An Investigation of Escherichia coli O157 Contamination of Cattle during Slaughter at an Abattoir

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ABSTRACT

The extent of contamination with Escherichia coli O157 was determined for 100 cattle during slaughter. Samples from 25 consecutively slaughtered cattle from four unrelated groups were collected from the oral cavity, hide, rumen, feces after evisceration, and postchill carcass. Ten random fecal samples were collected from the pen where each group of animals was held at the abattoir. E. coli O157 was detected using automated immunomagnetic separation (AIMS), and cell counts were determined using a combination of most probable number (MPN) and AIMS. E. coli O157 was isolated from 87 (14%) of the 606 samples collected, including 24% of 99 oral cavity samples, 44% of 100 hides, 10% of 68 fecal samples collected postevisceration, 6% of 100 prechill carcass swabs, and 15% of 40 fecal samples collected from holding pens. E. coli O157 was not isolated from rumen or postchill carcass samples. E. coli O157 was isolated from at least one sample from each group of cattle tested, and the prevalence in different groups ranged from less than 1 to 41%. The numbers of E. coli O157 differed among the animals groups. The group which contained the highest fecal (7.5 × 10⁵ MPN/g) and hide (22 MPN/cm²) counts in any individual animal was the only group in which E. coli O157 was isolated from carcasses, suggesting a link between the numbers of E. coli O157 present and the risk of carcass contamination. Processing practices at this abattoir were adequate for minimizing contamination of carcasses, even when animals were heavily contaminated with E. coli O157.

Escherichia coli serotype O157 is part of the enterohemorrhagic group of E. coli and has been recognized as a human pathogen for more than 20 years (25, 30). Shiga toxin–producing E. coli O157 (referred to hereinafter as E. coli O157) can cause disease ranging in severity from mild diarrhea through severe conditions such as hemolytic uremic syndrome, which can result in death (17). E. coli O157 colonizes the gastrointestinal tract of ruminants, including healthy adult cattle (16, 20), and beef carcasses may become contaminated during slaughter and processing (1). Meat and meat products have been associated with human foodborne outbreaks, emphasizing the need for control of this pathogen in all phases of meat production (7, 10, 23). The process of risk assessment is an important way to identify factors that may be manipulated to control the risk of consumer infection. Both qualitative and quantitative data are needed for risk assessments of E. coli O157 in red meat production (9, 11, 24), and this information is required for all stages of production.

The prevalence of E. coli O157 on hides and in oral cavities of cattle may be higher than that in feces (18, 28). Feces and hides of cattle are thought to be important sources of E. coli O157 contamination of carcasses during slaughter (3, 5, 14). There is no information available on the numbers or prevalence of E. coli O157 in the oral cavity and on the hide for cattle at slaughter within Australia. The major aims of this study were to measure the prevalence and population of E. coli O157 at different sites during the cattle slaughtering process. Such quantitative and qualitative data should lead to a greater understanding of the sources of carcass contamination and to the development of methods for reducing carcass contamination.

MATERIALS AND METHODS

Cattle. Cattle originating from four unrelated farms were sampled in this study. Each group consisted of 30 cattle selected from within a larger herd. These animals were transported to the abattoir via truck, with travel times between 7.25 and 11.75 h. After the cattle arrived at the abattoir, animals from each group were housed in a single pen, where they were held for 13 to 21 h prior to slaughter. Two groups of cattle were from feedlots, one group consisted of grain-assisted grass-fed cattle, and another group was grass fed. The cattle were of mixed breed, with the average percentage of Bos indicus for each group ranging from 25 to 87%. All of the cattle had short coats, and none had visible balls of mud or feces on their hides. Each group of cattle was sampled during a separate week. Samples were taken from all sites (where possible) from the first 25 animals slaughtered from each group, for a total of 100 cattle. Samples were collected from oral cavity, hide, feces (after evisceration), rumen, and pre- and postchill carcasses for each individual animal at slaughter. Ten fecal pads were sampled from the pen in which the animals were housed, but because these samples could not be traced to individual animals they were used only as an indication of the presence of E. coli O157 in the group.

Abattoir. The abattoir from which samples were collected was an establishment with a line speed of 72 head per hour (average speed for Australian export establishments). Although operations were designed for zero tolerance of E. coli O157 as per U.S. requirements, there were no specific interventions such as...
decontamination cabinets, carcasses were not washed during dressing, and knife trimming was the only intervention in place on the kill floor. Animals from groups 1 and 3 were washed with water before they were killed.

