Research Note

Escherichia coli O157 in Cull Dairy Cows on Farm and at Slaughter

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ABSTRACT

Cull dairy cattle both on the farm and at slaughter from herds in the states of Idaho, Oregon, and Washington were surveyed for *Escherichia coli* O157 by culturing fecal swab samples. A total of 205 cull cows from 19 dairy herds were sampled on the farm of origin; 7 (3.4%) tested positive for *E. coli* O157. A total of 103 cull cows from 15 dairy herds were sampled at slaughter; 4 (3.9%) were positive for *E. coli* O157. Eighty-nine cull cows were sampled both at the farm and at slaughter; 2 (2.2%) were positive in both locations, 3 (3.3%) only on the farm, and 2 (2.2%) only at the slaughter plant. Seven (7.9%) of the 89 cull cows tracked from farm to slaughter were positive in at least one location. This suggests a higher prevalence of *E. coli* O157 in cull dairy cattle than previously has been reported to occur in other ages and classes of cattle.

Key words: *E. coli* O157, cull dairy cattle

Public health investigations of *Escherichia coli* O157 outbreaks have demonstrated that ground beef is an important food vehicle for human infections *(1, 4, 5, 9, 10)*. These findings have been an impetus for research focused on the epidemiology of this organism in cattle operations, slaughter plants, and meat-processing facilities. Surveys for *E. coli* O157 in dairy cattle have shown postweaned animals to have a higher frequency of colonization than other ages of cattle in dairy herds *(6–8)*. Therefore, sampling of postweaned cattle is believed to be the most sensitive indicator of herd status for *E. coli* O157.

Although the status of postweaned heifers has been used to evaluate herd level risk factors for *E. coli* O157 on dairy operations, the status of this age group is hypothesized to be only indirectly related to the occurrence of contaminated ground beef. Cull dairy cattle are an important source of beef products: thus the incidence of *E. coli* O157 in cull dairy cattle would be a more direct indicator of the potential role that dairy cattle play in the occurrence of contaminated beef products.

Although the pathways for contamination of ground beef are still under investigation, it is reasonable to hypothesize a positive correlation between the prevalence of *E. coli* O157 in cull dairy cows entering slaughter plants and the prevalence of *E. coli* O157-contaminated ground beef produced from these cows. In order to begin exploring this hypothesis, a study was completed to determine the prevalence of Shiga toxin-positive *E. coli* O157 in cull dairy cows on the farm and after arrival to the slaughter plant. This study was part of a larger study which investigated various herd-level risk factors for *E. coli* O157 in dairy herds *(8)*.

MATERIALS AND METHODS

This study was performed in conjunction with another study that evaluated several herd-level risk factors for *E. coli* O157 in 36 dairy herds (12 each in Idaho, Oregon, and Washington) *(8)*. State or federal animal health officials visited each herd monthly and attempted to acquire a fecal sample from all cows in the herd which were targeted for culling within the following 7 days. When one or more cows were sampled from a herd, the animal health official attempted to determine the likely marketing destination (e.g., livestock market, buying station, or direct to slaughter plant). When a cull cow could be traced through marketing channels, the slaughter plant was notified of its impending arrival and another fecal sample was collected just prior to slaughter. Cull cows were identified on the farm using ear tags and this identification was correlated with back tags applied at livestock markets or buying stations when such marketing channels were known.

Fecal samples were collected from the rectum by using cotton-tipped swabs, which were placed in tryptic soy broth (Difco Laboratories, Detroit, MI) containing 40 µg of vancomycin (Abbott Laboratories, Chicago, IL) and 50 ng of cefixime (Wyeth-Ayerst, Pearl River, NY) per ml. These samples were refrigerated and shipped by overnight delivery to the laboratory. Laboratory identification of *E. coli* O157 was based on a lack of sorbitol fermentation and β-glucuronidase activity and on possession of the O157 antigen and Shiga toxin genes *(2, 11)*.

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TABLE 1. *Prevalence of* E. coli *O157 in dairy cattle on their farm of origin and at slaughter*

Cattle sampled at:	No. of herds sampled	No. of cattle sampled	No. (%) of positive samples
Farm of origin	19	205	7 (3.4)
Slaughter	15	103	4 (3.9)
Both farm of origin and at slaughter	15	89	2 (2.2)
Positive on farm only			3 (3.3)
Positive at slaughter only			2 (2.2)
Positive on farm or at slaughter			7 (7.9)

RESULTS

A total of 205 cull cows from 19 of the study herds were sampled at the farm of origin; 7 (3.4%) tested positive for *E. coli* O157 (Table 1). A total of 103 cull cows from 15 study herds were sampled at slaughter; 4 (3.9%) were positive. Eighty-nine cull cows were sampled both at the farm and at slaughter; of these 2 (2.2%) were positive in both locations, 3 (3.3%) only on the farm, and 2 (2.2%) only at the slaughter plant. Seven (7.9%) of the 89 cull cows tracked from farm to slaughter were positive in at least one location. The average time between sampling on farm and at slaughter was 2 days (range, 0 to 6 days) for all paired samples. All *E. coli* O157-positive samples from cull cows were from farms in which *E. coli* O157 had been identified in heifers during the risk-factor study *(8)*.

DISCUSSION

The number of samples collected in this study was limited by the logistics of identifying cull cows in the study herds, capturing these cows for sampling on-farm, and accurately tracking these cows through marketing channels for sampling at slaughter. On-farm sampling was affected by the time available for animal health officials to complete sampling, timing of monthly visits, and willingness of producers to arrange for capture of cull cows for sampling. These factors influenced the inability to get at least one cull cow sample from 17 of the 36 herds participating in the risk factor study. Also, some cull cows were slaughtered in plants located outside the 3 states participating in this study and it was not possible to make arrangements with plant personnel to sample those cattle.

During the slaughter process, beef products may become contaminated with *E. coli* O157 directly by fecal contamination during evisceration. Another mechanism of contamination is through fomites originating from *E. coli* O157-contaminated cattle hides. Thus, even a low prevalence of *E. coli* O157-infected cattle entering the slaughter process could become amplified through the soiling of cattle hides with *E. coli* O157 from the feces of infected cattle.

Although the cull cow sampling described in the present study was limited, the results suggest that these cows may be an important component of human food-borne exposure.

Among the 89 cows followed from farm to slaughter, 7.9% were positive for *E. coli* O157 on the farm and/or at the slaughter plant. Both the single-point sample prevalence and the two-point combined prevalences are higher than previously reported for adult cattle, and higher even than that observed in postweaned heifers (an age group that is considered to be the most readily colonized with *E. coli* O157) *(6–8)*. Among 4,762 adult dairy cattle fecal samples assayed for *E. coli* O157 in a study in the same region, 0.4% were culture positive *(7)*. In a longitudinal study in which cattle of all ages were sampled an average of 3.7 times, 4.9% of the cattle were positive at least once *(3)*. Although the findings of the present study must be interpreted with caution because of the limited sample size, they suggest that *E. coli* O157 prevalence may be higher in cull dairy cattle than in other classes of dairy cattle.

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