Environmental sources and transmission of *Escherichia coli* O157 in feedlot cattle

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Abstract — A study was conducted in 2 feedlots in southern Alberta to identify environmental sources and management factors associated with the prevalence and transmission of *Escherichia coli* O157:H7. *Escherichia coli* O157:H7 was isolated in preslaughter pens of cattle from feces (0.8%), feedbunks (1.7%), water troughs (12%), and incoming water supplies (4.5%), but not from fresh total mixed rations. Fresh total mixed rations did not support the growth of *E. coli* O157:H7 and *E. coli* from bovine feces following experimental inoculation. Within a feedlot, the feces, water troughs, and feedbunks shared a few indistinguishable subtypes of *E. coli* O157:H7. A few subtypes were repeatedly isolated in the same feedlot, and the 2 feedlots shared a few indistinguishable subtypes. The prevalence of *E. coli* O157:H7 in water troughs of preslaughter cattle in 1 feedlot was associated with season, maximum climatic temperatures the week before sampling; total precipitation the week before sampling, and coliform and *E. coli* counts in the water trough.

Résumé — Sources environnementales et transmission d'*Escherichia coli* O157 à des bovins en parc d'engraissement. Une étude a été menée dans deux parcs d'engraissement du sud de l'Alberta afin de détecter les sources environnementales et les facteurs de gestion associés à la prévalence et à la transmission d'*Escherichia coli* O157:H7. *Escherichia coli* O157:H7 a été isolée dans les fèces (0,8 %), les mangeoires (1,7 %), les abreuvoirs (12 %), et l'eau d'alimentation (4,5 %), des enclos où sont gardés les animaux sur le point d'être abattus, mais pas dans les mélanges de rations totales fraîches. Les mélanges de rations totales fraîches inoculées à titre expérimental ne permettent pas la croissance d'*E. coli* O157:H7 et d'*E. coli* provenant des fèces de bovins. Dans un parc d'engraissement, les fèces, les abreuvoirs et les mangeoires contenaient quelques sous-types communs d'*E. coli* O157:H7. Quelques sous-types ont été détectés plusieurs fois dans le même parc d'engraissement, et deux sous-types communs ont été isolés dans les deux parcs d'engraissement. La prévalence d'*E. coli* O157:H7 dans les abreuvoirs des animaux d'un parc d'engraissement qui étaient destinés à l'abattage était associée à la température saisonnière élevée et aux précipitations enregistrées la semaine précédant le prélèvement d'échantillons, ainsi qu'à la quantité de coliformes et d'*E. coli* dans les abreuvoirs.

(Traduit par Madame Suzanne Gasseau)

Can Vet J 2001;42:714–720

Introduction

The group of enterohemorrhagic *Escherichia coli*, the most common member of which is *E. coli* O157:H7, is the food-borne pathogen of greatest concern to the cattle industry. In 1996–97, the *Canadian Cattlemen — Quality Starts Here Program* conducted a study in Alberta to determine the prevalence of *E. coli* O157:H7 in the feces and rumen of cattle at processing (1). *Escherichia coli* O157:H7 was found in 12.4% of fecal samples from yearling cattle and in 2.0% of the fecal samples from cull cows. The prevalence of *E. coli* O157:H7 in yearling cattle rose from 1.4% in the winter to 40% in the summer. A similar summer peak was noticed in cull cows, where the prevalence rose from 0% in the winter to 5% in the summer. These results suggested that research efforts should be targeted at reducing the level of *E. coli* O157 in fed cattle during the summer.

A similar peak of *E. coli* O157 shedding in the summer has been noticed in the United States and England (2–8). The clear seasonal peak of fecal shedding of *E. coli* O157 in cattle may be due to a point source of infection; infections from several sources over the summer; or greater multiplication of the bacteria in a warm environment, resulting in more efficient transfer among animals. In a few studies, *E. coli* O157 has been isolated from water and feed, and scientific data show that the infection in cattle is of a short duration and that a chronic carrier state is probably not established (2–8).

Results from a U.S. feedlot study suggested that newly arrived cattle have a higher prevalence of *E. coli* O157 than cattle that have been on feed (4,7). There are no data in Canada that describe the prevalence of *E. coli* O157 in cattle during the feeding period and how or if transmission occurs between animals. Knowledge of this transmission is important in determining how to reduce infection in cattle and contamination in the environment.

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Funding provided by the Beef Industry Development Fund.