**Sample collection and processing.** Samples collected from consecutively slaughtered animals were kept chilled and were returned to the laboratory within 1 h of collection. Samples were diluted in buffered peptone water (BPW; Oxoid, Basingstoke, UK) immediately upon arrival at the laboratory or were stored at 2°C for up to 3 h until they were diluted. When immediate incubation was not possible, the BPW-diluted samples were kept chilled at 2°C for 16 to 18 h before incubation. Storage of samples had no effect on the number of bacteria present (15).

Fecal samples were randomly collected from 10 individual fecal pats in the abattoir holding pens (pen feces) 1 to 2 h before the animals were slaughtered. A 30-g sample of feces was diluted 1:10 with BPW, and 100 g of this dilution was enriched for 6 h at 42°C and used for detection and isolation of *E. coli* O157. The remaining part of the sample was stored at 2°C for enumeration studies. Oral cavity samples were collected after the animals had been stunned and hung by one hock. The oral cavity was sampled using a dehydrated Speci-Sponge (Nasco, Fort Atkinson, Wis.). Sterile gloves were used when handling the sponge, which was used to collect material from the oral cavity by swabbing around the tongue and mouth of each animal before returning the sponge to the Whirl-Pak bag (Nasco). A fresh glove and sponge were used for each animal. The Whirl-Paks were weighed before and after collection to determine the weight of saliva and oral material that had been collected. The amount of oral material collected per animal ranged from 1.9 to 11.1 g, with an average of 5.8 g. Oral material was diluted 1:10 with BPW and stomached for 1 min. A 6-ml volume of the suspension was removed and placed into a sterile 10-ml tube and stored at 2°C for enumeration studies. The remaining sample was incubated at 42°C for 6 h. Oral material from animal 91 was not tested because the sponge was lost in the face. An area (10 by 10 cm) of each site was sampled by moving a glove was used to hold the sponge while sampling the hide surface. Three sponges were used to sample sites 1 through 3, and another sponge was used to sample sites 4 and 5. Sponges were rehydrated with 10 ml of BPW prior to sampling. A sterile glove was used to hold the sponge while sampling the hide surface. One area (10 by 10 cm) of each site was sampled by moving the sponge laterally and vertically several times with moderate pressure (usually a small amount of dirt and hair was evident on the sponges after sampling). This protocol allowed 500 cm² of the hide to be sampled. After sampling, the two sponges corresponding to the same animal were combined, and 80 ml of BPW was added. The samples were stomached for 1 min, and 10 ml of the stomached solution was removed and placed into a sterile 10-ml tube and stored at 2°C for enumeration studies. The remaining sample was incubated at 42°C for 6 h.

The rumen of each animal was sampled in the paunch room by collecting about 50 g of material in a sterile 70-ml jar. A 20-g sample of rumen material was diluted 1:10 with BPW and mixed in a sterile Schott bottle. Half of this (approximately 10 g of rumen material) was incubated at 42°C for 6 h and the remainder was stored at 2°C for enumeration studies. A rumen sample was not collected from animal 23. Intestinal feces were collected after evisceration by cutting the intestine 15 to 30 cm from the bagged end and squeezing at least 30 g of material into a sterile jar. Intestinal fecal samples were processed following the same procedure used for pen feces. Feces were not always present in the intestine of the animals; only 68 fecal samples were obtained from the 100 cattle.

Carcasses were sampled prechill (immediately after processing but before entry into the chiller) and postchill (after 17 to 24 h of chilling). Carcass sides were sampled by alternating between left side of one animal and the right side of the next animal to eliminate bias from left- or right-handed workers. The side of the carcass not sampled prechill was sampled postchill. Pre- and postchill carcass samples were collected following the method and sites described for the export meat industry *E. coli* and *Salmonella* monitoring program of the Australian Quarantine Inspection Service (4). This method involved sampling three areas (10 by 10 cm) of the flank, brisket, and buttock using a Speci-Sponge as described for the sampling of hides. The samples were returned to the laboratory, where 90 ml of BPW was added to the sponge, the sample was stomached for 1 min, 10 ml was removed and stored at 2°C for enumeration, and the remainder was enriched for 6 h at 42°C.

