RESEARCH

"Development of multiplex recombinase polymerase amplification (RPA) assays for the detection of antimicrobial-resistant (AMR) bacterial pathogens causing bovine respiratory disease (BRD)"

REFINING NEW DIAGNOSTICS FOR BRD

PROJECT NO.: ANH.18.19
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Background: Traditional bacterial culture and antibiotic sensitivity tests that are available to diagnose which bacteria are causing a specific BRD case take weeks to produce results. By the time the diagnostic result is available, different bacteria may be responsible for the illness (if the animal is still alive). This delay in the availability of diagnostic information is not practical in large-scale, commercial feedlots. As a result, feedlot BRD treatment decisions are based on recent clinical trials, veterinary protocols and producer experience rather than an actual diagnosis.

Complicating things further, not all bacteria are equally capable of causing disease. For example, there are different serotypes (strains) of Mannheimia haemolytica (one of the main BRD bacteria). Serotypes 1 and 6 frequently cause BRD, whereas serotype 2 is typically found in healthy cattle. Some bacteria may also be carrying antibiotic resistance genes while others aren't, which requires a whole different diagnostic procedure. Sometimes clusters of antibiotic resistance genes are carried on mobile genetic elements that can be easily traded with other bacteria. This can lead to rapid spread of antibiotic resistance.

This project uses technology first developed in a previous ABP funded project and will be making further improvements and refinements.

Objectives: The objectives of this study are to:

1. Design recombinase polymerase amplification (RPA) assays to simultaneously detect Histophilus somni and Pasteurella multocida stains known to cause BRD, and identify mobile genetic elements and antimicrobial resistance genes associated with these bacteria
2. Describe the frequency of detection of the four main bacteria associated with BRD using RPA, the antimicrobial resistance genes and associated mobile genetic elements isolated from calves on arrival and five days post-feedlot arrival, as well as from calves that are sick and/or have died from BRD

Implications of the Research: Building on the previous project, this research will move new timely, accurate and cost-effective BRD diagnostics another step closer to being applied at the farm level, and will contribute to more appropriate and strategic antibiotic treatment options that improve animal health and welfare outcomes.

This project is also supported by the Beef Cattle Research Council, the Saskatchewan Agriculture Development Fund, the Saskatchewan Ministry of Agriculture and Genome Alberta/Canada.

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