The objectives of the study here were to identify environmental sources and management factors that may be associated with the fecal shedding of *E. coli* O157:H7 in feedlot cattle, and to determine the means of transmission of *E. coli* O157:H7 in feedlot cattle. This information may help the industry to target research at potential intervention strategies, such as improving water quality, inhibiting growth of *E. coli* O157 in feed by means of additives, and immunizing cattle to reduce their susceptibility to colonization by *E. coli* O157.

Materials and methods

Factors affecting the seasonal prevalence of *E. coli* 0157: September 1998 to August 1999

Two feedlots in southern Alberta were visited once a month for 1 y to look at the seasonal prevalence of *E. coli* O157. At each feedlot, samples were collected from cattle feces, water troughs, incoming water supplies, feedbunks, and the mixer wagon (fresh total mixed rations (TMR)) from 10 different pens of cattle within approximately 1 mo of slaughter. Thirty swab fecal samples from fresh manure patties were collected from each pen to estimate the prevalence of *E. coli* O157 in the feces in each pen. Thirty fecal samples per pen has been used before in a feedlot survey in the United States to obtain reliable estimates of the pen prevalence (4,7). Fecal swabs were placed in transport medium (trypticase soy broth with 50 μg/L cefixime and 40 mg/L vancomycin) and sent by courier to the Veterinary Infectious Disease Organization, Saskatoon, Saskatchewan, to be cultured the next day.

One hundred milliliters of water was collected from the water trough in each pen. The sample included biofilm from inside walls and sediments from the bottom of the troughs, since previous studies had shown that *E. coli* O157 is more likely to be found in these locations (5,9). Water was also collected from the incoming source of water to the feedlot (dugout) to see if *E. coli* O157 was present in the incoming water supply. One kilogram of feed was collected from each feed bunk. Five kilograms of fresh feed from the mixer wagon was collected for inoculation studies, to see if the feed would support the growth of *E. coli* O157 and generic *E. coli* of bovine fecal origin. Water and feed samples were sent overnight by courier to the laboratory at Washington State University for culture and inoculation studies.

Additional information was collected at each feedlot visit. Data on the local climate (temperature, rainfall on the day of collection and the preceding week) were collected from a nearby weather station. Information on a pen basis was collected from the feedlot on the incoming weight of the cattle, the number of days on feed, morbidity, mortality, feed medications, gender of cattle, and days on feed (DOF) of cattle in adjacent pens.

Transmission of *E. coli* O157 during the summer

The same 2 feedlots as above were visited in May to October 1999, during the high summer risk period for *E. coli* O157, so that transmission of the bacterium could be studied. At each feedlot, 10 pens of yearling cattle were followed from arrival to slaughter to determine the transmission of *E. coli* O157 in the feces, water troughs, and feedbunks. To determine the pen prevalence of *E. coli* O157:H7 in the feces, 30 fecal samples per pen were collected every month until slaughter, and 2 additional samples were collected when the cattle had been on feed for 2 wk and when their ration was changed to the final finishing ration; water trough samples and feed bunk samples were collected at the same time. Fecal samples were cultured for *E. coli* O157 at the Veterinary Infectious Disease Organization and water and feed samples were cultured at Washington State University.

Culture methods for detecting *E. coli* O157 in feces

Fresh fecal samples were taken with cotton swabs and each swab was placed in a tube containing 5 mL of tryptic soy broth (TSB; Difco, Detroit, Michigan, USA) supplemented with cefixime (Lederle Laboratories, Pearle River, New York, USA) (50 ng/mL) and vancomycin (40 μg/mL) (10). These were kept cool until arrival at the Veterinary Infectious Disease Organization. Upon arrival, the tubes were incubated overnight at 37°C. Samples were plated on sorbitol MacConkey's (SMAC) agar plates containing 50 ng/mL of cefixime and 2.5 μg/mL of potassium tellurite (Sigma Chemical Company, St. Louis, Missouri, USA). Colonies that did not ferment sorbitol were screened for β-glucuronidase production and their ability to ferment lactose. A duplicate sample was plated directly on rainbow agar O157 (Biolog, Hayward, California, USA) to detect β-glucuronidase-negative colonies, which were screened for their ability to ferment sorbitol and lactose. All colonies that did not ferment sorbitol, but fermented lactose, and did not produce β-glucuronidase were screened for reactivity with rabbit-anti O157 polyclonal antiserum by slide agglutination. Positive isolates were tested for reactivity with a monoclonal antibody specific for O157 lipopolysaccharide (LPS) (obtained from Malcolm Perry, National Research Council of Canada, Ottawa, Ontario). Samples were then screened with O157-specific antigen by using a latex agglutination kit as directed by the manufacturer (Oxoid, Nepean, Ontario). Tentative *E. coli* O157 isolates were further characterized at Washington State University using a multiplex polymerase chain reaction (PCR) assay for detection of genes coding for Shiga toxins 1 and 2, *eae*A, and H7 (11).

