

**PREVALENCE, ANTIBIOTIC SUSCEPTIBILITY, AND GENETIC DIVERSITY OF *SALMONELLA*, *CAMPYLOBACTER*, AND *ESCHERICHIA COLI* O157:H7 COLLECTED AT FOUR KANSAS BEEF CATTLE FEEDYARDS OVER 13 MONTHS<sup>1</sup>**

*D. R. Hyatt*<sup>2</sup>, *J. C. Galland*<sup>2</sup>, *S. Crupper*<sup>3</sup>,  
*L. Hawkins*, *N. V. Anderson*<sup>2</sup>, *G. L. Stokka*

**Summary**

*Salmonella*, *Campylobacter*, and *Escherichia coli* O157:H7 are important foodborne pathogens, but longitudinal studies of their prevalence in beef cattle feedyards have not been done. Our long-term study involved 24,556 samples taken from beef cattle feedyards found overall prevalences of 4.87% for *Salmonella*, 20.1% for *Campylobacter* in hospital pen fecal samples, and 0.20% for *E. coli* O157:H7. Yard and pen differences ( $P < 0.05$ ) were detected. All 53 *E. coli* O157:H7 isolates were resistant to Talmicosin and Erythromycin, two antimicrobials used in food animal medicine. Their genetic diversity was high and did not indicate the presence of resident strains at the yards studied. *Salmonella*, *Campylobacter*, and *E. coli* O157:H7 were probably brought into the yards by shipments of new cattle. Many of these organisms were susceptible to antibiotics commonly used to treat beef cattle.

(Key Words: Bacterial Infection, *Salmonella*, *Campylobacter*, *E. coli* O157:H7, Feedyards, Antibiotic Susceptibility.)

**Introduction**

Agricultural use of antibiotics has been suggested as the reason for the development of antibiotic resistance in strains of human pathogens. However, strong evidence to support this

hypothesis has not been presented. Knowing antibiotic susceptibility of genetically identical *Escherichia coli* O157:H7 isolates will help to determine 1) their feedyard sources, 2) which antibiotics could be effective for cattle therapy, 3) sources that have greatest resistance, 4) whether some genetically identical isolates are developing resistance over time, and 5) seasonal resistance patterns for each antibiotic tested. Knowing the genetic diversity of organisms such as *E. coli* O157:H7 aids investigators in determining if contamination is due primarily to resident or transient isolates and could help trace the source of disease outbreaks. Monitoring the prevalence, antibiotic susceptibility, and genetic diversity of foodborne pathogens at cattle feedyards is important for producers designing production animal (preharvest) Hazard Analysis Critical Control Points (HACCP) programs for pathogen reduction.

**Experimental Procedures**

Four large (>25,000 head) beef cattle feedyards in southwest Kansas were sampled every 3 weeks for 13 months for a total of 20 collections per yard. Pens typically had new lots of cattle every 155 days. Six composite fresh fecal pat samples (five pat samples/ composite) from the floor of approximately 30 home pens and all special pens were collected as well as a composite water sample from the pen's water

---

<sup>1</sup>The authors would like to acknowledge funding from USDA-CSRS grant #95-37201-2127.

<sup>2</sup>Food Animal Health and Management Center, College of Veterinary Medicine.

<sup>3</sup>Department of Biology, Emporia State University, Emporia, Kansas.

trough and a composite feed sample from the pen's feed bunk. Lagoon water and ration ingredients also were collected from each yard at each visit. Standard microbiological techniques were used to isolate *Salmonella*, *Campylobacter* and *E. coli* O157:H7. The susceptibility of the *E. coli* O157:H7 isolates to 16 antibiotics used in human medicine and eight antibiotics approved for use in food animals was determined by use of the Sensititre Accumed semi-automated system. Random amplification of polymorphic DNA (RAPD) was used to genetically characterize the *E. coli* O157:H7 isolates.

### Results and Discussion

Analysis of over 24,500 samples showed that prevalence of the three bacteria varied among yards; type of pen (home, hospital, other); and sample type (fecal, water, total ration, individual ration ingredients, and lagoon). *Salmonella* spp. were isolated from 4.87% of samples, and *E. coli* O157:H7 was isolated from 0.20%. *Campylobacter* was isolated from 20.1% of hospital pen fecal samples (n=2672). Total prevalences for all yards varied from 1.88% to 10.66% for *Salmonella*; from 0.06% to 0.36% for *E. coli*; and from 14.43% to 30.49% for *Campylobacter* (in hospital pens only). Over all four yards, *Salmonella* spp. were isolated from 6.3% of bunk ration samples (n=2921), 0.80% of drinking trough samples (n=3248), 5.44% of fecal samples (n=17494), 2.24% of ration ingredient samples (n=581), and 6.09% of lagoon samples (n=312). *E. coli* O157:H7 was isolated from 0.10% of rations, 0.03% of drinking water, and 0.26% of fecal samples but was not detected in any lagoon or ration ingredient samples. Total prevalence of *Salmonella* varied in different yards from 2.08% to 12.2% in fecal pat samples, 0.58% to 0.97% in water samples, 1.47% to 13.3% in ration samples, 0.67% to 3.82% in ingredient samples, and 2.7% to 8.77% in lagoon

samples. Hospital and other special pens had higher total prevalence of *Campylobacter* than home pens (P<0.05). No differences were detected in *E. coli* O157:H7 prevalence among pen types. All isolates of *E. coli* O157:H7 were resistant (Table 1) to Tilmicosin and Erythromycin. Most of the *E. coli* O157:H7 isolates were susceptible to Ceftiofur and Ampicillin. All but three isolates were susceptible to Trimethoprim sulfate, which was used widely in cattle feedyards 10 years ago but is used infrequently now.

Genetic diversity among 53 *E. coli* O157:H7 isolates was high (16 RAPD prints) and indicates that the strains found were brought in with loads of cattle and did not remain resident at these large well-managed feedyards. Pens rarely tested positive for *E. coli* O157:H7 twice. It was rarely isolated from feed and never isolated from water. Thus it was not persistent in these yards. *E. coli* O157:H7 was isolated from the same pen at different collections only three times. In two of those cases (separate yards), a genetic pattern found during collection 1 was found again in collection 15, which was made 42 weeks later.

**Table 1. Antimicrobial Susceptibility (Susceptible (S), Intermediate (I), or Resistant (R)) of 53 *E. coli* O157:h7 Isolates**

Antibiotic	S	I	R
Trimethoprim Sulfa	50	0	3
Ceftiofur	44	0	9
Ampicillin	44	0	9
Cephalothin	31	13	9
Tetracycline	28	2	23
Amoxicillin	11	0	42
Penicillin	0	3	50
Erythromycin	0	0	53
Tilmicosin	0	0	53