT[b]	—
41	—	<0.06	—	NT	—
42	—	—	—	—	0.31
43	—	<0.06	—	NT	—
45	—	—	—	—	<0.1
46	—	<0.06	—	NT	—
47	—	<0.06	—	—	—
48	<3	0.18	<3	<3	—
50	—	<0.06	—	—	—

[a] *Salmonella* was not detected in the sample.
[b] NT, sample was not tested, as these animals did not have sufficient fecal material for testing.

itive samples occurred in clusters. In addition, 83% of oral samples, 76% of rumen samples, and 73% of fecal samples occurred in clusters. All of the carcasses that were contaminated with *Salmonella* occurred as isolated samples.

Enumeration of *Salmonella*. The counts of *Salmonella* in the feces obtained from the holding pens have not been tabulated and are described in the following text. Counts were generally low, with the highest count (23 MPN/g) obtained from the holding pen in which group 3 cattle were housed; two other fecal samples from this group of cattle had counts of 3.6 MPN/g. There was one count of 9.2 MPN/g in a fecal sample from group 1 and one count of 3.6 MPN/g in a fecal sample from group 4. The other 14 positive fecal samples obtained from the holding pens had *Salmonella* counts that were <3 MPN/g. The numbers of *Salmonella* present in samples collected during processing from animals in group 1 (the group with the highest prevalence) were generally low (Table 2). The highest fecal count occurred in the feces of animal 24 (93 MPN/g), and the highest rumen count occurred in animal 10 (43 MPN/g). All feces, rumen, and oral material from cattle in group 2 had counts below the limit of detection of the MPN method (Table 3). The only hide sample having a count of *Salmonella* above the limit of detection was from animal 48, which had a count of 0.18 MPN/cm^2. This was the only animal in group 2 from which multiple sites yielded *Salmonella*; these included the oral cavity, rumen, and feces, but the counts in these samples were below the limit of detection (Table 3). *Salmonella* was isolated from three chilled carcasses from this group of animals; these included the carcasses of animals 39 (<0.1 MPN/cm^2), 42 (0.31 MPN/cm^2), and 45 (<0.1 MPN/cm^2).

Group 3 cattle had the highest *Salmonella* counts for any of the 99 oral cavity and 100 hide samples collected in the study (Table 4). Animal 58 had the highest *Salmonella* count from a hide (4.8 MPN/cm^2) and was the only animal from group 3 to have *Salmonella* isolated from its feces and rumen. The highest oral cavity count of *Salmonella* (23 MPN/g) was from animal 63, which also had *Salmonella* isolated from its hide and prechill carcass. The highest count of *Salmonella* found in this study was 1.1×10^4 MPN/g, which was in the rumen of animal 85 (group 4). *Salmonella* was isolated from the rumen of two other cattle from this group, animals 83 and 86, with counts of 23 and 43 MPN/g, respectively (Table 5). One fecal sample from this group was positive for *Salmonella* (<3 MPN/g, animal 85), and of the five positive hide samples from this group, that of animal 92 had a count of 0.07 MPN/cm^2, while the others were <0.06 MPN/g. Only two cattle from this group had *Salmonella* isolated from multiple sites, including animal 85 (rumen and feces) and animal 86 (hide and rumen).

Characterization of *Salmonella enterica* isolates. Fourteen *Salmonella* serotypes were isolated from cattle in this study, with different serotypes associated with each of

TABLE 4. *Counts of* Salmonella *in positive samples collected between stunning and carcass chilling from group 3 cattle*

Animal no.	Oral (MPN/g)	Hide (MPN/cm^2)	Rumen (MPN/g)	Feces (MPN/g)	Prechill carcass (MPN/cm^2)
51	—[a]	<0.06	—	—	—
52	<3	<0.06	—	NT[b]	—
53	—	<0.06	—	—	<0.1
54	<3	0.07	—	—	—
55	—	0.18	—	—	—
56	—	<0.06	—	NT	—
57	—	0.15	—	—	—
58	<3	4.8	<3	93	—
59	<3	0.85	—	—	—
60	<3	0.85	—	—	—
61	9.2	1.9	—	—	—
62	<3	1.9	—	NT	—
63	23	0.85	—	NT	<0.1
65	<3	—	—	—	—
66	<3	0.46	—	—	—
67	<3	0.46	—	NT	—
68	<3	0.46	—	NT	—
69	<3	0.85	—	—	—
70	<3	0.15	—	NT	—
71	<3	0.46	—	—	—
72	<3	0.46	—	NT	—
73	—	0.15	—	—	—
74	<3	0.07	—	NT	—
75	<3	0.07	—	NT	—

[a] *Salmonella* was not detected in the sample.
[b] NT, sample was not tested, as these animals did not have sufficient fecal material for testing.