Culture methods for detecting *E. coli* O157 in animal feed

Bunk feed was collected from the feed bunks of each pen on each sampling date. Prior to feeding, a sample was collected of the fresh TMR. These collections were kept cool until they were processed at Washington State University, where 10 g of each feed sample was sterilely placed into a new sterile bag and 90 mL of TSB was added to the sample. All bags were then incubated at 37°C for approximately 18 h. In addition, another set of samples collected in August and September 1999 were assayed in TSB using an incubation temperature of 44.5°C (9). After overnight incubation, all the samples were assayed for *E. coli* O157 by using an immunomagnetic separation method that utilized Dynabeads anti-*E. coli* O157 (Dynal, Oslo, Norway), following

the manufacturer's directions. This included plating on SMAC, containing 50 ng/mL cefixime and 2.5 μg/mL potassium tellurite (Sigma Chemical Company), and assaying up to 10 sorbitol-negative colonies/sample for their ability to ferment lactose, the lack of β-glucuronidase activity, and the possession of O157 antigen. Tentative *E. coli* O157 isolates were further characterized by using a multiplex PCR assay, as described above for animal feces.

Culture methods for detecting *E. coli* O157 in water

Water (60 to 80 mL) from a water trough in each pen was collected on each sample collection date using sterile 100-mL Nalgene bottles. These were kept cool until processed at Washington State University. Upon arrival at the laboratory, 30 mL of 2X TSB was added to sterile specimen cups with an equal volume of sample water. All water samples were then incubated at 37°C for approximately 18 h. In addition, another set of water samples collected in August and September were assayed utilizing an incubation temperature of 44.5°C (9). After overnight incubation in TSB, the samples were assayed for *E. coli* O157 by using an immunomagnetic separation method, and tentative *E. coli* O157 isolates were further characterized by a multiplex PCR assay as described above for animal feed.

Replication of *E. coli* O157 and fecal origin *E. coli* in total mixed rations

Fresh TMR samples were inoculated with *E. coli* from bovine feces and with naladixic acid-resistant strains of *E. coli* O157:H7. Concentrations of these organisms were targeted at 100 to 1000 colony-forming units (cfu)/g of TMR. For each TMR sample, a mix of 5 different isolates of *E. coli* O157:H7, each resistant to naladixic acid, and 1 g of bovine feces were inoculated into separate 500-g aliquots of TMR sample. The inoculum was delivered in enough sterile saline to raise the total moisture of the TMR to between 27% and 35%. Inoculums were evenly mixed into the TMR by hand and then left at room temperature for the duration of the assay. Total cfu/g of *E. coli* O157 and *E. coli* were determined at times 0 and 24 h after inoculation. This was done using the following methods: 25 g of TMR was added to 225 mL of buffered peptone water and placed on an orbital shaker for 15 min at 200 rpm. One milliliter, 0.1 mL, 0.01 mL, and 0.001 mL were plated onto separate 150-mm MacConkey agar plates containing 2.5 μg/mL naladixic acid (MacNal; Sigma Chemical Company) to enumerate total *E. coli* O157:H7, and onto 150-mm violet red bile agar plates containing 100 μg/mL 4-methylumbelliferyl-β-D-glucuronide (MUG) to enumerate total coliforms and *E. coli*. Presumptive *E. coli* O157:H7 were confirmed by using a latex agglutination assay to detect O157 antigen. Lactose-positive colonies were enumerated for total coliform counts and lactose-positive/MUG-positive colonies were used to enumerate total *E. coli*. The amount of feed assayed, the dilution plated, and the number of screened suspect colonies that were confirmed as either *E. coli* O157:H7, coliforms, or *E. coli* were used to determine the total cfu/g of target organism in the TMR at each time point. Times 0 and 24 h were compared to determine if replication of the target organism occurred.

Subtyping *E. coli* O157 isolates by pulsed field gel electrophoresis

Escherichia coli O157 isolates were subtyped by using pulsed field gel electrophoretic (PFGE) patterns of *XbaI* cleaved chromosomal DNA. Chromosomal DNA of each *E. coli* O157 isolate was prepared by using the Center for Disease Control Pulse Net protocol (12). Agarose-embedded chromosomal DNA for each isolate was cleaved with the endonuclease *XbaI* (Gibco-BRL, Gaithersburg, Maryland, USA) following the manufacturer's directions. Pulsed field gel electrophoresis was carried out (CHEF-DRII PFGE; BioRad, San Diego, California, USA) by using the following parameters; separation on 1% agarose-TBE (Tris/boric acid/EDTA buffer) gels (Sea Kem gold agarose; Bio Whittaker, Rockland, Massachusetts, USA) at 13°C for 20 h at 6 V/cm and a linear ramp of 5.2 to 54.2 s.

