

## Antimicrobial Drug Resistance of *Salmonella* and *Escherichia coli* Isolates from Cattle Feces, Hides, and Carcasses

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### ABSTRACT

To determine patterns of cross-contamination and antibiotic susceptibility of microorganisms commonly associated with cattle, 60 cattle shipped to a commercial abattoir (20 in each of three separate trial periods) were followed through processing. Samples for bacterial isolation were collected from the feces and hides immediately before shipping, from the hides at the abattoir after exsanguination, and from the carcasses before evisceration and in the cooler. Samples were cultured for *Salmonella* and non-type-specific *Escherichia coli*. *Salmonella* was identified in 33.9% ( $n = 20$ ) of the fecal samples and on 37.3% ( $n = 22$ ) of the hides before shipment. At the abattoir, the proportion of hides from which *Salmonella* was isolated increased ( $P < 0.001$ ) to 84.2% (48 hides). Nonspecific *E. coli* and *Salmonella* were recovered from 40.4 and 8.3% of preevisceration carcass samples, respectively. No *Salmonella* or nonspecific *E. coli* were recovered from hotbox carcass samples. Isolates were tested for antimicrobial drug susceptibility. For nonspecific *E. coli*, 80.3% ( $n = 270$ ) of the isolates were resistant to at least one antimicrobial drug. For *Salmonella*, 97% ( $n = 101$ ) of the isolates were resistant to at least one antimicrobial drug; however, only 4.0% were resistant to two or more. The most common resistance was to sulfamethoxazole. These results indicate that the presence of microorganisms resistant to antimicrobial drugs is common in cattle and beef. Further studies are needed to identify the sources and causes of this drug resistance.

Numerous research studies have been conducted to determine common bacterial species associated with cattle and beef products. These studies have concentrated mainly on pathogenic strains of bacteria that may be a cause of concern for human or animal health. Many researchers have attempted to estimate the prevalence of *Escherichia coli* O157:H7 in cattle at the feedlot, at the packing plant, and on the final processed products (1, 2, 9, 10). The actual prevalence may vary and is dependant on many factors. Non-type-specific or biotype I *E. coli* is commonly associated with cattle and beef products, but pathogenic strains are less common. *Salmonella* also is prevalent in cattle. In one study, the prevalence of *Salmonella* on hides and in feces of cattle at the packing plant was 86.9 and 43.4%, respectively (1). Others have reported that approximately 70% of fecal samples taken from 60 animals by rectal-colonial palpation were positive for *Salmonella* (9). The prevalence of *Salmonella* on preevisceration carcasses has been reported at 23 to 27% (10). Although prevalence estimates vary, these bacteria clearly are commonly associated with cattle.

Antimicrobial drug resistance in bacterial isolates that have the potential to enter our food supply is a growing public health concern. There appears to be an increasing number of bacterial isolates that are resistant to multiple common antimicrobial drugs used for treatment of life-threatening illnesses (7). However, the exact causes of the emergence of these resistant strains have yet to be pinpoint-

ed. One potential source of antimicrobial drug resistance is nonpathogenic strains of drug-resistant bacteria, which can contaminate beef products and be subsequently consumed. These bacteria can then possibly transfer resistance capabilities to other bacteria, including pathogens, in the human gastrointestinal tract. The exchange of genetic information between bacteria could result in the development of antimicrobial drug resistance in normal gastrointestinal microflora without direct antimicrobial drug challenge and may lead to transfer of resistance to pathogenic microorganisms, making it difficult to treat human illnesses associated with that pathogen. Treatment of a patient with antibiotics may select for potentially pathogenic strains that would otherwise stay susceptible without the selective pressure of an antibiotic but, under these conditions, can proliferate and cause illness and sometimes death.

