Diving Deep Into Liver Abscesses

Project Code: ANH.02.19
Completed: *In Progress. Results expected in 2025.*

Project Title:

Application of a multi-omics strategy to investigate liver abscess development in beef cattle

Background

The most common theory about the origin of liver abscesses is that feeding high grain finishing diets leads to rumen acidosis. If ulcers form, some rumen bacteria may enter the bloodstream. When the liver tries to filter those bacteria out of the blood, some bacteria (Fusobacterium necrophorum and Truperella pyogenes) infect the liver, resulting in liver abscesses.

This theory hasn't ever been confirmed. For example, although Fusobacterium is often isolated from liver abscesses, it's unknown whether they actually cause the abscess, or whether they are simply opportunistic bacteria that join the party later. We don't have a very good understanding of what causes liver abscesses from a microbiological perspective, or why different animals vary in their susceptibility to liver abscesses.

Objectives

- Apply meta-omics to determine if the microbial ecology of liver abscesses vary between animals,

- Apply host transcriptomics to study gene expression in the liver impacted by abscess development and identify factors predisposing animals to this disease,

- Apply genomics to examine the relationship between the rumen microbial community, rumen fermentation, and the development of liver abscesses.

- Study if gene expression in the liver changes throughout feeding and is this linked to abscess development

- Identify targets for future vaccine/drug design and/or recommend changes in management practices

What they will do

This team will collect monthly blood, physiological, and rumen from 48 cannulated steers at 8 points through the backgrounding (40% concentrate) and finishing (90% concentrate) period as well as post-slaughter. Liver samples will be collected at the end of the backgrounding period, one and three months after the cattle have adjusted to the finishing diet, and post-slaughter. The microbial community in healthy and diseased

livers (taxonomic profile, microbial function, antibiotic resistance genes, etc.) and rumen (including microbiome profile, taxonomy, metabolic potential and starch digesting enzymes) will be assessed. Bacteria in liver abscesses will be compared among cattle with differing severity of abscesses, and the Fusobacterium and Truperella from liver abscesses will be compared to rumen strains to see if they are genetically identical. Gene expression will be compared in healthy and diseased livers to identify biomarkers for disease susceptibility.

Implications

The combination of genomic and metabolic data from both bacteria and animals will provide insights into how liver abscesses develop, help identify vaccine or drug development targets, and potentially contribute to better diagnostic techniques.

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