Topography of the respiratory tract bacterial microbiota in cattle

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Video Byte

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Abstract

Bovine respiratory disease, also known as shipping fever, is a primary cause of morbidity and mortality in feedlots. Although pneumonia-causing bacteria are thought to be located in the nasopharynx, contributions from other parts of the upper respiratory tract remain poorly characterized. A recent study characterized the composition of different respiratory bacterial communities in beef cattle. Researchers sequenced DNA from different respiratory samples collected from 15 healthy feedlot steer calves. They found that microbiota composition differed across sampling locations. The lung was more similar to the nasopharynx than to the oropharynx or any other sampling location. And one metacommunity found in the lung and nasopharynx was dominated by *Mycoplasma dispar*, a bacterium of potential significance in bovine respiratory microbiota research. Further studies are needed to determine how bovine respiratory disease affects the relationships between different respiratory bacterial communities. But the study suggests that the nasopharynx is likely the most important location to target when developing novel therapeutics to control respiratory disease in cattle. Such therapeutics would allow the cattle industry to minimize its use of antimicrobials while promoting better animal health and welfare.