Meta-transcriptomic Insight Into Resistome, Virulome, And Microbial Diversity In Calves

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Abstract:

Microbial communities in dairy calves significantly impact their health, influencing the occurrence of enteric and respiratory diseases. A deeper understanding of microbial diversity in health and disease is critical for improving diagnostic and treatment approaches.

This study aimed to explore the microbial diversity and gene expression patterns of various virulence and antimicrobial factors in rectal samples from dairy calves with varying health conditions and 4 different age groups sampled across 72 farms in New South Wales, Australia. A total of 593 rectal samples including 167 from animals with diarrhea were analysed using high-throughput RNA sequencing. Bacterial taxonomy was assessed using MetaPhlAn-4, calculating alpha and beta diversity. Virulence factors and antimicrobial resistance gene expression were also assessed within each age group and disease status.

The analysis revealed a complex microbial landscape characterized by approximately 1,000 distinct bacterial genera with top genera including Anaerovibrio, Prevotella, and Segatella. Healthy calves had significantly higher diversity compared to symptomatic animals. Differential expression analyses showed that although antimicrobial resistance genes (e.g., cfxA, Sul2, TetQ, dfrA-12, and aph(6)-la) were present across different age groups, they were significantly greater in calves with diarrhea compared to the healthy ones. Similarly, virulence factors such as afaE VIII, espB, espD, ompA 28, and PorA were distinctly elevated in symptomatic animals compared to asymptomatic ones. This study highlights bacterial diversity in dairy calves and its link to disease, virulence factors, and antimicrobial resistance, offering insights for calf health and antimicrobial stewardship.

Keywords: Metatranscriptomics, virulence factors, enteric disease

Declaration:

This work has been submitted to the American Dairy Science Association (ADSA) 2025 Annual Meeting for consideration. The abstract has been slightly reduced in length while maintaining its original content and significance.