The exact reason for the emergence of antimicrobial drug-resistant strains of bacteria remains unknown, but selective pressure is partially to blame. It has been suggested, but not proven, that the use of subtherapeutic doses of antimicrobials in animal feedstuffs has led to an increase in the number of resistant strains of common and pathogenic bacteria. Approximately 50% of antimicrobial drug use occurs in animal agriculture (14). A common theory is that subtherapeutic doses given over a long period have made it possible for these bacteria to adapt in a stepwise fashion to many of these drugs (6). The most common types of antimicrobial drugs used for cattle feed supplementation are monensin, tylosin, and chlortetracycline (13), which are

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used as growth promoters in cattle at the feedlot. The benefits of these growth promoters include improved feed efficiency, better efficiency of rumen fermentation, greater rate of weight gain, control of coccidiosis, reduced liver abscesses, and increased ability of cattle to obtain more energy from any ration. Some of these antimicrobial drugs are very similar in chemical form to many of the antibiotics that are used to treat life-threatening illnesses. The concern is that the use of these antimicrobial drugs in cattle feces is somehow connected to the rising prevalence of resistant bacterial strains associated with human illness. To begin to answer some of these questions, we must first create a baseline on the prevalence and antimicrobial drug susceptibility profiles of common bovine bacteria in a commercial processing system. The objective of the present study was to determine the prevalence of antimicrobial drug-resistant *Salmonella* and nonspecific *E. coli* in cattle feces and on cattle hides and carcasses after processing.

## MATERIALS AND METHODS

**Sample collection.** Sixty mixed-breed steers (20 per replication) from a single source with a mean initial body weight of approximately 340 kg were purchased and delivered to the Burnett Center for Beef Cattle Research and Instruction. After their arrival at the center, the steers were weighed, given sequentially numbered ear tags, and routinely processed. Steers were housed in dirt-floor pens and fed a 70% concentrate starter diet for approximately 7 to 10 days. Finishing diet consisted of steam-flaked corn-based meal with either alfalfa or cottonseed hulls as the roughage source. Antimicrobial growth promoters included in this diet were Rumensin (30 g/ton) and Tylan (8 g/ton) (Elanco Animal Health, Greenfield, Ind.). Intermediate body weights were recorded on days 28, 84, and 112 of the study. Weights also were recorded on day 56 when the cattle were reimplemented and again on the day of shipment to the slaughter plant.

Ten grams of fecal material was aseptically collected via rectal palpitation immediately before the cattle were shipped to a commercial abattoir. Each sample was placed aseptically in a labeled sterile plastic container. During this same time period, a sample area measuring 30 by 30 cm from the perineal hide was swabbed with a gauze pad (10 by 10 cm) soaked in sterile buffered peptone water (BPW), which was placed in a separate labeled sterile container. All samples were placed on ice in a cooler and transported back to the laboratory for further analysis.

At the commercial abattoir, the carcass order was recorded to link the animal tag number back to its respective carcass during processing. Carcasses were sent through the plant in groups of 5 for a total of 20 animals per replication with 20 nonstudy carcasses between each group to allow time to swab each carcass and prepare for the next set of carcasses. Upon entry into the plant the opposite side of the perineal hide was swabbed as described above. Immediately after hide removal and before the hot-water wash, a carcass swab sample was collected from an area (30 by 30 cm) of the hindquarter near the rectal opening. After entry into the hotbox, a second carcass swab sample was collected from the opposite hindquarter in the perineal area. Swabs were then transferred into individually labeled sterile bags and placed in a cooler on ice for transport back to the laboratory for analysis.

**Microbial analysis.** Upon arrival at the laboratory, the samples were processed for isolation for two bacterial genera: non-type-specific *E. coli* and *Salmonella*. U.S. Department of Agriculture and Food and Drug Administration methodology was used for recovery of all organisms.

**Fecal samples.** A 10-g portion of fecal matter was aseptically transferred into 90 ml of BPW and shaken for 1 min. To recover commensal *E. coli*, 0.1 ml of the diluted sample was streaked onto a prepped plate of violet red bile agar (VRBA) for isolation. *Salmonella* was isolated by aseptically transferring 0.2 ml of the BPW sample into 10 ml of Rappaport-Vassiliadis medium (RV), which was incubated at 40°C for 24 h.

