Lung Tissue-based Analysis Of Pathogen Dynamics In Feedlot Cattle

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Abstract:

Bovine respiratory disease (BRD) is a major cause of morbidity and mortality in feedlot cattle, yet pathogen interactions remain poorly understood.

This study examined bacterial and viral contributions to BRD using 10 lung tissue samples and paired tracheal samples from cattle that died from BRD or other causes. Bacterial isolation, histopathology, immunohistochemistry (IHC), and RNA sequencing were conducted to assess lesions, detect BRD-associated pathogens, and characterize viral communities.

RNA sequencing showed significant differences in viral composition and virulence gene abundance between BRD-affected and non-BRD cattle. Jouyvirus ev207, Peduovirus P22H1, and Moineauvirus D1024 were predominantly found in BRD cases, likely due to viral tropism, co-infections, immune modulation, and environmental stress. BRD-affected samples contained significantly more virulence genes, suggesting a more virulent viral community. Known BRD-associated viruses, including Bovine Alphaherpesvirus 1 (BoHV1) and Bovine Respiratory Syncytial Virus (BRSV), were also detected in BRD cases, whereas Bovine Viral Diarrhea Virus (BVDV) was present in both groups.

These findings highlight the complex microbial landscape of BRD and the need for further research into pathogen interactions.

Keywords: Viral metagenomics; RNA sequencing; virulence genes; BRD; pathogen detection.