Pulsed field gel electrophoresis patterns for each isolate were compared by using scanned images of photographs of agarose gels. A restriction fragment length polymorphism (RFLP) analysis software program (PRO-RFLP; DNA ProScan, Nashville, Tennessee, USA) was used to generate an estimated size in kilobase pairs (Kb) for the largest 12 bands of DNA for each isolate. An SAS clustering procedure (SAS Institute, Cary, North Carolina, USA) was then used to narrow the number of possible indistinguishable subtypes on each separate gel. Comparison of individual isolates within clusters was made in a spreadsheet by utilizing the data on DNA band size. This comparison allowed for a 5% margin of error in DNA bands < 150 Kb and a 10% margin of error in DNA bands ≥ 150 Kb. A subtype of *E. coli* O157 was defined as an isolate with indistinguishable PFGE patterns of *XbaI* digested chromosomal DNA (6).

Statistical analysis

All data were entered into a spreadsheet (Microsoft Excel; Microsoft Corporation, Seattle, Washington, USA) and then transferred to an analytical software program (Statistix 4.1 for Windows; Analytical Software, Tallahassee, Florida, USA). The unit of analysis was the pen. Simple descriptive statistics were used to describe the pen prevalence of *E. coli* O157 in feces, water troughs, and feedbunks. Coliform and *E. coli* counts were log-transformed. Associations among the pen prevalence of *E. coli* O157:H7 in the feces, water troughs, and feedbunks, and the independent management and climatic variables were assessed by feedlot by using simple associative tests, such as the chi-squared test and the *t*-test. The paired *t*-test was used to determine whether growth of *E. coli* O157:H7 occurred during feed inoculation and incubation.

Results

Factors affecting the seasonal prevalence of *E. coli* O157: September 1998 to August 1999

The pen prevalence of *E. coli* O157:H7 was 0.8% (2/240) in the feces of preslaughter pens of feedlot cattle. In the yearling feedlot, the fecal pen prevalence

was 0% (0/120), and in the calf feedlot, it was 1.7% (2/120). *Escherichia coli* O157:H7 was isolated in only 2 fecal samples, each from a different feeding pen. *Escherichia coli* O157:H7 was found in 1.7% and 1.0% of the feedbunks in the yearling feedlot and calf feedlot, respectively (Table 1). Overall, 12% of the water troughs in the preslaughter pens were positive for *E. coli* O157:H7, 11% in the yearling feedlot and 14% in the calf feedlot. In the source water, *E. coli* O157:H7 was found only once in the calf feedlot (10%), and *E. coli* O157:H7 was not found in fresh TMR in either feedlot.

In the preslaughter pens of cattle, 12 different subtypes of *E. coli* O157:H7 were identified in the water troughs; 4 different subtypes of *E. coli* O157:H7 were identified in the feedbunks; and 2 different subtypes were identified in the feces (Table 2). Subtypes 1, 3, 12, 13, 14, and 15 were very similar, differing by only 1 to 3 bands. Subtype 5 and subtype 16 were distinct from all other subtypes. The yearling feedlot shared 2 indistinguishable subtypes between the water troughs and feedbunks (subtypes 1, 8). In the calf feedlot, subtypes 12 and 18 were found in the feces and in the water troughs. In one case, subtype 12 was found in the water 3 mo before it was found in the feces. In another case, subtype 18 was found in the feces 9 mo before it was found in the water. The subtype found in the source water of the calf feedlot (subtype 16) was distinct from the subtypes found in the feces, water troughs, or feedbunks. Two of the subtypes were repeatedly isolated from the yearling feedlot for 4 (subtype 8) and 7 (subtype 1) mo, and 3 subtypes were repeatedly isolated from the calf feedlot for 4 (subtype 9), 5 (subtype 5), and 11 (subtype 1) mo. The 2 feedlots shared 3 indistinguishable subtypes of *E. coli* O157:H7 in the water troughs (subtypes 1, 9, 12). Subtype 1 was commonly isolated from water troughs at both feedlots.