TABLE 5. *Counts of* Salmonella *in positive samples tested between stunning and chilling of carcasses from group 4 cattle*

Animal no.	Oral (MPN/g)	Hide (MPN/cm^2)	Rumen (MPN/g)	Feces (MPN/g)
79	—[a]	<0.06	—	NT[b]
80	—	<0.06	—	—
83	—	—	23	NT
85	—	—	11,000	<3
86	—	<0.06	43	NT
90	—	<0.06	—	—
92	—	0.07	—	—

[a] *Salmonella* was not detected in the sample.
[b] NT, sample was not tested, as these animals did not have sufficient fecal material for testing.

TABLE 6. *Serotypes of* Salmonella *in positive samples collected between stunning and fabrication from four different cattle groups*

Samples	*Salmonella* serotypes
Group 1	
Oral	Anatum (2),[a] Bahrenfeld (1), Bredeney (3), Kottbus (3), Zanzibar (1)
Hide	Anatum (3), Bredeney (9), Give (3), Kottbus (2), Senftenberg (4), Tennessee (2), Zanzibar (2)
Rumen	Anatum (1), Give (2), Mbandaka (5), Orion (4), Senftenberg (6)
Feces	Give (1), Mbandaka (2), Orion (2), Senftenberg (3)
Pen feces	Infantis (1), Mbandaka (3), Senftenberg (2)
Group 2[b]	
Oral	Senftenberg (1)
Hide	Anatum (1), Bredeney (1), Give (6), Saintpaul (2), Senftenberg (1), Virchow (6)
Rumen	Muenchen (1), Senftenberg (2)
Feces	Senftenberg (1)
Chilled carcass	Bredeney (1), Give (2), Mbandaka (2), Muenchen (1)
Pen feces	Anatum (2), Bredeney (1), Give (2), Virchow (2)
Group 3	
Oral	Muenchen (17), Zanzibar (1)
Hide	Muenchen (19), Zanzibar (4)
Rumen	Zanzibar (1)
Feces	Zanzibar (1)
Prechill carcass	Muenchen (2)
Pen feces	Muenchen (1), Zanzibar (6)
Group 4	
Oral	
Hide	Muenchen (1), Virchow (3), Zanzibar (1)
Rumen	Muenchen (2), Saintpaul (1)
Feces	Muenchen (1)
Pen feces	Anatum (1), Zanzibar (1)

[a] Numbers in parentheses are the number of samples from which the *Salmonella* serotype was isolated.
[b] Multiple *Salmonella* colonies from a single sample were serotyped, and up to three *Salmonella* serotypes were present in one sample.

the animal groups (Table 6). The largest number of *Salmonella* serotypes (11 different serotypes) was isolated from group 1 cattle, while only two serotypes (Muenchen and Zanzibar) were isolated from group 3 cattle. *Salmonella* Bredeney was isolated from the majority of positive hides of animals in group 1, and, along with *Salmonella* Kottbus, these were the most common serotypes found in oral cavities. In contrast, these serotypes were not isolated from the rumen or feces with the *Salmonella* Senftenberg, *Salmonella* Mbandaka, or *Salmonella* Orion isolated from most of these samples. Of the two serotypes of *Salmonella* isolated from cattle in group 3, Muenchen was predominantly found in oral cavities and on hides, while Zanzibar was isolated from both intestinal and holding pen feces and rumen material. The *Salmonella* isolated from the carcasses of animals 53 and 63 was *Salmonella* Muenchen, but each isolate had a unique PFGE pattern that differed from each other by three bands. The patterns from animals 53 and 63 differed from that of the other *Salmonella* Muenchen isolated from the hides, oral cavities, rumen, and feces from the holding pen by two and three bands, respectively (data not shown). Only four *Salmonella* serotypes were isolated from cattle in group 4: *Salmonella* Muenchen was isolated from hide, rumen, and fecal samples; *Salmonella* Zanzibar was isolated from a hide and pen feces sample; *Salmonella*

Virchow was isolated from hides; and *Salmonella* Saintpaul was isolated from a rumen.

