



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

## DIVING DEEP INTO LIVER ABSCESS DEVELOPMENT

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**Background:** The most common theory about the origin of liver abscesses is that feeding high grain finishing diets leads to ruminal acidosis, where the pH of the rumen is decreased. This decrease in pH may cause damage to the rumen wall, and if ulcers form, some rumen bacteria may enter the bloodstream. When the liver tries to filter those bacteria out of the blood, some bacteria (most commonly *Fusobacterium necrophorum* and *Truoperella pyogenes*) infect the liver, resulting in liver abscesses.

While this is the most prevailing theory, it hasn't been scientifically confirmed. For example, although *Fusobacterium* is often isolated from liver abscesses, it's unknown whether they cause the abscess, or whether they are simply opportunistic bacteria that join in on creating the infection. 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:

1. Apply meta-omics to determine if the microbial ecology of liver abscesses vary between animals
2. Apply host transcriptomics to study gene expression in the liver impacted by abscess development and identify factors predisposing animals to this disease

3. Apply genomics to examine the relationship between the rumen microbial community, rumen fermentation, and the development of liver abscesses
4. Study if gene expression in the liver changes throughout feeding and is this linked to abscess development
5. Identify targets for future vaccine/drug design and/or recommend changes in management practices

**Implications of the Research:** 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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