All samples were tested for *E. coli* O157 using automated immunomagnetic separation (AIMS) after 6 h of enrichment using anti- *E. coli* O157 beads (Dynal, Oslo, Norway) and the Bead-Retriever (Dynal), according to the manufacturer’s instructions. Collected beads were plated onto sorbitol MacConkey agar (SMAC; Oxoid) containing 0.05 mg liter⁻¹ cefsulodin and 2.5 mg liter⁻¹ tellurite (CT-SMAC) (31) and CHROMagar O157 (CHROMagar, Paris, France). Colonies with the appropriate morphology, i.e., colorless on CT-SMAC or mauve on CHROMagar O157, were serotyped using an *E. coli* O157 latex agglutination kit (Oxoid). Isolates that tested positive with the agglutination kit were streaked onto nutrient agar (Oxoid) and characterized.

**Enumeration of *E. coli* O157.** *E. coli* O157 was enumerated in all samples that tested positive for this bacterium. Enumeration was performed as previously described (15) using a combination of a 5- × 3-tube most probable number (MPN), followed by AIMS. An MPN tube was considered positive when a colony on the selective and differential media had the correct colony morphology and agglutinated with the specific antiserum. MPN values were calculated using MPN Calculator Build 22 (Mike Curiale, http://members.ync.net/mcuriale/mpn/index.html). The lowest count possible using the MPN-AIMS method (e.g., a single positive MPN tube from the dilution series) was 3.6 MPN/g for oral cavity, fecal, and rumen samples, 0.07 MPN/cm² for hides, and 0.12 MPN/cm² for carcasses (pre- and postchill). Samples from which *E. coli* O157 was isolated but where no count was obtained (all MPN tubes were negative) were recorded as having counts of <3 MPN/g for feces, oral cavity material, and rumen samples, <0.06 MPN/cm² for hides, and <0.1 MPN/cm² for carcasses.

**Characterization of *E. coli* O157.** One *E. coli* O157 isolate from each sample was characterized; this isolate was obtained from the initial isolation and not from the enumeration study. All *E. coli* O157 isolates were tested for genes encoding the O157 rfb (13), Shiga toxins (stx₁ and stx₂), *E. coli* attaching and effacing factor (eaeA), and enterohemolysin (ehxA) (22). *E. coli* O157 isolates were tested for the presence of the H7 antigen by incubating inoculated motility medium at 25°C for up to 1 month (26) and serotyping motile strains using the RIM *E. coli* H7 test antiserum (Remel, Lenexa, Kans.). Nonmotile strains were repassaged through motility medium at least twice. Clonal relationships between isolates from different samples were determined by analysis of pulsed-field gel electrophoresis (PFGE) patterns. PFGE
plugs were prepared following the method of Böhm and Karch
(8) and were digested and run for 22 h under the conditions
described by Davis et al. (12) using a CHEF DR III (Bio-Rad, Her-
cules, Calif.) and pulsed-field certified agarose (Bio-Rad). PFGE
patterns were analyzed using Molecular Analyst Fingerprinting
software (version 1.6, Bio-Rad) with the DICE similarity coeffi-
cient and clustering by the unweighted pair group method using
arithmetic averages. For the purposes of this study, isolates that
had indistinguishable PFGE patterns (100% similar) were consid-
ered as belonging to the same PFGE type. When patterns differed
from other patterns by one or more bands, they were considered
as belonging to a different PFGE type.

RESULTS

A total of 606 samples were collected from the four
groups of cattle studied. Eighty-seven (14%) samples con-
tained E. coli O157, and E. coli O157 was isolated from at
least one sample in each group of cattle. Hides were the most
frequently contaminated site (E. coli O157 isolated from 44% of samples) followed by oral cavities (E. coli 
O157 isolated from 24% of samples). E. coli O157 was not
isolated from rumen or postchill carcass samples. The
prevalence of E. coli O157 in samples differed among cattle
groups and among sites sampled within cattle groups (Fig.
1). Group 1 cattle had the lowest prevalence of E. coli O157
(0.7%), with only one hide sample testing positive, and
group 4 cattle had the highest prevalence, with 41% of all
samples collected containing E. coli O157.

