Mycoplasma ovipneumoniae in farmed white-tailed deer

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Introduction

Mycoplasma ovipneumoniae is an infectious cause of respiratory disease, previously assumed to cause disease only in members of the subfamily Caprinae (sheep, goats, muskox). This bacterium has sporadically been isolated from other species, including captive white-tailed deer (WTD); however, little is known about the incidence or significance of *M. ovipneumoniae* in this species. Chronic respiratory disease is a common problem in captive WTD, and due to the fastidious nature of *M. ovipneumoniae*, infections with this bacterium may be overlooked as a contributing factor. The objective of this study is to characterize the incidence of *M. ovipneumoniae* infection and its association with respiratory disease in an intensively managed captive WTD herd. Additionally, future multi-locus and full genome sequence analyses will elucidate relatedness between *M. ovipneumoniae* isolates from WTD and other species.

Materials and methods

This study focuses on an approximately 200-head, intensively managed, captive WTD herd in the Midwestern United States that has a 2-year history of chronic respiratory disease. Nasal swabs from clinically ill WTD or lung swabs from WTD that succumbed to respiratory disease were screened for *M. ovipneumoniae* by real-time PCR and samples were cultured using broth and agar appropriate for *Mycoplasma* spp. growth. *M. ovipneumoniae* specific real-time PCR was performed on subsamples of culture broths and colonies at Kansas State Veterinary Diagnostic Laboratory. Additionally, for WTD that succumbed to respiratory disease, histopathologic evaluation of respiratory tract lesions and routine aerobic culture on lung samples was performed.

Results

Samples were obtained from 58 captive WTD (37 female, 27 male), ranging in age from 4-months-old to 13.5-years-old. All but 2 sampled animals had varying clinical symptoms of respiratory disease, including nasal drainage, sneezing, coughing, raspy or labored breathing, and open-mouthed breathing. Six, 4-6-month-old female fawns had received no antimicrobial therapy, the remaining WTD had received varying protocols of antimicrobial therapy. *M. ovipneumoniae* was detected by real-time PCR in a total of 38 samples from 34 WTD (58.36% tested animals), including from 8 lung or lung swab samples and 2 post-mortem nasal swabs from deceased WTD. The remaining 28 positive samples were nasal swabs from living animals *M. ovipneumoniae* was detected in 23 female WTD (62%) and 11 males (41%). All of the *M. ovipneumoniae*-positive females were under 1 year of age, whereas 2 positive males were 1.5 and 2.5-years-old, respectively.

M. ovipneumoniae was detected in 9 of 10 WTD that succumbed to respiratory disease. In 3 of the deceased WTD, *M. ovipneumoniae* was the sole pathogen detected at postmortem evaluation. Bacterial co-infection of the lungs was detected in 5 *M. ovipneumoniae*-positive WTD, with *Trueperella pyogenes* (n = 2), *Bibersteinia trehalsoi* (n = 1), *Escherichia coli* (n = 1), and mixed bacterial flora (n = 4) isolated by aerobic culture. The following potential respiratory pathogens were not detected by real-time PCR in the 9 deceased WTD tested; *Histophilus somni, Mannheimia haemolytica, Mycoplasma bovis, Pasteurella multocida*, bovine respiratory syncytial virus, bovine viral diarrhea virus, bovine coronavirus, and bovine herpes virus-1.

Histopathologic evaluation of the lungs in the 9 *M. ovipneumoniae*-positive WTD revealed a patchy to diffuse, chronic, lymphoplasmacytic to histiocytic interstitial pneumonia with variable alveolar edema, occasional type-II pneumocyte hyperplasia, bronchiolar respiratory epithelial hyperplasia, bronchiolar-associated lymphoid tissue (BALT) hyperplasia and/or depletion, and peribronchiolar lymphohistiocytic infiltrates and atelectasis. In cases where co-infections were identified, there was cranioventral, multifocal to coalescent, acute necrotizing and suppurative bronchopneumonia with mixed Gram-negative bacilli and Gram-positive coccobacilli.

Significance

This study confirms that captive WTD are susceptible to infection with *M. ovipneumoniae*, and that this bacterium likely contributes to chronic respiratory disease in this intensively managed herd. Within *M. ovipneumoniae*-positive WTD in this herd, females and animals under a year of age were over-represented. Consistent with previous reports, this bacterium was challenging to isolate in culture, and real-time PCR of nasal and lung swabs is a more sensitive method of detection.

Microscopic lesions in *M. ovipneumoniae*-positive WTD that succumbed to respiratory disease were strikingly similar to those reported in sheep and goats with pulmonary *M. ovipneumoniae* infection. As typical with *M. ovipneumoniae* associated respiratory disease, multiple other bacterial agents were identified in the lung tissue of most of the *M. ovipneumoniae*-positive WTD in this study.

In summary, these findings provide evidence that *M. ovipneumoniae* contributes to clinical respiratory disease in captive white-tailed deer, both as a sole pathogen and in polymicrobial respiratory infections.