A description of the data collected from preslaughter pens of cattle is shown in Table 1. In the yearling feedlot, there were no significant ($P > 0.05$) associations between prevalence of *E. coli* O157:H7 in the water trough and the day, month, or season on which the sample was taken; the pen size; the arrival weight; the gender; the days on feed; the days since the water trough was cleaned; the water temperature in the trough; whether adjacent pens contained new arrivals (< 30 d on feed); the prevalence of *E. coli* O157 in feed or feedbunks; the coliform and *E. coli* counts in the water troughs or feedbunk; the outside temperature on the sample date; precipitation on the sample date; the minimum outside temperature during the preceding week; the maximum outside temperature during the preceding week; the average daily temperature the preceding week; the total precipitation during the preceding week; the feed medications; and the morbidity or mortality.

In the calf feedlot, the prevalence of *E. coli* O157:H7 in the water troughs of pens of preslaughter cattle was significantly ($P < 0.05$) associated with the day, month, and season when the sample was taken; the maximum climatic temperature in the week preceding the sample collection; the total precipitation in the week preceding the sample collection; the coliform counts in the water trough; and the *E. coli* counts in the water trough (Table 3).

Table 1. Descriptive data from 2 feedlots in southern Alberta from preslaughter pens of cattle from November 1998 to October 1999

Pen variable	Yearling feedlot	Calf feedlot
Average pen size (*s*)	288 (92)	154 (44)
Average arrival weight kg (*s*)	392 (31)	341 (80)
Gender %		
heifers	13%	0%
steers	88%	100%
Average days on feed (*s*)	130 (21)	186 (56)
Average morbidity % (*s*)	14% (6)	36% (16)
Average mortality % (*s*)	0.8% (0.5)	1.1% (1.2)
Feed medications %		
Rumensin[a], Tylan[b]	75%	35%
Rumensin, Tylan, Terramycin[c]	0%	15%
Rumensin, Terramycin	0%	50%
Posistac[d], Tylan	25%	0%
% adjacent pens less than 30 d on feed	19%	9%
Average water trough temperature (°C) (*s*)	9 (6)	10 (4)
Average outside temperature (°C) on sample date (*s*)	6 (12)	7 (9)
Average minimum outside temperature (°C) in week preceding sample collection (*s*)	-6 (10)	-2 (10)
Average maximum outside temperature (°C) in week preceding sample collection (*s*)	17 (8)	17 (8)
Average outside temperature (°C) in week preceding sample collection (*s*)	3 (10)	7 (9)
Average precipitation on sample date mm (*s*)	0 (0)	0 (0)
Average precipitation (mm) in preceding week of sample collection (*s*)	1 (10)	3 (12)
Average coliform counts in feedbunks (log cfu)[e] (*s*)	3.5 (1.4)	2.8 (1.1)
Average *E. coli* counts in feedbunks (log cfu) (*s*)	2.8 (1.7)	1.1 (1.0)
Average coliform counts in water troughs (log cfu) (*s*)	3.0 (10.4)	2.5 (0.9)
Average *E. coli* counts in water troughs (log cfu) (*s*)	2.7 (1.5)	2.3 (1.0)
Pen fecal prevalence of *E. coli* O157:H7 (%)	0% (0/120)	1.7% (2/120)
Fresh total mixed ration prevalence of *E. coli* O157:H7 (%)	0% (0/12)	0% (0/7)
Feedbunk prevalence of *E. coli* O157:H7 (%)	1.7 % (2/120)	1.7% (2/120)
Incoming water source prevalence of *E. coli* O157:H7 (%)	0% (0/11)	10% (1/10)
Water trough prevalence of *E. coli* O157:H7 (%)	11% (12/109)	14% (15/110)
summer (Jun to Aug)	7% (2/30)	13% (5/40)
fall (Sept to Nov)	7% (2/30)	35% (7/20)
winter (Dec to Feb)	5% (1/19)	0% (0/20)
spring (Mar to May)	20% (6/30)	10% (3/30)

[a]Monensin (Elanco Animal Health, Guelph, Ontario)
[b]Tylosin (Elanco Animal Health)
[c]Oxytetracycline hydrochloride (Pfizer Canada, London, Ontario)
[d]Salinomycin sodium (Pfizer Canada)
[e]log colony-forming units

Table 2. Subtypes of *E. coli* O157:H7 isolated from preslaughter pens of cattle in 2 feedlots in southern Alberta

Source	Yearling feedlot	Calf feedlot
Feces	No isolates	12, 18
Feedbunks	1, 8	11, 14
Water troughs	1, 1, 1, 8, 8, 8, 8, 9, 10, 12, 13, 15	1, 1, 1, 1, 1, 1, 3, 5, 5, 7, 9, 9, 12, 17, 18
Source water	No isolates	16

Table 3. Variables significantly ($P < 0.05$) associated with the prevalence of *E. coli* O157:H7 in water troughs in a calf feedlot of preslaughter cattle

