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BEEF CATTLE RESEARCH COUNCIL

RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

Beef Science Cluster



Evaluating the potential contribution of beef cattle to antimicrobial resistance

Project Title:

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

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Background

Increasing public concern regarding antimicrobial use (AMU) and resistance (AMR) in livestock is leading to increased pressure on livestock producers, veterinarians, industry groups, processors, foodservice companies and governments to address these concerns. Science-based, epidemiologically sound research is critical for sound industry policy and communication, legislation, and educated consumer choices.

Objectives

To determine how antibiotics used in the beef industry travel through the environment and how that contributes to antimicrobial resistance (AMR) in humans and cattle.

What They Did

This study focused on antimicrobials classified as being of high and very high importance in human medicine. AMU records were collected from Alberta feedlots. *E. coli* and enterococci were also isolated from bovine feces, manure drainage/catchment basins at feedlots, downstream surface water and retail beef, and compared to isolates obtained from human clinical samples. The

zoonotic potential of these species and any link between AMU in livestock and humans colonized by antibiotic resistant enterococci was examined. Advanced genotyping techniques will be used to evaluate similarities and differences between enterococci species isolated from cattle and humans, as well as the genetic sequences of genes associated with AMR in cattle and human clinical cases.

Additional samples were collected within the feedlot environment to assess the degree to which antimicrobial residues that are not absorbed or metabolized by the animal enter the environment via manure, how long they persist in the environment, and whether manure management practices like composting or stockpiling affect how quickly and completely antimicrobial residues are broken down.

What They Found

Different species of enterococci thrive in different environments. For example, one species (*E. hirae*) accounted for 90% of the enterococci found in fecal samples from cattle but less than 1% of the enterococci in humans. In contrast, *E. faecium* and *E. faecalis* accounted for over 95% of the enterococci found in humans, but less than 5% of the enterococci in cattle. This suggests that cattle-associated enterococci may have a hard time making their way into humans.

The predominant *Enterococcus* species gradually shifted as sample collection sites moved from the cattle to the human environments. The farther the sampling moved away from the feedlot, the less common the cattle-associated *E. hirae* became. The closer the sampling moved towards the human environment, the more common the human-associated *E. faecium* and *E. faecalis* became. A big shift happened at processing and retail, where the human-adapted species suddenly increased to 75% of the enterococci collected. Human-adapted enterococci may move from people to beef in those environments, rather than from cattle to beef.

Antimicrobial resistance patterns also differed between environments. Resistance to macrolides (High Importance in Human Medicine) and tetracycline (Medium Importance) were commonly found in enterococci from feedlot samples, probably because of the extensive use of in-feed Tylan and chlortetracycline to control liver abscesses. Compared to samples from cattle-associated environments, enterococci from clinical patients and treated sewage treatment showed resistance to macrolides as well as antibiotics of Very High Importance in human medicine (e.g. antibiotics related to Baytril, Excede, Excenel and others). The antibiotic resistance patterns observed in cattle-associated environments reflected the types of antibiotics that are used in cattle, while the patterns observed in human-associated environments reflected the antibiotics used in human medicine.

Comparisons of stockpiled to composted manure found that composting was an effective way to dissipate antibiotic residues and degrade antibiotic resistance genes. A wide variety of antibiotic resistance genes was found in soil samples. This isn't too surprising – many of the antibiotics used in human and veterinary medicine were originally discovered in soil bacteria. Bacteria naturally produce antibiotics to attack other bacteria and invade habitats that have better moisture, temperature or nutrient conditions, and they naturally develop antibiotic resistance to protect themselves from the antibiotics that other bacteria produce. As a result, microbiologically active soils appear to play an important role in degrading antibiotics and antibiotic resistance genes originating from manure.

What it Means:

Antibiotic resistant bacteria and genes are unlikely to flow from cattle to people through the environment when antibiotic use, manure and runoff are appropriately managed. Responsible antibiotic use slows the rate with which [antibiotic resistance](#) develops. Practices like manure composting help degrade antibiotic residues and antibiotic resistance genes. Adopting and documenting recommended antibiotic use and manure management practices will become increasingly important as public interest in and concern about beef production practices grows.

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