Multiple *Salmonella* colonies (at least five colonies per positive sample) were obtained from the isolation media of cattle in group 2, with eight different serotypes of *Salmonella* isolated from these samples. All five colonies were the same serotype of *Salmonella* in 19 of the 26 positive samples. The seven samples that contained multiple serotypes of *Salmonella* included three hides, those from animals 29 (Bredeney and Saintpaul), 37 (Anatum and Virchow), and 40 (Give and Virchow); two chilled carcasses from animals 39 (Bredeney, Give, and Mbandaka) and 42 (Give and Mbandaka); and two fecal samples collected in the holding pen (one containing the serotypes Anatum, Bredeney, and Virchow and the other containing Give and Anatum). The isolates of *Salmonella* Muenchen and *Salmonella* Bredeney obtained from carcasses and other samples within this group of cattle had indistinguishable PFGE patterns (data not shown). However, two different PFGE types of *Salmonella* Give were found among group 2 animals; those on the hides and in the pen feces were indistinguishable from each other but differed by several bands from the pattern obtained from the *Salmonella* Give isolated from the chilled carcasses (data not shown).

DISCUSSION

The prevalence of *Salmonella* within the groups of cattle was highly variable, both between the different groups of animals and among the different sites tested, while the concentration of *Salmonella* was generally low, with only one count (from a rumen) exceeding 100 MPN/g and none exceeding 5 MPN/cm^2. In each group, the hides were contaminated most often. *Salmonella* is known to be present on the hides of cattle, and contamination has been shown to increase after transportation from the farm or feedlot to the slaughter facility *(4).* The contamination rate of hides in the current study was 68%, with individual groups varying between 20 and 100%. In other studies, between 15 and 98% of cattle hides have been contaminated with *Salmonella* at slaughter *(1–3, 23, 24),* although methods for sampling and detection differ between studies, and direct comparisons cannot be made. Such data support findings that hides are potentially a major source for contamination of beef carcasses *(3, 24). Salmonella* was frequently isolated from the oral cavities of cattle, and it is possible, depending on slaughter practices, that oral cavities contribute to the contamination of other sites during processing.

The prevalence of *Salmonella* was high in the oral cavities and hides of two groups of cattle. It is unclear if there was a relationship between the contamination of these sites or if one site was the source of contamination for the other (e.g., oral cavities may become contaminated from cattle hides if the animals lick each other). *Salmonella* was isolated from 25% of the rumen samples tested, and this has been demonstrated in other studies *(26–28).* The detection of *Salmonella* in the rumen and feces did not correspond to the contamination of hides, because when hide prevalence was high, the isolation of *Salmonella* from feces and rumen material from the same group of cattle was low. Most of the positive oral, hide, rumen, and fecal samples occurred in clusters (e.g., adjacent animals within the same site positive for *Salmonella*), which may be related to the cross-contamination of different sites during slaughter or a result of social behavior between animals prior to slaughter. When cattle form small social groups and are constantly grooming each other, it is likely that cross-contamination will occur between these animals. Oral cavities may become contaminated from hides through cattle licking each other rather than from the regurgitation of rumen material, while hides are possibly contaminated from the farm and abattoir pen environments more often than directly from the feces of the cattle. This was supported by the serotyping data, as the same serotypes of *Salmonella* were often isolated from the hide and oral cavities, which were frequently different from the serotypes found in the feces and rumen of the same cattle. The highest count of *Salmonella* was obtained from a rumen, but despite the high number present in this rumen sample, hides and oral cavities were not heavily contaminated in this group of cattle. This further supports rumen material being of minor importance to hide and oral cavity contamination.

The enumeration of *Salmonella* suggested a relationship between the numbers present on hides and in oral cavities and the contamination of carcasses. Group 3 cattle had the highest counts of *Salmonella* on hides and in oral cavities, and prechill carcasses were contaminated, although at very low levels. It is possible that high counts on hides and in oral cavities contribute to the risk of contamination of carcasses. However, three chilled carcasses from group 2 cattle were contaminated with *Salmonella,* but the numbers of *Salmonella* present in other samples were mostly below the level of enumeration. The highest prevalence of *Salmonella* was found in group 1 cattle, but again, the counts of *Salmonella* in samples from these cattle were low, with no counts exceeding 100 MPN/g or 0.5 MPN/cm^2.