E. coli O157 was detected on six prechill carcasses
(animals 92, 93, 94, 95, 99, and 100), all from animals in
group 2 where the highest prevalence of E. coli O157 was
found. All positive carcass samples were obtained from an-
imals that had E. coli O157:H7 on their hides. In three
animals (animals 93, 94, and 95), E. coli O157 was also
present in fecal samples. During the collection of samples,
the carcasses of animals 92 and 93 were removed to the
retaining rail and further trimmed before rejoining the main
line out of sequence but before animal 100 was processed.
The specific reason for these two carcasses being placed on
the retaining rail is unknown, but this area is used for car-
casses that require further inspection by plant veterinarians

because of surface contamination from feces, rumen, or
urine or because the animal is thought to be diseased.

Samples positive for E. coli O157 occurred in clusters
(i.e., at least one adjacent animal with a positive sample
from the same site) more frequently than as individual posi-
tive samples (i.e., no adjacent animal with a positive sam-
ple site). The majority of all hide (89%) and oral (92%) samples positive for E. coli O157 occurred in clusters, but
only 43% of positive fecal samples were clustered. Clus-
tering of positive carcasses occurred for animals 94, 95, 99,
and 100; however the percentage of clustered carcasses
could not be determined because carcasses 92 and 93 were
removed to the retaining rail and their exact return position
was unknown.

Enumeration of E. coli O157. The ranges of E. coli
O157 counts from positive samples collected from individ-
ual animals were <3 MPN/g to 4.6 × 10^5 MPN/g for pen
feces, <3 to 3.6 MPN/g for oral cavities, <0.06 to 22
MPN/cm² for hides, 3.6 MPN/g to 7.5 × 10^5 MPN/g for
feces, and <0.1 to 0.12 MPN/cm² for prechill carcasses.
The highest E. coli O157 count was detected in the feces
of animal 93 (group 4): 7.5 × 10^5 MPN/g. Only one sample
from group 1 tested positive for E. coli O157; this was the
hide of animal 14, which had a count of 0.07 MPN/cm².
E. coli O157 was isolated from one pen fecal sample (<3
MPN/g) and four animal samples from cattle in group 2;
the hides of animals 30 and 37 (0.15 and <0.06 MPN/cm²,
respectively) and the feces of animals 44 and 49 (430 and
7.4 MPN/g, respectively). Counts of E. coli O157 on the
hides of animals from group 3 ranged from <0.06 to 9.2
MPN/cm² (Table 1), and counts in oral cavities were <3
MPN/g.

Cattle from group 4 had the highest prevalence of E.
coli O157 and the highest count of E. coli O157 in feces

<table>
<thead>
<tr>
<th>Animal no.</th>
<th>Count (MPN/g)</th>
<th>PFGE type</th>
<th>Count (MPN/cm²)</th>
<th>PFGE type</th>
</tr>
</thead>
<tbody>
<tr>
<td>55</td>
<td>ND</td>
<td>0.15</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>58</td>
<td>ND</td>
<td>0.46</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td>60</td>
<td>ND</td>
<td>&lt;0.06</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>61</td>
<td>ND</td>
<td>0.07</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>62</td>
<td>ND</td>
<td>9.2</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>63</td>
<td>&lt;3</td>
<td>&lt;0.06</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>64</td>
<td>ND</td>
<td>0.85</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>65</td>
<td>ND</td>
<td>0.29</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>66</td>
<td>ND</td>
<td>0.46</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>67</td>
<td>ND</td>
<td>&lt;0.06</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>68</td>
<td>ND</td>
<td>&lt;0.06</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td>69</td>
<td>ND</td>
<td>&lt;0.06</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>70</td>
<td>ND</td>
<td>0.18</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>72</td>
<td>&lt;3</td>
<td>0.07</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>73</td>
<td>ND</td>
<td>&lt;0.06</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>75</td>
<td>ND</td>
<td>0.18</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

* ND, E. coli O157 was not detected in the sample.
and on hides, and this group included the only animals from which *E. coli* O157 was isolated from carcasses. Counts of *E. coli* O157 from various sites for group 4 animals are shown in Table 2. There were five positive fecal samples collected from the pen in which group 4 animals were held, with counts of 3.6, 23, 74, 93, and 46,000 MPN/g of feces.

**Characterization of *E. coli* O157 isolates.** All of the *E. coli* O157 isolates in this study carried the *eaeA* and *ehxA* genes. The majority (74.7%) carried the gene encoding Shiga toxin 2, 19.5% carried the gene for Shiga toxin 1, and only 5.8% carried both Shiga toxin genes. Most (76%) isolates were of the *E. coli* O157:H7 serotype. This serotype was isolated from cattle in groups 1, 2, and 4. The isolates from group 3 animals were all *E. coli* O157:H−, as was one isolate from group 2 (feces of animal 49) and two isolates from group 4 animals (oral cavity of animal 84 and hide of animal 89).

