



Insights into environmental transmission of antimicrobial resistance and metal tolerance in *Escherichia coli* in beef production

HOW DOES ANTIMICROBIAL RESISTANCE SPREAD THROUGH THE ENVIRONMENT

PROJECT NO.: 2021F098R

LEAD RESEARCHER: Sylvia Checkley (University of Calgary Faculty of Veterinary Medicine)

COLLABORATORS: Susan Cork, Karen Liljebjelke (University of Calgary Faculty of Veterinary Medicine); Sheryl Gow (Public Health Agency of Canada, Canadian Integrated Program for Antimicrobial Resistance Surveillance); Tim McAllister, Rahat Zaheer (Agriculture and Agri-Food Canada); Cheryl Waldner (Western College of Veterinary Medicine)

Background: Antibiotics are a critical component of animal health management, and we need to be able to maintain their effectiveness to treat sick animals. But the use of antibiotics also generally provides selection pressure for bacteria to become resistant to antibiotics. Bacteria have several methods of developing resistance, and many of them are genetic in nature. Some of these genetic elements can be “swapped” amongst different species of bacteria causing resistance to spread further

Objectives:

1. Determine genetic relatedness of *E. coli* isolated from numerous sources (feedlot, retail meat, well water, wastewater)
2. Characterize antimicrobial resistance (AMR) gene and mobile genetic element (MGE) frequency and other patterns across sources, including metal tolerance phenotypes and genotypes
3. Compare the characteristics of *E. coli* from the gastrointestinal tract with those from environmental sources to assess their ability to act as reservoirs and/or play a role in resistance transmission

4. Assess associations between multidrug resistance, AMR genes, and risk factors including antibiotic use, compare phenotype and genotype for antibiotic resistance and metal tolerance
5. Model transmission of resistant *E. coli* along the beef production chain to help determine the effects of different management factors environmental AMR transmission.

Implications of the Research: In Canada we have surveillance systems that work to monitor trends in AMR at different points in the production chain (e.g., CIPARS, on-farm). But, there is a lack of knowledge around how AMR spreads throughout the environment. A previous study looking at *Enterococcus* bacteria demonstrated that different species with different AMR patterns were predominant in different environments, and the same was true for extended-spectrum beta-lactamase producing (ESBL) *E. coli*. However, given that the transmission of AMR is extremely complicated, and the ability of bacteria to assemble multiple AMR genes on a MGE, it is important to learn as much as we can about the potential spread of AMR throughout the environment.

This project is also supported by Results Driven Agricultural Research, Major Innovation Fund, the Beef Cattle Research Council, and NSERC.



www.albertabeef.org