Do Bacteria from Cattle Contribute to Antibiotic Resistance in Human Medicine?

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Project Title:
Surveillance of E. coli, enterococci, antimicrobial resistance (AMR) and Enterococcus species distribution in beef operations and associated environments

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Published:
Whole Genome Sequencing Differentiates Presumptive Extended Spectrum Beta-lactamase Producing Escherichia coli isolates from various sources of the One Health Continuum

Background
E. coli live in the digestive tracts of warm-blooded animals and birds. Most are harmless, some are beneficial, and some (like E. coli O157:H7) can be very dangerous. E. coli are also involved in antibiotic resistance.

“Extended-spectrum beta lactamase producing” (ESBL) E. coli are a major concern in human medicine. These bacteria are resistant to many antibiotics used both human and veterinary medicine. Ordinary E. coli can cause urinary tract or bloodstream infections in people. They’re usually quite easy to treat with antibiotics. But ESBL E. coli are responsible, the infections can’t be easily treated with antibiotics, and the illnesses can be much worse or even fatal.

E. coli rarely causes disease in feedlot cattle. But ESBL E. coli are still a concern, because antibiotic resistance genes are often located on “mobile genetic elements” that bacteria can trade with each other, even with completely unrelated bacteria. So antibiotic resistant E. coli bacteria from feedlots can carry and transmit genes for resistance to other E. coli from cattle or even to E. coli from different sources.

Dr. Tim McAllister and other researchers from Agriculture and Agri-Food Canada, the University of Calgary, the Public Health Agency of Canada, the Canadian Food Inspection Agency, Alberta Agriculture and Forestry, Feedlot Health Management Services and the University of Calgary looked for ESBL E. coli isolates from environments and compared them to ESBL E. coli isolated from human environments. The results of this Beef Cluster study have been published (Whole Genome Sequencing Differentiates Presumptive Extended Spectrum Beta-lactamase Producing Escherichia coli isolates along Segments of the One Health Continuum, doi:10.3390/microorganisms8030448).

What They Did
Over two years, 7,537 E. coli isolates were collected at four southern Alberta feedlots (pen floor feces, catch basin water and surface streams), a packing plant (hides, washed carcasses, conveyor belts, trim, whole muscle cuts and ground beef), sewage treatment plants (Calgary and Medicine Hat) and human patients (Calgary Laboratory Services). About 80% of the E. coli isolates from feedlots and packing plant samples were from pens and could only be found after they were exposed to multiple antibiotics. In contrast, E. coli from feedlots and packing plants only rarely carried any mobile genetic elements. But DNA sequencing revealed that different antibiotic resistance genes predominated in ESBL E. coli from different environments. Of the 11 antibiotic resistance genes that differed between ESBL E. coli from cattle- and human-associated samples, 11 were more common in E. coli E. coli isolated from human-associated samples. This seems to suggest that the ESBL E. coli that prevailed in sewage and human samples probably didn’t originate from cattle.

Three main “families” emerged when genetic relatedness was compared among the ESBL E. coli isolated from different sources. Three isolates from feedlot pens, three from cattle processing and municipal sewage were closely related to each other. Those from the packing plant were closely related to each other, and those from clinical patients and municipal sewage were closely related to each other. But there was very little relatedness between genetic clusters in the three groups. Like other bacteria, E. coli evolve to fit their environment, and it can be difficult for one E. coli from one environment to thrive in another.

Integrative conjugative elements (ICE), one group of mobile genetic elements bacteria use to carry and trade antibiotic resistance genes, are rarely found in ordinary E. coli. But ICE were found in all 502 of the ESBL E. coli isolates in this study. Genetic analyses revealed that most of these genomes likely originated from different bacteria like Vibrio, Pseudomonas, Salmonella or Yersinia. Although environmental challenges and food safety interventions all help to prevent ESBL E. coli from moving from cattle to people, bacteria may still be able to “bucket bounce” their antibiotic resistance genes from one environment to another.

What It Means
This study adds to a growing body of evidence that antibiotic resistance in bacteria associated with beef cattle likely doesn’t drive antibiotic resistance associated with bacteria in humans.

But it also emphasizes the importance of appropriate antibiotic use. When bacteria manage to assemble multiple antibiotic resistance genes on the same ICE element, the stage is set for rapid spread of multi-drug resistance among a lot of different bacteria, whether on the farm or in the hospital.

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