Can chute-side disease diagnostics reduce antibiotic use in beef cattle?

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Project Title:

Exploring options for BRD diagnostics 2.0 – a point-of-care metagenomic nanopore sequencing pilot study

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Objective

To determine whether existing technologies can be used chute side to determine and expedite optimal antibiotic treatment.

Background

Bovine respiratory disease (BRD) is one of the most common diseases in feedlot cattle and as a result is the most common need for antibiotic treatment. Currently there is no practical way to test for the presence of BRD; lab tests take days which postpone treatment decisions that alleviate suffering. Currently feedlot workers base treatment options on presence of clinical signs and previous experience. Since no test is available to tell for sure which specific pathogen to treat there is a chance that workers e may not select the optimal treatment based on the specific type of BRD. An ideal BRD test would be rapid, easy to use, cost effective, and comprehensive enough to detect both common and less frequently seen pathogens that cause BRD.

What they did

In preliminary work, researchers were able to analyze BRD samples in less than 6 hours. This pilot study aims to reduce that time further and test an existing technology that could automate the sample handing procedure so that the work can be carried out in a veterinary clinic or on farm.

Samples for this pilot study were obtained from clinical cases submitted by practicing veterinarians as well as a group of calves from a feedlot chronic pen at the end of the season. Researchers evaluated a methodology for metagenomic sequencing that describes all the DNA in a diagnostic sample. It is a type of non-targeted diagnostics that does not require you to know what bacteria you are looking for before you start the analysis. This contrasts with most other techniques that look for precise small DNA targets in diagnostic samples. This technology can be used both outside and within a

traditional laboratory.

Researchers collected clinical samples from feedlot cattle and compared the results from conventional culture and antimicrobial sensitivity testing to the result of DNA sequencing

What they learned

This group found that in almost all cases, sequencing detected the same organisms as culture or more. They were also able to detect gene-encoded determinants of antimicrobial resistance, but additional optimization of this approach will be necessary to link resistance genes to specific bacteria. This methodology seems to perform most reliably in samples with high bacterial load. Further work is necessary to improve efficiency in lower biomass samples, so that this tool can be used more effectively for surveillance and evaluating pre-symptomatic animals.

Additionally, researchers tested the field compatibility of sequencing technology and found that while most of the process can be reliably performed in the field with limited equipment, there are still some more intensive steps (removal of calf DNA and extraction of the bacterial DNA) that are currently still challenging outside of a laboratory environment but that could potentially be undertaken in a veterinary clinic.

This technology has the potential to have a major impact on the Canadian beef industry. The ability to use chute-side diagnosis in feedlots would reduce the number of animals who are misdiagnosed. As a result, it would enable more rapid treatment while decreasing antibiotic use.Such an improvement is critically needed to maintain consumer confidence in beef quality and safety, address the increasing antimicrobial stewardship requirements, and maintain global market access.

What it means

In comparison with classical microbiological techniques like culturing and antimicrobial sensitivity testing, DNA sequencing is a promising diagnostic method that can offer faster answers and increased sensitivity for the detection of BRD pathogens, even in low biomass samples. Researchers found that sequencing performs well in terms of its ability to detect relevant pathogens of interest, compared to culture. However, initial sample preparation and sequencing efforts were less consistent at resolving information about antimicrobial resistance; meaning this method is currently able to report potential pathogens involved in a BRD infection but will require additional development (currently underway as part of a follow up project) to provide information about what antimicrobials may be best suited for treatment.

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