



## Detection Error and Demographic Variability Amid Pervasive Pneumonia Pathogens in Bighorn Sheep

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**ABSTRACT:** Respiratory disease (pneumonia) has been a persistent challenge for bighorn sheep (*Ovis canadensis*) conservation and its cause has been attributed to numerous bacteria including *Mycoplasma ovipneumoniae* and several *Pasteurellaceae* family species. This study sought to investigate efficacy of diagnostic protocols in detecting *Pasteurellaceae* and *Mycoplasma ovipneumoniae*, generate sampling recommendations for different protocols, assess the distribution of these disease agents among 21 bighorn sheep populations in Montana and Wyoming, and evaluate what associations existed between detection of these agents and demographic performance of bighorn sheep populations. Analysis of replicate samples from individual bighorn sheep revealed that detection probability for regularly used



diagnostic protocols was generally low (<50%) for *Pasteurellaceae* and was high (>70%) for *Mycoplasma ovipneumoniae*, suggesting that routine pathogen sampling likely mischaracterizes respiratory pathogen communities. Power analyses found that most pathogen species could be detected with 80% confidence at the population-level by conducting regularly used protocols multiple times per animal. Each pathogen species was detected in over half of the study populations, but after accounting for detection probability there was low confidence in negative test results for populations where *Pasteurellaceae* species were not detected. Eighty percent of study populations hosted both *Mycoplasma ovipneumoniae* and leukotoxigenic *Pasteurellaceae* pathogens, yet a number of these populations were estimated to have recruitment rates greater than 30% and positive population growth. The results of this work suggest that disease severity is influenced by ecological factors and/or differences in pathogen communities that cannot be assessed using methods currently available to most wildlife managers. These results also suggest that continued respiratory disease epizootics may be caused by pathogens already resident in bighorn sheep populations as well as by the introduction of novel pathogens. We present a framework to evaluate these hypotheses and develop management strategies aiming to minimize the effects of respiratory disease in bighorn sheep amid pervasive respiratory pathogens.

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**KEY WORDS** Bighorn sheep; *Ovis canadensis*; pneumonia; *Mycoplasma ovipneumoniae*; *Pasteurellaceae*; detection probability; recruitment.