The prevalence of *Salmonella* on chilled carcasses from this study was 3%. This is similar to the findings of other studies; however, caution must be used in comparing results between studies because of the different methods used. In a study of carcasses from culled cows in France, 3% of 160 were contaminated with *Salmonella* Typhimurium *(23).* In other studies of beef carcasses, 1.5% of 200 carcasses from Northern Ireland *(17)* and 1.3% of 320 beef carcasses from the United States *(1)* were contaminated with *Salmonella.* There appeared to be no association between fecal carriage and carcass contamination in this study, as no positive carcasses were detected in group 1, even though this group had the highest number of *Salmonella* isolations. The concentration of *Salmonella* may be a more important factor for carcass contamination, as the numbers of *Salmonella* in group 1 cattle, particularly the hide samples, were low compared to the numbers detected on hides among group 3 cattle from which positive carcasses were found.

Three of the five *Salmonella*-positive carcasses were derived from animals from which *Salmonella* had not been isolated preprocessing. The *Salmonella* serotypes found on carcasses were isolated from within the same group of cat-

tle, although they were not isolated from other sites from the same animal. However, when the isolates were characterized by PFGE, only two isolates from the eight obtained from contaminated carcasses had PFGE patterns that were indistinguishable from others of the same serotype isolated from within the animal group. The source of contamination of these carcasses may not have been the animals themselves, but rather, the environment (including equipment) or personnel within the abattoir *(6, 7, 20).* When only a single PFGE pattern was observed within one serotype, it is possible that other molecular typing methods or combinations of methods provided further discrimination between *Salmonella* isolates *(16).* It is also possible that these *Salmonella* colonies were present in the group of cattle but were not isolated during the study, as only a single colony was typed from groups 1, 3, and 4. The results of a study of *Salmonella* in eight groups of cattle, with 10 individuals per group, showed that *Salmonella* was present in hair samples (hair collected from the hide around the brisket and aitch-bone region) and in the feces and lymph nodes. Ground meat produced from these animals was also contaminated with *Salmonella.* The authors suggest that the presence of *Salmonella* in the lymph nodes is predictive of meat contamination *(23).* Lymph nodes were not tested in this study; thus, no conclusions can be made about whether they were responsible for the contamination of the carcasses.

Comparisons of the *Salmonella* serotypes among these cattle show that most groups contained a diverse range of *Salmonella,* as groups 1, 2, and 4 had five or more different serotypes. Two of these groups were feedlot cattle, while the other group was from pasture. The serotypes isolated from the feedlot cattle included those commonly associated with cattle *(21).* In addition, *Salmonella* serotypes Senftenberg, Tennessee, Infantis, and Mbandaka were isolated. These four serotypes are commonly found in animal feedstuffs, including canola, grain, and cottonseed meal *(21).* It is possible that the source of the serotypes isolated from feedlot cattle (groups 1 and 2) was their feed, as *Salmonella* transmission to animals through feed has been observed *(10–12).* Even though the prevalence of *Salmonella* in cattle from group 3 was high, only two serotypes were isolated, Muenchen and Zanzibar. These cattle were grain-assisted organic-fed animals. This experiment was not designed to investigate the effect of feed on *Salmonella* serotypes, but it is possible that the differences observed in the diversity of serotypes between the different groups of cattle is, at least in part, the result of diet *(5).*

In addition to *Salmonella,* the presence of *Escherichia coli* O157 in these cattle was investigated *(13).* Similar to *Salmonella, E. coli* O157 contaminated hides and oral cavities more than other sites, but in contrast to *Salmonella,* it was not detected in any rumen material. This suggests that burst rumen are at a greater risk for contamination of carcasses with *Salmonella* than with *E. coli* O157. The prevalence of *E. coli* O157 and *Salmonella* contrasted between the different groups of cattle, with those in which *Salmonella* was frequently isolated yielding few samples containing *E. coli* O157 *(13).* Although cattle presented for slaughter at the abattoir in this survey had a high prevalence of pathogens, particularly on hides, carcasses were infrequently contaminated, indicating that the slaughter process and chilling practices at this abattoir prevented or reduced contamination in most cases. The relationships between the prevalence and numbers of these pathogens present at various sites on cattle and the potential risk of carcass contamination require further investigation to formulate suitable control interventions.

ACKNOWLEDGMENTS

The management and staff of the abattoir used for these studies are gratefully acknowledged for their assistance and support of this work. The cooperation of this abattoir has been invaluable for achieving the objectives of this study. This work was funded by both the Commonwealth Scientific and Industrial Research Organization (CSIRO) and Meat and Livestock Australia (MLA).

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