There were 14 different PFGE patterns (types 1 to 14) among the 87 *E. coli* O157 isolates from these cattle (Table 3). Most (64%) *E. coli* O157 isolates belonged to two PFGE patterns (types 1 and 2), these isolates were mostly from group 4 cattle, but one isolate came from group 2 cattle. PFGE types 1, 2, and 5 were all clonally related; these patterns differed by only one or two bands. *E. coli* O157 isolates of PFGE type 2 were obtained from all but one of the carcasses; an isolate with PFGE type 1 was found on the carcass of animal 99 (Table 2). *E. coli* O157 isolates of PFGE type 1 were obtained from the majority of sites sampled from animals 76 through 88, and those of PFGE type 2 were obtained from the majority of sites sampled from animals 80 through 100. In some cases, the *E. coli* O157 isolated from different samples taken from the same animal were of different PFGE types, whereas in other cases only one PFGE type was isolated from multiple sites for the same animal.

The PFGE type of the *E. coli* O157 isolate from group 1 (type 10) was not found in any other group of animals. There were four different PFGE patterns (types 1, 4, 11, and 13) represented among the five *E. coli* O157 isolates obtained from cattle in group 2; the fecal samples from the pen and the intestines had indistinguishable PFGE patterns. An isolate with this PFGE pattern (type 4) was also obtained from the hide of animal 97 in group 4. Two PFGE patterns (types 3 and 6) were present in the *E. coli* O157:H− isolates from group 3 cattle (Table 1). Two isolates of type 6 were present on hides (animals 58 and 68), and the remaining 16 isolates belonged to type 3. All isolates from group 3 cattle were *E. coli* O157:H−.

**DISCUSSION**

There was variability among the different animal groups with respect to the prevalence of *E. coli* O157. There did not appear to be any consistent pattern across the individual groups, except that hides were the most commonly contaminated site. Clustering of positive samples occurred, i.e., adjacent animals in the processing line were contaminated with *E. coli* O157. This finding may be related to cross-contamination of different sites during slaughter or to social behavior among animals prior to slaughter. Cattle are thought to form small social groups, even within a small herd. If animals enter the slaughter line in these groups in which they had close social contact, all the animals in the group may be contaminated with the same strain of *E. coli* O157.

*E. coli* O157 was more often isolated from hides and oral cavities of cattle than from feces. The prevalence of *E. coli* O157 on the hides of cattle from different groups ranged from 4 to 100%, with an overall average of 44%. This result is similar to that in another study, where the prevalence of *E. coli* O157 on hides from individual groups or pens of cattle ranged from 25 to 93% (18, 28). In the same study, the prevalence of *E. coli* O157 in the oral cavities of feedlot cattle was 75% (of 139 animals), with values ranging from 50 to 95% within individual groups of cattle (18). The prevalence of *E. coli* O157 in the oral cavities of cattle in the present study (24%) was lower than that reported in the United States, and the prevalence within individual groups ranged more widely (0 to 100%). The animals studied in this survey were a mixture of feedlot and grass-fed cattle. The highest prevalence occurred in group 4 cattle, which were grass fed; however, because the experiment was not designed to compare prevalence of pathogens in cattle from different production systems, no conclusions can be made concerning pathogen carriage and specific production systems.

Cattle carrying *E. coli* O157 on their hides but notshedding detectable numbers in their feces were found in this study and others (14, 18, 28). Indirect hide-to-hide contamination between cattle has been suggested as a major route of transmission of *E. coli* O157, with direct feces-to-hide contamination of an individual playing only a minor role (28). A correlation between hide and fecal *E. coli* O157 prevalence and carcass contamination has been demonstrated (14), and carcass contamination occurring during hide removal and bung tying has been found in some abattoirs (19). The source of both generic *E. coli* and *E. coli* O157 on carcasses is thought to be the feces and hides of animals within the group (3, 6). This hypothesis is supported by the results of the present study; *E. coli* O157 carcass isolates had PFGE patterns indistinguishable from those of hide and fecal isolates from the same group of animals. The feces of other animals transported in the same vehicle or held in the same pen may also be sources of hide contamination. *E. coli* O157 was not detected in any of the rumen samples; this finding is consistent with *E. coli* O157 colonization of only the lower intestine (16, 20). *E. coli* O157 has occasionally been isolated from rumen fluid (29), particularly in the first few days after *E. coli* O157 inoculation (16). The results from the present study suggest that the risk of carcass contamination with *E. coli* O157 from a ruptured rumen is low.