**Hide and carcass samples.** Hide and carcass samples were processed in a manner similar to that for fecal samples. A 90-ml volume of BPW was poured into each labeled bag containing a swab sample, and the bag was manually massaged for 1 min. The hide sample was immediately cultured for commensal *E. coli* and *Salmonella* as described for fecal samples. Samples taken from the carcasses were subjected to a preenrichment step by holding for 18 h at 37°C prior to selective plating. Previous studies and our preliminary data indicate that this step improved recovery, possibly by allowing injured cells time to recover. Bacteria may be injured when subjected to intervention strategies such as acid or hot-water washes, steam cabinets, or steam vacuuming. Our collaborating plant used steam vacuums, steam pasteurization, and various carcass washes at multiple sites along the chain. Previsceration (after sample collection), carcasses proceed through a hot-water wash. After evisceration and before entering the hot box, carcasses are subjected to a hot-water wash and an acid wash and passed through a steam cabinet.

**Confirmation.** Following preenrichment, three morphologically typical coliform colonies from VRBA plates (purple to red, 0.5 mm or larger, surrounded with a zone of precipitate) were selected and restreaked for further isolation. Typical colonies were Gram stained and subjected to biochemical analyses. Final confirmation was conducted using a commercial test kit (Enterotube II, Becton Dickinson, Sparks, Md.), which is a convenient cluster of biochemical tests. The Enterotube II was inoculated according to the manufacturer's instructions and incubated at 37°C for 24 h. Results were read and processed according to typical reactions expected with this test kit.

A portion of the RV broth was streaked onto XLT4 (xylose lactose tergitol) agar plates for *Salmonella* isolation. Plates were then incubated at 37°C for 24 h. Typical colonies were transferred to triple sugar iron agar slants, incubated for 24 h, and then observed for typical reactions. Serological agglutination tests were used to confirm *Salmonella* identity (to serogroup). *Salmonella* isolates were then sent to the National Veterinary Services Laboratory (Ames, Iowa) for serotyping.

**Antimicrobial drug testing.** Susceptibilities of isolates to antimicrobial drugs were determined using a broth microdilution technique (Sensititre, TREK Diagnostics, Westlake, Ohio). This system is designed to determine the MIC of both gram-positive and gram-negative organisms. Sets of 96-well microdilution plates were designed specifically based on desired antimicrobial drug panels (Table 1) The concentrations of the antimicrobial drugs were diluted serially across the plates. This method meets Clinical and Laboratory Standards Institute (CLSI; formerly NCCLS) guidelines (8).

Isolated colonies were grown on appropriate media. Three well-isolated colonies were placed into 10 ml of sterile deionized water and adjusted to a 0.5 McFarland standard. A 10- $\mu$ l portion of the suspension was transferred into Mueller-Hinton broth and mixed by vortexing. An eight-channel multipipettor was used to deliver the culture into the 96-well plates. Plates were covered with the adhesive provided with the test kit and incubated at 35°C for 18 to 24 h. Plates were manually read and exposed to natural light on the underside of the wells to more easily discern visible growth. The MIC was reported as the lowest concentration of the antimicrobial drug that inhibited visible growth. Appropriate CLSI quality control organisms were used during each replication to ensure that methods utilized fell within quality control ranges (8).

TABLE 1. Sensititre custom plate format for gram-negative organisms

Antimicrobial drug	Concn (µg/ml)
Bacitracin <sup>a</sup>	8–128
Ciprofloxacin	0.12–4
Chloramphenicol	2–32
Erythromycin	0.5–8
Flavomycin <sup>a</sup>	1–32
Gentamicin	128–1,024
Kanamycin <sup>a</sup>	128–1,024
Linezolid	0.5–8
Penicillin	0.5–16
Quinupristin/Dalfopristin	1–32
Streptomycin	512–2,048
Salinomycin <sup>a</sup>	1–32
Tetracycline	4–32
Vancomycin	0.5–32
Lincomycin <sup>a</sup>	1–32
Tylosin tartrate <sup>a</sup>	0.25–32
Nitrofurantoin	2–128

<sup>a</sup> Drug for which there is no current CLSI standard.

**Statistical analysis.** This study yielded data from five observations associated with each sample location or type. Each animal was sampled at five different locations for recovery of three different bacteria. No area of the animal was swabbed or sampled more than once. A sample was considered positive when the identity of one or more of the isolates recovered was confirmed. In this way, a categorical table was created with either a positive or negative result for each sample type at each sampling location for each organism. Descriptive statistics were then generated using various procedures in SAS (version 8.2, SAS Institute, Inc., Cary, N.C.) and a chi-square analysis. On several occasions, a day effect was observed for a particular sample type, and data were then analyzed separately for each sampling day for that sample type. The variation in the likelihood of recovery of organisms within

each sampling location (1 through 5) was evaluated with logistic regression techniques.