Variable[a]	Water troughs positive for *E. coli* O157:H7	Water troughs negative for *E. coli* O157:H7
Season		
summer	13%	87%
fall	35%	65%
winter	0%	100%
spring	10%	90%
Average maximum climatic temperature in week preceding sample collection	22°C	18°C
Median total precipitation in week preceding sample collection	0 mm	3.4 mm
Coliform count in water trough (log cfu)[b]	3.1	2.5
E. coli count in water trough (log cfu)	2.9	2.3

[a]Date and month samples were also significantly associated ($P < 0.05$) with water trough prevalence of *E. coli* O157:H7 in preslaughter pens of feedlot cattle
[b]log colony-forming units

The prevalence of *E. coli* O157:H7 was too low in the feces and feedbunks to assess associations between climatic and management variables. The fresh TMR did not support the growth of *E. coli* or *E. coli* O157:H7 from bovine feces.

II. Transmission of *E. coli* O157 during the summer

Escherichia coli O157:H7 was not found in the feces of any of the pens in either feedlot while the cattle were on feed (Table 4). The bacteria were found in 2% of the feedbunks in the calf feedlot during the first 2 mo on feed. Only 1 subtype was found in the feedbunks (subtype 5). Subtype 5 was found in the feedbunks of 2 different pens on days 26 and 48, and this subtype was indistinguishable from isolates collected from both the feedbunks and water trough.

Escherichia coli O157:H7 was isolated from 22% of the water troughs in the yearling feedlot, and most isolates were found during the first month on feed (Figure 1). Subtypes 1, 2, 3, and 13 were very similar, differing by only 1 to 3 bands. Subtypes 5 and 6 were very similar to each other, differing by only 1 band, but they were very different from all other subtypes. Four different subtypes of *E. coli* O157:H7 were identified in the water troughs (subtypes 1, 2, 8, 13). Subtype 1 was most commonly isolated in the yearling lot, and it was found

Table 4. Prevalence of *E. coli* O157:H7 in pens of feedlot cattle from arrival to slaughter in a yearling feedlot and in a calf feedlot in southern Alberta

Pen prevalence	Yearling feedlot	Calf feedlot
Pen fecal prevalence of *E. coli* O157:H7	0 % (0/55)	0 % (0/83)
Water trough prevalence of *E. coli* O157:H7	22 % (11/50)	8 % (7/83)
Subtypes of *E. coli* O157:H7 in water troughs	1, 1, 1, 1, 1, 1, 1, 2, 8, 8, 13	1, 3, 4, 5, 5, 5, 6
Feedbunk prevalence of *E. coli* O157:H7	0 % (0/50)	2 % (2/83)
Subtypes *E. coli* O157:H7 in feedbunks	No isolates	5, 5
Feedbunk prevalence of *E. coli* O157:H7 by days on feed (DOF)	No isolates	
26 DOF		10% (1/10), subtype 5
48 DOF		10% (1/10), subtype 5
76 DOF		0% (0/10)
104 DOF		0% (0/10)
136 DOF		0% (0/10)
170 DOF		0% (0/10)
196 DOF		0% (0/10)
218 DOF		0% (0/8)
245 DOF		0% (0/5)

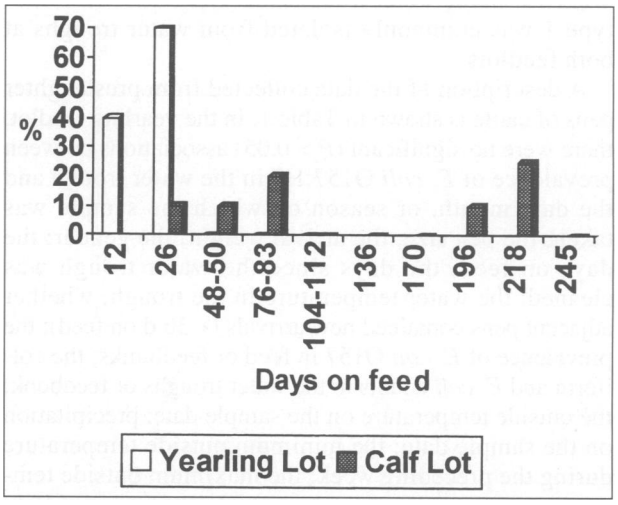

Figure 1. Prevalence of *E. coli* O157:H7 in water troughs in a yearling feedlot and a calf feedlot in southern Alberta by days on feed.

in the water troughs of both feedlots. In the yearling feedlots' water troughs, subtypes 1 and 8 were isolated on day 12, and subtypes 1, 2, and 13 were isolated on day 26. Two water troughs were positive for *E. coli* O157:H7 on days 12 and 26, but different subtypes were identified each time (subtypes 1, 8). In one water trough, the same subtype was identified repeatedly on days 12 and 26 (subtype 1). Eight of the 10 water

troughs in the yearling feedlot were positive for *E. coli* O157:H7 at least once while the cattle were on feed.

