

Research Summaries

Evolution of the nasopharyngeal bacterial microbiota from spring processing to 40 days after arrival at the feedlot in beef calves

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Introduction

The stability of the bovine nasopharyngeal bacterial microbiota has been shown to play a crucial role in respiratory health. The combination of microbiota-based inhibitory effects and the protective effects of the host's immune system creates a stable environment in the nasopharynx. However, a loss of stability in the microbiota may decrease the host's ability to contain opportunistically pathogenic bacteria and increase the risk of foreign pathogens colonizing the upper respiratory tract. These pathogens can proliferate and progress into the lower respiratory tract, potentially leading to pneumonia. Different factors, including antimicrobial usage, commingling, stress, and concurrent viral infection can have an impact on the stability of nasopharyngeal microbiota. In humans, it has been shown that the respiratory bacterial microbiota evolves toward an adult-like profile within the first months of life. Certain bacterial profiles, once established, can remain stable over time, demonstrating a resiliency against respiratory infection. Previous longitudinal studies looking at the evolution of the nasopharyngeal bacterial microbiota in beef cattle have only centered around significantly stressful events, such as weaning and arrival at a feedlot, limiting our understanding of how respiratory microbiota evolve from an early age. Therefore, the objective of this study was to characterize the nasopharyngeal bacterial microbiota and its evolution from spring processing to 40 days after arrival at the feedlot.

Materials and Methods

A total of 120 crossbred beef-crossed steer calves, comprising three groups (40 calves/group), were enrolled to a study in southern Alberta at the time of first vaccination (spring processing). The 3 groups of calves originated from different ranches and were placed in different feedlots. Deep nasopharyngeal swab samples were collected from calves at the time of spring processing, feedlot arrival, and a targeted 40 days after feedlot arrival. Total DNA was extracted from the swabs and the V4 region of the 16S rRNA gene was sequenced. Sequencing data were processed using DADA2 to infer exact

sequence variants, and the resulting variants were used to evaluate the microbiota.

Results

The composition of the nasopharyngeal microbiota differed among calf groups. Each group showed different relative abundances of a total of 963 observed sequence variants. Across all groups, the most abundant genus was *Mycoplasma* and the most abundant species was *Mycoplasma dispar*. The next most abundant genera included *Lactococcus*, *Moraxella*, *Histophilus*, and *Pasteurella*, while the next most abundant species included *Lactococcus lactis*, *Pasteurella multocida*, *Histophilus somni*, and *Moraxella bovoculi*. The order of these genera and species by relative abundance differed by calf group. Over time, there was a distinct shift in the composition of the microbiota for all calf groups, including both alpha and beta diversity; however, changes in microbiota composition were unique to each calf group and each individual calf. Based on a PERMANOVA, time was a significant ($p < 0.001$) source of variation across all groups and remained a significant ($p = 0.003$) source of variation when pairwise comparisons of all time point combinations were made. Calf group was also a significant ($p < 0.001$) source of variation across all time points.

Significance

While some commonalities among the calf groups existed, in general the composition of the nasopharyngeal bacterial microbiota differed among groups and over time. A clear and distinct evolution of the nasopharyngeal bacterial microbiota was observed over time in all three groups. However, the patterns of change observed differed for each calf group. These variations in both microbiota composition and temporal changes of sequence variants indicates that the respiratory microbiota of beef cattle may lack a common pattern of evolution from ranch to feedlot, and that future studies should account for potential group effects.