To classify the bacterial isolates as resistant or susceptible, variables were created with any MIC that was greater than the highest concentration or lower than the lowest concentration of antimicrobial drug in the Sensititre 96-well plates. When growth was visible at the highest concentration of antibiotic in the well, a number twice that concentration was entered, which resulted in classifying that organism as resistant. For example, for an organism that grew at a chloramphenicol concentration of 32 µg/ml, which was the highest concentration in the wells, an MIC of 64 µg/ml was assigned. For organisms that did not grow at even the lowest drug concentration, the lowest concentration was assigned and resulted in a classification of susceptible. With these guidelines and various adjustments, a categorical response to each antimicrobial for each bacterium was generated and an overall susceptibility profile was recorded for each isolate collected. From these profiles, general descriptive statistics were created with various procedures in SAS and a chi-square analysis. Patterns were evaluated for the most commonly occurring phenotypes within each organism and sample type.

**RESULTS AND DISCUSSION**

The proportion of samples that were culture positive for *Salmonella* was higher ( $P < 0.001$ ) for hide samples taken at the plant (SPH) than hide samples taken from the same cattle at the feedlot (SFH). This increase, averaged for all three sampling periods, was  $37.3\% \pm 25\%$  SFH to  $84.2\% \pm 20\%$  SPH (Fig. 1). This increase may have been the result of cross-contamination of the cattle during transport or may have been directly related to stress factors, which can increase shedding of *Salmonella*. This result is consistent with findings of other researchers (1, 3). For all three sampling periods, the same increase was observed. For the first sampling date, the proportion of hides that were culture positive for *Salmonella* was 55.0% SFH and 100.0% SPH. A similar increase was observed for the second sampling period, at 31.6% SFH and 95.0% SPH. The

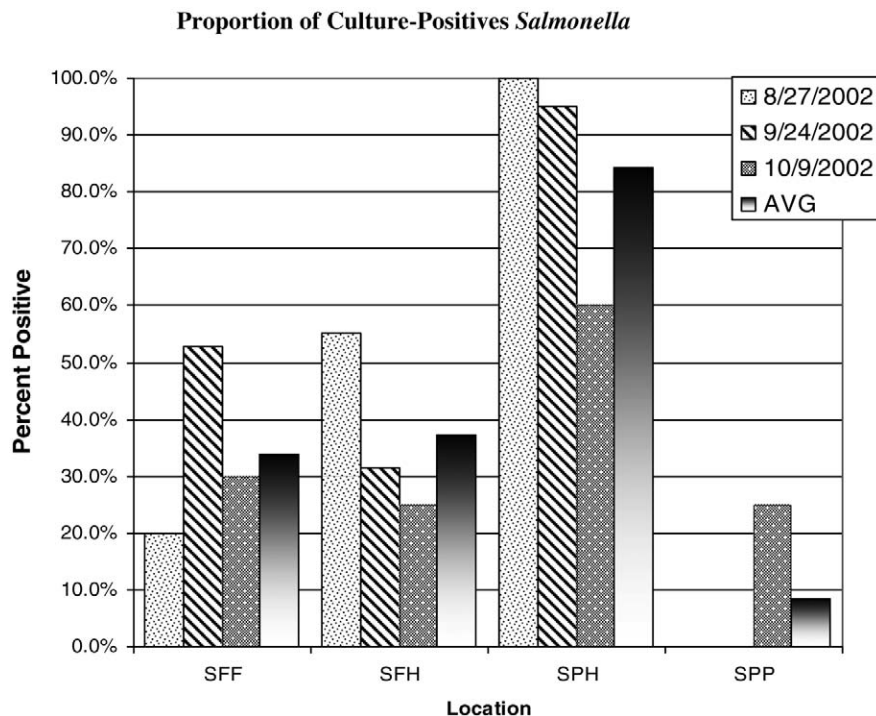
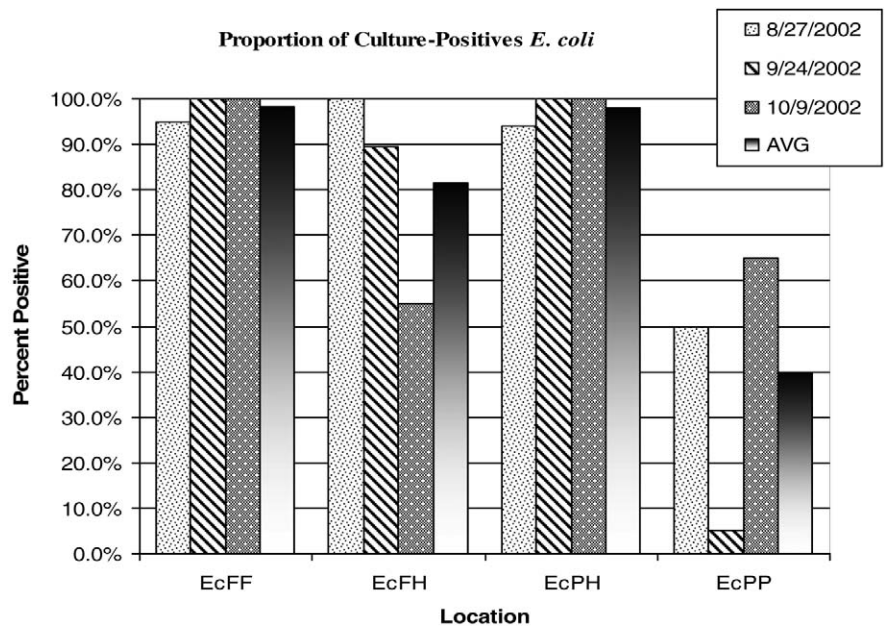