In the calf feedlot, *E. coli* O157:H7 was isolated from 8% of the water troughs (Table 4). *Escherichia coli* O157:H7 was isolated on days 26, 48, 76, 196, and 218 (Figure 1), and 6 water troughs had *E. coli* O157:H7 at least once while the cattle were on feed. Five different subtypes were identified in the water troughs (subtypes 1, 3, 4, 5, 6), and one of these subtypes (subtype 5) was found on days 26, 48, and 76. The other 4 subtypes were isolated only once. Subtype 6 was isolated on day 76, subtype 3 was isolated on day 196, and subtypes 1 and 4 were isolated on day 218. One water trough was positive repeatedly on days 26 and 76, but a different subtype was isolated on each sample date (subtypes 5, 6). Subtype 5 was isolated in the feedbunk and water trough from the same pen on day 26. The calf and yearling feedlots shared one common subtype in the water troughs (subtype 1).

Discussion

Escherichia coli O157:H7 was isolated from the feces, feedbunks, drinking water, and incoming water. The pen prevalence of *E. coli* O157:H7 was low in the feces of preslaughter pens. *Escherichia coli* was not isolated in the feces of cattle from the yearling feedlot, but it was isolated at low levels in the calf feedlot, which may reflect higher fecal levels in younger animals, as previously reported (1,3,8). In slaughter yearling cattle, the prevalence of *E. coli* O157:H7 was lower than that previously reported in Alberta (1). This may be due to natural variation by feedlot or by year, or it may reflect differences in culture techniques, such as failure to use immunomagnetic separation for isolation of the bacterium from fecal samples. *Escherichia coli* O157:H7 was found occasionally in the feedbunks and more commonly in the water troughs, as previously reported (5,8). Fresh TMR did not support the growth of *E. coli* O157:H7 or *E. coli* from bovine feces, which suggests that the silage and grain rations had inherent factors, such as pH, organic acids (5), or feed medications, that inhibited the growth of *E. coli*; all feeds from these 2 feedlots contained ionophores and antimicrobial drugs for the control of liver abscess. Alternatively, the sample size may have been too small to identify growth.

The feces, water troughs, and feedbunks shared some common subtypes of *E. coli* O157:H7, suggesting transmission of *E. coli* O157:H7 among these sites. In one instance, the incoming water contained *E. coli* O157:H7, suggesting further study to identify sources of water contamination of dugouts and to determine whether treatment of incoming water sources for cattle is plausible. A few subtypes were isolated repeatedly, suggesting that they were either endemic in the feedlot or repeatedly introduced from a common source. The 2 feedlots also shared a few indistinguishable subtypes, suggesting either common sources between the feedlots or independent sources that contained the same subtype. A shared or common source of animals entering the feedlots could not be identified. The only potential common source identified between the 2 feedlots was wild birds and, possibly, flying insects, although the feedlots were approximately 100 km apart. In England, birds are known to carry and transmit *E. coli* O157:H7 (8). Ducks and geese were commonly observed on the dugout of one feedlot, and they are prevalent in the summer in southern Alberta. As well, *E. coli* O157 has been isolated in the United States from pigeons, flies, and rodents (8), and they are common in feedlots in Alberta. Further studies will need to be conducted to determine what role wildlife, such as wild birds, flying insects, and rodents, play in the transmission of *E. coli* O157:H7 among feedlot cattle through contamination of water, feed, or soil.

In the calf feedlot, climatic temperature and weekly precipitation affected the prevalence of *E. coli* O157:H7 in the water troughs. Climatic changes may partly explain seasonal differences observed in the prevalence of *E. coli* O157:H7 in water and feedlot cattle, as previously suggested (8). The association between coliform and *E. coli* counts and *E. coli* O157:H7 prevalence in the water troughs, which indicates fecal contamination, suggests that coliform and *E. coli* counts in water could be measured as a surrogate measure to determine effective water quality intervention strategies for reducing *E. coli* O17:H7. Coliform and *E. coli* counts are generally much higher; thus, it is easier to assess statistically significant differences among intervention strategies using these bacterial counts as the outcome rather than those of *E. coli* O157:H7, which are usually much lower.

