



# RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

## Antimicrobial Resistance in Campylobacter

### Project Title:

Development of a Longitudinal Antimicrobial Resistance and Antimicrobial Use Surveillance Program for the Feedlot Sector in Western Canada

### Project Code:

6.41

### Completed:

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### Researchers:

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### Background:

*Campylobacter* bacteria can cause intestinal cramping, abdominal pain, fever, nausea, headaches and bloody diarrhea, especially in very young people or those with weak immune systems. Some infected people show no symptoms at all. Electrolytes and fluids are the most commonly prescribed treatment, although antibiotics may be prescribed in severe cases.

Southern Alberta has the highest rates of human campylobacteriosis and the largest cattle population in Canada, leading some people to blame cattle for human illness. *Campylobacter jejuni* does not typically cause illness in cattle, so these bacteria are not deliberately targeted when cattle are treated. However, *Campylobacter* can rapidly develop resistance to some antibiotics. Fluoroquinolone drugs like ciprofloxacin are of very high importance in human medicine. Although rarely used in beef cattle, Baytril (a fluoroquinolone) is approved to treat bovine respiratory disease. It is important to assess whether routine feedlot health management practices may contribute to human health risks in cattle producing areas.

### Objectives

- I. Determine how antimicrobial resistance in *C. jejuni* changes over time in feedlot cattle,
- II. genetically compare *C. jejuni* found in beef cattle and humans living in southern Alberta, and
- III. determine which genetic factors contribute to fluoroquinolone resistance in *C. jejuni*.

### What they did

*C. jejuni* was isolated from individual fecal samples collected from 4,427 cattle at four commercial feedlots in Southern Alberta. Samples were collected on arrival, with a second sample collected after 60 days on feed. *C. jejuni* was also isolated from stools of human patients with enteritis in Southern Alberta. Isolates were DNA-fingerprinted to see if the *C. jejuni* found in cattle were the

same as those found in humans. Antimicrobial resistance was also evaluated in *C. jejuni* isolated from the cattle and humans. Mutations in *C. jejuni*'s *gyrA* gene are involved in ciprofloxacin resistance, so ciprofloxacin resistant *C. jejuni* from cattle and humans were DNA sequenced to determine if they carried the same *gyrA* mutations.

### What they learned

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Prevalence: *C. jejuni* was found in 27% of the cattle samples at arrival, and 61% after 60 days on feed. Of the 290 people in the Chinook Health Region diagnosed with enteritis over a one-year period; less than 11% were infected with *C. jejuni*.

*C. jejuni* in cattle and humans: Of the 592 genetically distinct types of *C. jejuni* found, 306 types were found in cattle, and 286 types were found in human patients. Only 54 genetic types were found in both cattle and humans, but these overlapping genetic types were very common. The overlapping genetic types accounted for 69% of the *C. jejuni* isolated from cattle and 43% of those from human patients.

Antimicrobial resistance to ciprofloxacin increased slightly (from 5.8 to 8.8%) between feedlot entry and 60 days on feed in cattle. The reason for this is unclear. Only 11 animals in one feedlot were treated with Baytril, and ciprofloxacin resistant *C. jejuni* was only isolated from one of these animals. The degree of ciprofloxacin resistant *C. jejuni* in cattle in this study was also higher than the 2.4% reported from fecal samples collected from healthy cattle entering abattoirs in the ongoing Public Health Agency of Canada's Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) study.

Antimicrobial resistance was higher in *C. jejuni* from human patients than in *C. jejuni* from cattle samples for five of the seven antimicrobials tested in this study, and six out of seven tested in the CIPARS study.

Genetics of resistance differed between antimicrobial resistant *C. jejuni* from cattle and humans. The specific mutations in the *gyrA* gene found in antimicrobial resistant *C. jejuni* from cattle were very rarely found in antimicrobial resistant *C. jejuni* from humans (and vice versa). Three mutations accounted for over 75% of the ciprofloxacin resistant *C. jejuni* isolates from cattle, but these three mutations were found in less than 3% of the human isolates. Similarly, seven mutations accounted for over 75% of the ciprofloxacin resistant *C. jejuni* isolates from humans, but these seven mutations were found in less than 20% of the cattle isolates.

### What it means:

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Cattle may not be the primary reservoir of *C. jejuni* (including antimicrobial resistant *C. jejuni*) responsible for the high rates of campylobacteriosis in Southern Alberta. Together with Alberta Health Service, these researchers are using more complex DNA techniques to identify important reservoirs of human infectious *C. jejuni* and transmission mechanisms.

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