FIGURE 1. Proportion of samples that were culture positive for *Salmonella*. Samples were collected from feces, hides, and carcasses before and after transport to a commercial processing facility. SFF, *Salmonella* recovered from fecal samples at the feedlot; SFH, *Salmonella* recovered from hide samples at the feedlot; SPH, *Salmonella* recovered from hide samples at the plant; SPP, *Salmonella* recovered from preevisceration carcass samples at the plant.

FIGURE 2. Proportion of samples that were culture positive for nonspecific *E. coli* biotype I. Samples were collected from feces, hides, and carcasses before and after transport to a commercial processing facility. EcFF, *E. coli* recovered from fecal samples at the feedlot; EcFH, *E. coli* recovered from hide samples at the feedlot; EcPH, *E. coli* recovered from hide samples at the plant; EcPP, *E. coli* recovered from preevisceration carcass samples at the plant.



last sampling period had the lowest proportion of culture-positive hides, at 25.0% SFH and 60.0% SPH. This result may indicate that fewer animals testing positive for *Salmonella* at the feedlot will result in lower numbers at the plant after transportation; however, the number of animals testing positive will likely increase during transportation.

The proportion of fecal samples that were culture positive for *Salmonella* at the feedlot was 33.9% (SFF) for all sampling periods combined. The proportion of fecal samples that were positive for *Salmonella* was 20.0, 52.6, and 30.0% for sampling periods 1, 2, and 3, respectively. An increase in the number of *Salmonella*-positive fecal samples after transport was previously observed in another study (1). Based on the short transportation time in the present study, it is unlikely that the number of culture-positive fecal samples would increase. No fecal samples were taken at the commercial processing facility, so this effect could not be tested.

For nonspecific *E. coli*, the proportion of fecal samples (EcFF) for all sampling periods that were positive at the feedlot was  $98.3\% \pm 9.1\%$  (Fig. 2), which was expected because *E. coli* is a normal inhabitant of the gastrointestinal tract of these animals and the actual proportion is more likely 100%. However, in this study, three colonies were selected from each agar plate, and in a few instances none of these colonies were confirmed to be *E. coli*. If additional colonies had been tested, it is likely that we would have identified *E. coli*. The isolates were nonspecific *E. coli* and not necessarily pathogenic. For *E. coli*, there was a day effect for number of hide samples that tested positive at the feedlot. In the third sampling period, only 55.0% of the animals were positive compared with approximately 90 to 100% in the first two sampling periods. When analyzed individually, in the third sampling period a significantly higher number of hides ( $P < 0.001$ ) were culture positive at the plant (EcPH) than at the feedlot (EcFH) (Fig. 2). Because of the lower number of culture-positive hides in the third sampling period at the feedlot, when the sampling periods were combined there was an overall significant in-

crease ( $P < 0.001$ ) observed from the feedlot to the commercial abattoir. However, the day effect could account for this difference, and when this effect was observed the individual sampling days were analyzed separately.