A higher prevalence of *E. coli* O157:H7 was found in the feedbunks and water troughs in yearling cattle and calves early on in the feeding period, as previously reported (4,7). This higher prevalence may be due to increased fecal excretion of *E. coli* O157 by cattle, secondary to stresses such as ration changes, although evidence is inconclusive on the effects of ration composition or ration changes on the prevalence of *E. coli* O157:H7 (8). Alternatively, it may be due to age, incoming infected animals, or other yet to be identified management practices. In the calf feedlot, there was a spike of *E. coli* O157:H7 contamination of water troughs late during the feeding period, during days 196 to 218. At this time, the feedlot was cleaning its dugout. Possibly the increase in bacteria was due to disturbances in the soil sediment in the dugout during cleaning, even though *E. coli* O157:H7 were not identified in the dugout (source) water at that time. Since only a few water samples were taken from the dugout at that time, failure to find *E. coli* O157:H7 was not surprising.

In conclusion, many different subtypes of *E. coli* O157:H7 were isolated from the feces, water, and feed in pens of feedlot cattle. Transmission of the bacterium appeared to occur among cattle, water, and feed, and the 2 feedlots shared some common subtypes, suggesting either a common source of contamination, such as wild birds or flying insects, or contamination from 2 independent sources that shared the same subtypes. These results suggest that methods to control *E. coli* O157:H7 in feedlot cattle will have to focus not only on reducing fecal shedding of *E. coli* O157:H7 in cattle but also on the potential of reinfection from environmental sources, such as water and feed, both at the feedlot and before the cattle arrive on the premises. What role wildlife, such as birds and, possibly, insects and rodents,

play in the transmission of *E. coli* O157:H7 within and among different feedlots remains to be determined.

Acknowledgments

The researchers thank the 2 feedlots in southern Alberta who participated in the study. Research technicians from Lakeside Research are thanked for collecting feedlot samples. The laboratory staff from Washington State University is thanked for the laboratory analyses.

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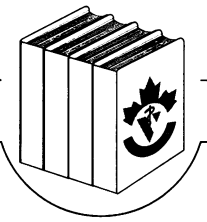
BOOK REVIEW



COMPTE RENDU DE LIVRE

Turner DC, Bateson P, eds. ***The Domestic Cat: The Biology of its Behavior, 2nd ed.*** Cambridge University Press, New York, 2000, 256 pp, ISBN 0-521-63648-5, US$19.95.

If you are a cat aficionado, or if you are fascinated by this species, this is a book worthy of your attention. The book is, for the most part, very readable, despite its being a compilation of the results of a very large number of scientific studies. I was surprised (and delighted) to learn that such a vast amount of work has been done looking at the biology of the behavior of cats. Most of this work has been done over the last 30 years and the lion's share is out of Europe and the United Kingdom. As a veterinarian, I have focused so much on health and illness and, when behavior is the issue, behavior problems, that I have completely missed this wonderful, objective information on what makes cats "tick" and why they have developed the way that they have. Not only is this interesting, but it also helps with trying to understand illness and "inappropriate" behaviors.

Following an introduction, there is a section on the development of young cats (behavioral development, factors influencing the mother-kitten relationship, individuality in the domestic cats), which I found fascinating. Professor Bateson's descriptions of the developmental timeline of sensory needs of kittens (thermoregulation, tactile, olfactory, auditory, and visual responses) goes beyond anything I had ever read before. He considers why these stages develop in the order that they do and what factors affect whether they are earlier or later, such as litter size and maternal factors. I learned that the ability to right the body in mid-air while falling (the so-called "air-righting reaction") starts to appear during the 4th week and is in place by the 6th week. Play and interaction with the queen develop differently in kittens of larger litters than in solo kittens. After this section on the emergence of behavior and the genetic, evolutionary, interactive, and nutritional influences on the development of behavior, the social life of cats is reviewed. This looks in depth at the signaling repertoire and compares that of the domestic cat with that of its undomesticated relatives. A section on group-living (sociobiology and epidemiology) follows. Fascinating!

Hunting behaviors are affected by early experiences, but, surprisingly, even if a cat has not had play opportunities, it will still be an effective hunter. He/she will develop the behaviors by alternative paths. The effects of hunting and their impact on the prey populations is extensively examined.

The book concludes with a superb section about cats and people. This section is very easy to read and tours through the domestication and rocky history of the cat in human society, human-cat relationship and ends with a look at feline welfare issues. Why is any of this important to a veterinarian? Any increased awareness and attempts to understand the species we work with helps us to be better care providers. This impacts on how we think about the individual cat in a single cat household, as well as in the larger multicat or cattery/shelter living situation. I hope you enjoy this book as much as I did.

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