Carcasses contaminated with *E. coli* O157 were found only in group 4 cattle. This group had the highest prevalence of *E. coli* O157 at all the sites tested. All six positive carcass samples were obtained from animals that had *E. coli* O157:H7 on their hides, whereas only three animals (animals 93, 94 and 95) shed detectable *E. coli* O157:H7 in
TABLE 2. E. coli O157 counts and PFGE types in samples collected between stunning and processing of cattle in group 4

<table>
<thead>
<tr>
<th>Animal no.</th>
<th>Oral cavity (MPN/g)</th>
<th>PFGE type</th>
<th>Hide (MPN/cm²)</th>
<th>PFGE type</th>
<th>Feces (MPN/g)</th>
<th>PFGE type</th>
<th>Prechill carcass (MPN/cm²)</th>
<th>PFGE type</th>
</tr>
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<tbody>
<tr>
<td>76</td>
<td>3.6</td>
<td>1</td>
<td>0.29</td>
<td>1</td>
<td>NT</td>
<td>2</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>77</td>
<td>&lt;3</td>
<td>1</td>
<td>0.46</td>
<td>1</td>
<td>NT</td>
<td>2</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>78</td>
<td>&lt;3</td>
<td>1</td>
<td>0.18</td>
<td>2</td>
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<td>ND</td>
<td>ND</td>
<td></td>
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<tr>
<td>79</td>
<td>ND</td>
<td></td>
<td>0.18</td>
<td>1</td>
<td>NT</td>
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<td>&lt;3</td>
<td>1</td>
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<td>0.46</td>
<td>1</td>
<td>NT</td>
<td>ND</td>
<td>ND</td>
<td></td>
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<tr>
<td>84</td>
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<td>7</td>
<td>&lt;0.06</td>
<td>1</td>
<td>ND</td>
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<tr>
<td>85</td>
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<td>ND</td>
<td></td>
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<tr>
<td>86</td>
<td>&lt;3</td>
<td>5</td>
<td>0.07</td>
<td>1</td>
<td>NT</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>87</td>
<td>&lt;3</td>
<td>14</td>
<td>0.46</td>
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<td>ND</td>
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<td>ND</td>
<td>ND</td>
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<td>90</td>
<td>&lt;3</td>
<td>1</td>
<td>0.46</td>
<td>2</td>
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<td>ND</td>
<td>ND</td>
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</tr>
<tr>
<td>91</td>
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<td>ND</td>
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<td>&lt;3</td>
<td>2</td>
<td>0.46</td>
<td>2</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>93</td>
<td>&lt;3</td>
<td>2</td>
<td>0.85</td>
<td>2</td>
<td>750,000</td>
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<td>94</td>
<td>3.6</td>
<td>2</td>
<td>4.8</td>
<td>2</td>
<td>930</td>
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<td>0.12</td>
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</tr>
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<td>95</td>
<td>&lt;3</td>
<td>2</td>
<td>22</td>
<td>2</td>
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<td>ND</td>
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<tr>
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<td>&lt;3</td>
<td>2</td>
<td>4.8</td>
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<td>NT</td>
<td>ND</td>
<td>ND</td>
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<tr>
<td>98</td>
<td>&lt;3</td>
<td>2</td>
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<tr>
<td>99</td>
<td>&lt;3</td>
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<td>ND</td>
<td>ND</td>
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<tr>
<td>100</td>
<td>&lt;3</td>
<td>2</td>
<td>0.46</td>
<td>1</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
</tbody>
</table>

a E. coli O157 was not isolated from rumen or postchill carcass samples.

b NT, samples were not tested because insufficient sample was available (feces) or sample was lost (oral cavity).

c ND, E. coli O157 was not detected in the sample.

92 and 93 were removed to the retaining rail during dressing; however, the reason for this removal was not provided by the abattoir. Carcasses that have visible signs of gross contamination (e.g., burst rumen or contamination with visible digesta) are removed to the retaining rail, but there may be other reasons for removal as well.