For preevisceration carcass samples (EcPP), the proportion of culture-positive samples was  $40.0\% \pm 26\%$  for all sampling periods (Fig. 2). However, there was also a day effect observed; the second sampling period resulted in only one positive sample (5.0%) from the 20 carcasses swabbed. The reason for this difference is unclear, but it may be an indication that preevisceration numbers can fluctuate greatly depending on the day and the source of cattle. Regardless of the number of *E. coli* on the carcasses at the preevisceration stage, no *E. coli* was recovered from carcasses in the cooler in this study. This result indicates that in-plant interventions targeted to reduce microbial contamination were effective for *E. coli* and *Salmonella*. The procedure for the third sampling period was altered in the lab to include a nonselective preenrichment step to increase the likelihood of recovering injured bacteria. For *E. coli* and *Salmonella*, this alteration in procedure had no effect for cooler carcass samples, and no *E. coli* or *Salmonella* were recovered during this study. Another limitation that could have led to reduced recovery of these bacteria on the carcasses was the fact that only a small portion of the total carcass was swabbed, in particular an area of only 30 by 30 cm near the rectal opening.

**Antimicrobial susceptibility patterns.** Approximately 97% of *Salmonella* isolates (101) were resistant to at least one antimicrobial drug. The majority of these isolates (96.08%) were resistant to sulfamethoxazole followed by streptomycin (17.65%). Twenty-one (20.5%) of the 102 isolates were resistant to two or more antimicrobial drugs. Eight distinctive *Salmonella* serotypes were isolated. Of the 102 total isolates, 28 were *Salmonella* Muenster, 19 were *Salmonella* Cerro, 14 were *Salmonella* Montevideo and *Salmonella* Kentucky, 13 were *Salmonella* Meleagridis, 5 were *Salmonella* Anatum, 3 were *Salmonella* Mbandaka, and

1 was *Salmonella* Muenchen. The remainder of the isolates were reported as untypeable or nonviable. Two of the five *Salmonella* Anatum and 1 of the 13 *Salmonella* Meleagridis isolates were susceptible to all antimicrobials tested, but all other serotypes were resistant to at least one antimicrobial. The most common resistance profile was sulfamethoxazole resistance alone (75.49%) followed by sulfamethoxazole resistance combined with streptomycin resistance (17.65%). One isolate was resistant to amoxicillin–clavulanic acid and sulfamethoxazole, one isolate was resistant to nalidixic acid and sulfamethoxazole, and one isolate was resistant to trimethoprim-sulfamethoxazole and sulfamethoxazole. All *Salmonella* Kentucky isolates were resistant to streptomycin.

According to the Centers for Disease Control and Prevention (CDC) *Salmonella* annual report (4), the most common *Salmonella* serotypes reported from human sources were Typhimurium (21.9%, 7,062 cases), Enteritidis (15.8%, 5,116 cases), Newport (13.0%), Heidelberg (6.1%), Javiana (3.7%), Montevideo (2.2%), Muenchen (1.8%), and 13 others each making up about 1% of the total. From the top 20 most frequently isolated human serotypes, only *Salmonella* Montevideo and *Salmonella* Muenchen were recovered from cattle during this study. The 20 most common nonclinical nonhuman serotypes reported to the CDC included 7 of the 8 serotypes recovered during the course of this study (excluding *Salmonella* Muenchen). From these results, a majority of the isolates recovered would not be a common causative agent of gastrointestinal disease or risk to human health. *Salmonella* Montevideo is the most significant overlapping serotype between human isolates and cattle strains in this study, although this overlap is fairly insignificant and the real risk to human health would more likely be sharing of virulence factors and/or antimicrobial drug resistance gene cassettes with other more virulent pathogens.

