



# RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

## IN PROGRESS

### Characterizing the microbiome of beef cattle to identify risk factors that affect respiratory health

#### Project Title:

Characterizing the microbiome of beef cattle to identify risk factors that affect respiratory health

#### Researchers:

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#### Project Code:

AMR.10.17

#### Completed:

*In Progress. Results expected in March 2023.*

#### Background:

Some bacteria naturally present in the respiratory tract of beef cattle help to prevent pathogenic bacteria or viruses from invading. Factors like stress and antimicrobials can disrupt the protection that these 'good' bacteria provide. However, we need to know more about which bacteria have protective effects, and how their populations can be maintained or restored.

#### Objectives:

Characterize the bovine nasopharyngeal microbiota from birth to weaning and define animal, management, and environmental elements that influence the nasopharyngeal microbiota of and how those elements correlate with animal health.

#### What They Will Do:

Animal, management and environment effects: 4,000 calves entering 10 feedlots will be sampled using deep nasal swabs. Upper respiratory tract microbiota will be compared between groups differing in BRD risk, weight, sex, origin, season, distance travelled and BRD outcome. Treatment, morbidity and mortality data will be collected. Relationships between upper respiratory tract microbiota and health outcomes will be assessed.

Nasopharyngeal microbiota from birth to weaning: 45 cows will have deep nasal swabs collected at calving, and their calves will be sampled within 3 weeks, at 2 months, 3-4 months, and 6 months of age. Calf microbiota will be compared to the dam. Changes in respiratory microbiota and relationships to health outcomes will be compared over time.

Mapping bacterial communities along the respiratory tract: 30 feedlot steers (15 healthy and 15 with BRD) will be sampled at 13 sites along the respiratory tract. The bacteria populating different regions of the respiratory tract will be identified and compared between healthy and sick cattle.

Changes in bacterial communities during BRD development: 50 feeder steers at high risk of developing BRD will be studied in the first 60 days on feed. Deep nasal swabs will be collected on arrival, and a rumen bolus will be given to monitor and identify temperature changes indicative of BRD before visible signs of illness appear. In animals displaying elevated temperatures for 24 hours, repeated blood and respiratory tract samples will be collected until visual signs of illness develop or the animal recovers. Sick calves will be treated and resampled 4 to 8 days later. Microbiota will be assessed and compared between sick and healthy calves, between treated calves and calves that recover on their own, between different time points of sickness and recovery, and between different locations in the respiratory tract.

Effect of on-farm vaccination on feedlot BRD: 50 vaccinated and 50 non-vaccinated calves from AAFC Lacombe will be shipped to AAFC Lethbridge 5 weeks after weaning. Blood samples will be collected on arrival to measure antibody levels. Deep nasal swabs will be collected on arrival, 14 and 30 days on feed. Microbiota and health outcomes will be compared between vaccinated and non-vaccinated calves.

Effect of stress: Preconditioned and non-preconditioned calves from AAFC Lacombe (50 head each) will be shipped to AAFC Lethbridge. The two groups will be kept separate, but commingled with auction mart calves. Deep nasal swabs will be collected pre-shipment and 2, 7, 15 and 30 days after feedlot placement. Stability of the respiratory microbiota, health and treatment outcomes will be compared between groups.

### **Implications:**

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This project will help the beef industry to maintain animal health with less reliance on antimicrobials by improving our understanding of what constitutes a healthy respiratory microbiome and how management practices can disrupt or support the respiratory microbiome and affect its ability to resist bovine respiratory disease.

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