TABLE 3. Characterization of all E. coli O157 isolates from cattle samples

<table>
<thead>
<tr>
<th>PFGE type</th>
<th>Shiga toxin gene</th>
<th>Serotype</th>
<th>No. of isolates</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>O157:H7</td>
<td>1</td>
<td>Group 2: hide</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>O157:H7</td>
<td>22</td>
<td>Group 4: hides, oral, feces, and carcasses</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>O157:H−</td>
<td>16</td>
<td>Group 3: hides and oral</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>O157:H7</td>
<td>2</td>
<td>Group 2: feces (pen and intestinal)</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>O157:H7</td>
<td>2</td>
<td>Group 4: oral and feces</td>
</tr>
<tr>
<td>6</td>
<td>1, 2</td>
<td>O157:H−</td>
<td>2</td>
<td>Group 3: hides</td>
</tr>
<tr>
<td>7</td>
<td>1, 2</td>
<td>O157:H−</td>
<td>1</td>
<td>Group 4: oral</td>
</tr>
<tr>
<td>8</td>
<td>2</td>
<td>O157:H7</td>
<td>1</td>
<td>Group 4: pen feces</td>
</tr>
<tr>
<td>9</td>
<td>2</td>
<td>O157:H7</td>
<td>1</td>
<td>Group 4: pen feces</td>
</tr>
<tr>
<td>10</td>
<td>2</td>
<td>O157:H7</td>
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<td>Group 1: hide</td>
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<td>11</td>
<td>2</td>
<td>O157:H7</td>
<td>1</td>
<td>Group 2: hide</td>
</tr>
<tr>
<td>12</td>
<td>1, 2</td>
<td>O157:H−</td>
<td>1</td>
<td>Group 4: hide</td>
</tr>
<tr>
<td>13</td>
<td>1</td>
<td>O157:H−</td>
<td>1</td>
<td>Group 2: feces</td>
</tr>
<tr>
<td>14</td>
<td>1, 2</td>
<td>O157:H7</td>
<td>1</td>
<td>Group 4: oral</td>
</tr>
</tbody>
</table>

their feces. Hides and oral cavities were the most frequently contaminated sites and a likely source of carcass contamination. A relationship has been demonstrated between the prevalence of E. coli O157 on hides and contamination of preevisceration carcasses (2, 14). The carcasses of animals
have been other reasons the carcasses were removed that were not related to visible contamination. *E. coli* O157 was not isolated from the carcasses after chilling, possibly because carcasses were sampled on the opposite side from where prechill samples were obtained. It is also possible that chilling reduced the numbers of *E. coli* O157 to undetectable levels (19).

The highest carcass count for *E. coli* O157 was on the carcass of animal 94. The *E. coli* O157 PFGE type found in the feces of animal 94 was different from that found on the carcass. This animal may have been carrying multiple PFGE types of *E. coli* O157 in its feces, of which only one type was isolated, or the carcass may have been contaminated with *E. coli* O157 from another site of this animal or from a different animal or source, such as the abattoir environment. Only one isolate from each sample was characterized, and other PFGE types may have been present in the samples but not characterized. *E. coli* O157 of PFGE types 1 and 2 were clonally related. Their patterns differed by only one band (27), indicating that these isolates may all have originated from the same source or may have mutated by a single band during the process of isolation and characterization.

The *E. coli* O157 count in the feces from animal 93 was \(7.5 \times 10^5\) MPN/g. This was the highest count recorded in the study, and this animal could be considered a “super shedder” (20, 21). *E. coli* O157 of PFGE type 2 was shed by this animal. A small amount of feces from animal 93 may have contaminated the majority of carcasses from animals 92, 93, 94, 95, and 100, either through direct contact or by cross-contamination of equipment or personnel; all of these carcasses contained *E. coli* O157 isolates of PFGE type 2. In other studies, adjacent carcasses often have been contaminated with indistinguishable strains of *E. coli* O157 (19).

The cattle presented for slaughter at the abattoir in this survey had a high pathogen prevalence on the hide and in the oral cavity. Prechill carcasses had a low prevalence and were contaminated with small numbers of *E. coli* O157; this pathogen was not detected on postchill carcasses. The high prevalence of *E. coli* O157 on animals entering slaughter and the failure to detect this pathogen on chiller carcasses suggests that the slaughter process and chilling practices were able to prevent or reduce contamination of carcasses significantly in the majority of cases.

**ACKNOWLEDGMENTS**

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**REFERENCES**