A total of 267 isolates of nonspecific *E. coli* were isolated at the three sampling periods. Similar to *Salmonella*, the most common resistance was to sulfamethoxazole (79.03%), followed by trimethoprim-sulfamethoxazole (trisulfa) (29.96%), tetracycline (13.48%), cephalothin (5.62%), streptomycin (5.62%), kanamycin (4.87%), ampicillin (1.12%), and several others that were less than 1% of the total. No resistance was found to the antimicrobial drugs amikacin, ceftriaxone, ciprofloxacin, and gentamicin. Most isolates (226) were resistant to at least one antimicrobial drug tested, but 41 isolates were not resistant to any of the agents tested. Approximately half of the 226 isolates that showed some resistance were resistant to only one antimicrobial drug, which indicates that a large number of isolates would not be considered multidrug resistant. The most common pattern of resistance was to sulfamethoxazole alone (35.58%). Ninety isolates were resistant to two drugs, and the most common pattern associated with two-drug resistance was resistance to sulfamethoxazole and trisulfa (65%), followed by sulfamethoxazole and tetracycline (5.62%). Twenty-one isolates were resistant to three antimicrobial drugs, and the most common pattern was resistance to sulfamethoxazole and to the combination of trisulfa and tetracycline (3.75%). Six isolates were resistant to four or more antimicrobial drugs tested, and only one isolate was

resistant to six drugs: ampicillin, trisulfa, kanamycin, sulfamethoxazole, streptomycin, and tetracycline. Two isolates were pentaresistant; one was resistant to amoxicillin–clavulanic acid, cephalothin, trisulfa, sulfamethoxazole, and tetracycline, and the other was resistant to cephalothin, trisulfa, sulfamethoxazole, nalidixic acid, and ceftiofur.

Analysis also was conducted to determine any resistance patterns associated with sample type or location. There was no significant difference in antimicrobial drug resistance between sample types ( $P = 0.18$ ). Whether the sample came from the feces, hide, or carcass, our experimental design revealed no indication of selection for a specific pattern of resistance, and the variability of patterns was consistent across sampling locations. This finding suggests that resistance patterns are conserved throughout the processing environment. No drastic changes were observed in isolates collected at the feedlot compared with those collected at the commercial abattoir. A similar analysis also was conducted to determine whether the number of resistant isolates varied depending on sample type; no significant difference was found ( $P = 0.26$ ). Thus, isolates from different sample types would not be considered different in the number of agents that they were resistant to. For example, a hide *E. coli* isolate would have a similar chance of being resistant to the same number of antimicrobial drugs as would a fecal *E. coli* isolate. Analysis was also conducted by sampling date, and no significant difference was found ( $P = 0.27$ ), indicating little variability between the three replications in terms of resistance profiles. These results indicate that resistance profiles of *E. coli* tend to be consistent throughout the processing environment and do not vary greatly from one day to the next for cattle from the same feedlot source.

Food animals are known reservoirs for *Salmonella* and *E. coli*, which are common inhabitants of the gastrointestinal tract of most animals, including cattle. Beach and coworkers (3) examined the antibiotic profiles of *Salmonella* isolates coming from feedlot and nonfeedlot beef cattle. *Salmonella* was isolated from rectal grabs, hides, the environment, and carcasses. Serotypes were determined for all isolates. The most common *Salmonella* serotype recovered from feedlot cattle was Anatum (18.3%) followed by Kentucky (17.5%), Montevideo (9.2%), Senftenberg (8.3%), and Mbandaka (7.5%). For nonfeedlot cattle the most common *Salmonella* serotypes were Kentucky (35.4%), Montevideo (21.7%), Cerro (7.5%), Anatum (6.8%), and Mbandaka (5.0%). These isolates, with the exception of *Salmonella* Senftenberg, were similar to those in our study. Antimicrobial drug susceptibility testing by Beach and coworkers (3) revealed that 21.7% of the isolates from feedlot cattle were resistant to tetracycline. None of the other *Salmonella* isolates from the feedlot cattle were resistant to any other antimicrobials tested, but 6.2% of the nonfeedlot cattle were resistant to more than four antimicrobials tested. These researchers did not test for sulfamethoxazole resistance except in conjunction with trimethoprim, for which they did find some resistance in nonfeedlot cattle. Antimicrobial drug testing was performed using the disk diffusion method as opposed to the microdilution method as utilized by our study. In a study by Edrington and coworkers (5), dairy cattle were examined for the presence of *Salmonella*, and their resistance profiles were ana-

