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Impact of respiratory microbiota disruption on mucin glycosylation during influenza D virus-associated polymicrobial infection

Inhalt

Bovine respiratory disease (BRD) results from complex interactions between the host, the respiratory microbiota, and multiple respiratory pathogens, including influenza D virus. Mucins, the major structural components of respiratory mucus, constitute the first line of defense against inhaled pathogens. They carry O-glycans whose terminal sialic acid residues mediate interactions between influenza viruses and their host. However, the spatiotemporal changes in mucin glycosylation during respiratory infection remain poorly characterized.

The aim of the study is to evaluate the impact of respiratory microbiota disruption on mucin glycosylation remodeling during polymicrobial respiratory infection. To address this question, an in vivo calf model was established in which animals, treated or not with antibiotics were challenged with a combination of influenza D virus, bovine coronavirus and Mycoplasma bovis. Nasal swabs and bronchoalveolar lavages samples were collected over time to monitor changes in O-glycans and sialic acids profiles along the respiratory tract using glycomic approaches.

Preliminary analyses of non-infected animals showed that antibiotic treatment reshapes the global O-glycan profile, with coordinated changes across multiple glycan structures. Analyses of infected animals are ongoing and will determine how microbiota disruption influences respiratory mucin glycosylation during influenza D virus-associated polymicrobial infection.

Keywords

Glycans, sialic acids, glycomic, mucins, influenza D virus, polymicrobial infection, microbiota disruption

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Professional status of the speaker

PhD student

Junior scientist status

Yes, I am a junior scientist.

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