lyzed. Serotypes recovered were similar to those reported here, and the most frequent resistance was to sulfamethoxazole, tetracycline, streptomycin, kanamycin, chloramphenicol, and ampicillin. These results indicate that resistance profiles may vary from study to study and that streptomycin resistance and sulfamethoxazole resistance are fairly common. Variations likely occur as a result of cattle management practices, age of animals, and source of the animals.

Another study was performed to determine the prevalence of antimicrobial drug-resistant *E. coli* in retail meats in Washington, D.C. (12). Samples were taken from retail beef, chicken, pork, and turkey, and 472 *E. coli* isolates were recovered and subjected to antimicrobial tests. Approximately 59% of these isolates were resistant to tetracycline followed by sulfamethoxazole (45%), streptomycin (44%), cephalothin (38%), and ampicillin (35%). Resistance was also observed, but to lesser extent, to gentamicin (12%), nalidixic acid (8%), chloramphenicol (6%), ceftiofur (4%), and ceftriaxone (1%). The authors concluded that retail meats are often contaminated with drug-resistant *E. coli*.

In a similar study, 752 *E. coli* isolates from human and animal agriculture sources in several countries also were evaluated for their antimicrobial susceptibility patterns (11). Of the resistant phenotypes, the highest frequencies were found in isolates from human and turkey samples. Of the isolates from humans, 59% were resistant to sulfamethoxazole, 59% to streptomycin, 56% to ampicillin, 56% to tetracycline, 50% to cephalothin, 38% to trimethoprim-sulfamethoxazole, 34% to chloramphenicol, and 18% to amoxicillin-clavulanic acid. For turkeys, 84% were resistant to sulfamethoxazole, 82% to streptomycin, 71% to tetracycline, 49% to ampicillin, 39% to cephalothin, 28% to amoxicillin-clavulanic acid, 24% to gentamicin, and 20% to nalidixic acid. The resistance profiles for cattle, chicken, and swine were similar; approximately 50% of cattle isolates were resistant to streptomycin, 47% to tetracycline, 46% to sulfamethoxazole, and 15% to ampicillin. Of all the isolates tested, approximately half were resistant to one or more antimicrobials. The authors stated that the data provided by that study were in accordance with those of other studies and suggested that the use of antimicrobial drugs has been a key factor in selecting for these resistant *E. coli* strains. However, no evidence was provided to support this hypothesis. They also noted that 40% of the *E. coli* isolates from humans were resistant to trimethoprim-sulfamethoxazole, which is a recommended combination for treating a range of human infections, including urinary tract infections. The authors suggested that resistance to this combination drug should be closely monitored because its use for treatment of disease may result in failure to cure. The authors also noted that 20% of the *E. coli* isolates from turkeys were resistant to nalidixic acid, which is a quinolone type of drug. Currently, fluoroquinolones are used to treat a range of *E. coli* infections in humans, and resistance to this class of antimicrobial drugs is alarming. Results from our study indicated little or no resistance to nalidixic acid along with other quinolones tested with *E. coli* and *Salmonella*.

Resistance to trisulfa was more common in *E. coli* isolates recovered in this study and could be a cause for concern if these bacteria can make it through the processing environment and contaminate meat products consumed by humans.

Sulfamethoxazole is generally not prescribed without trimethoprim in humans, and the high level of resistance observed in this study may therefore not be considered too alarming.

The results of previous studies and this study clearly indicate that nonspecific *E. coli* and *Salmonella* can carry and disseminate antimicrobial resistance genes. The increase in the number of resistant bacteria is a cause for concern in both food animals and humans. Concern over nonpathogenic strains of these bacteria is equally merited because these strains may be able to transfer resistance to pathogenic and commensal bacteria in the human and animal gastrointestinal tract.

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