Evaluating Alternative Hypotheses to Explain Bighorn Sheep Respiratory Disease Events

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ABSTRACT Respiratory disease has been a major challenge for bighorn sheep conservation and is a dominant factor influencing management decisions of bighorn sheep. However, much about the disease process remains unknown. Decades of research have compiled considerable evidence that domestic sheep and goats transmit the disease to bighorn sheep. There is also strong evidence for several bacterial organisms commonly carried by domestic sheep and goats as causative agents for the disease. However, the bacterial agents linked to respiratory disease have been detected in several of the most robust bighorn sheep populations, such as the Missouri Breaks of Montana or the Greater Yellowstone Area of Wyoming. Further, the immediate cause of disease events often remains undetermined. We consider two general hypotheses to explain observed disease events in wildlife populations: 1) A disease event is caused by introduction of a novel pathogen from neighboring or sympatric host populations; or 2) A disease event is caused by certain conditions which trigger resident pathogens to increase in virulence or transmissibility. In the case of bighorn sheep respiratory disease, we consider resident pathogens to be pathogens that originated from domestic sheep or goats and likely caused a respiratory disease upon introduction to naive bighorn sheep populations, but continue to persist in a bighorn sheep population for an extended time period with minimal effects on the population. Although the extent to which these different hypotheses explain observed respiratory disease events in bighorn sheep is unknown, the appropriate management actions to address disease events caused by these processes are very different. Rigorous pathogen surveillance in populations with and without evidence of respiratory disease is necessary to evaluate the relative roles novel and resident pathogens play in causing respiratory disease. The pathogen community hosted by bighorn sheep populations prior to respiratory disease epizootics must be understood in order to conclude whether the epizootic was caused by novel or resident pathogens. Limited evidence suggests that diagnostic protocols used to detect respiratory pathogens in bighorn sheep have low detection probability (i.e. sensitivity) and may falsely indicate some pathogens are not present in a sampled population. The detection probability of diagnostic protocols must be known in order to design rigorous respiratory pathogen surveillance programs. We collected multiple nasal swab and tonsil swab samples from 476 live bighorn sheep in Montana and Wyoming and employed several diagnostic protocols to detect *Mycoplasma ovipneumoniae* and relevant *Pasteurellaceae* organisms. This effort will estimate detection probabilities for diagnostic protocols commonly used by wildlife agencies to assess presence of respiratory pathogens in bighorn sheep, provide the ability to estimate confidence in negative test results at the population-level, and provide recommendations for rigorous pathogen surveillance programs. Initial findings confirm previous studies that suggested detection probability for *Pasteurellaceae* organisms is generally low (<40%), but varies among diagnostic protocols. In contrast, initial findings indicate that detection probability for *Mycoplasma ovipneumoniae* is generally high (>60%). The disparity in detection probability among the different pathogens may be explained by the availability of polymerase chain reaction (PCR) tests, which are not available through fee-for-service labs for *Pasteurellaceae* samples from bighorn sheep. These findings and concepts will be applied to a pathogen surveillance effort across Montana and Wyoming that aims to sample approximately 800 bighorn sheep from 17 populations (Figure 1).

Biennial Symposium of the Northern Wild Sheep and Goat Council 20:65-67.

KEY WORDS bighorn sheep, demography, die-offs, disease, health, Montana, *Ovis canadensis*, novel pathogen, pneumonia, recruitment, respiratory pathogens, Wyoming

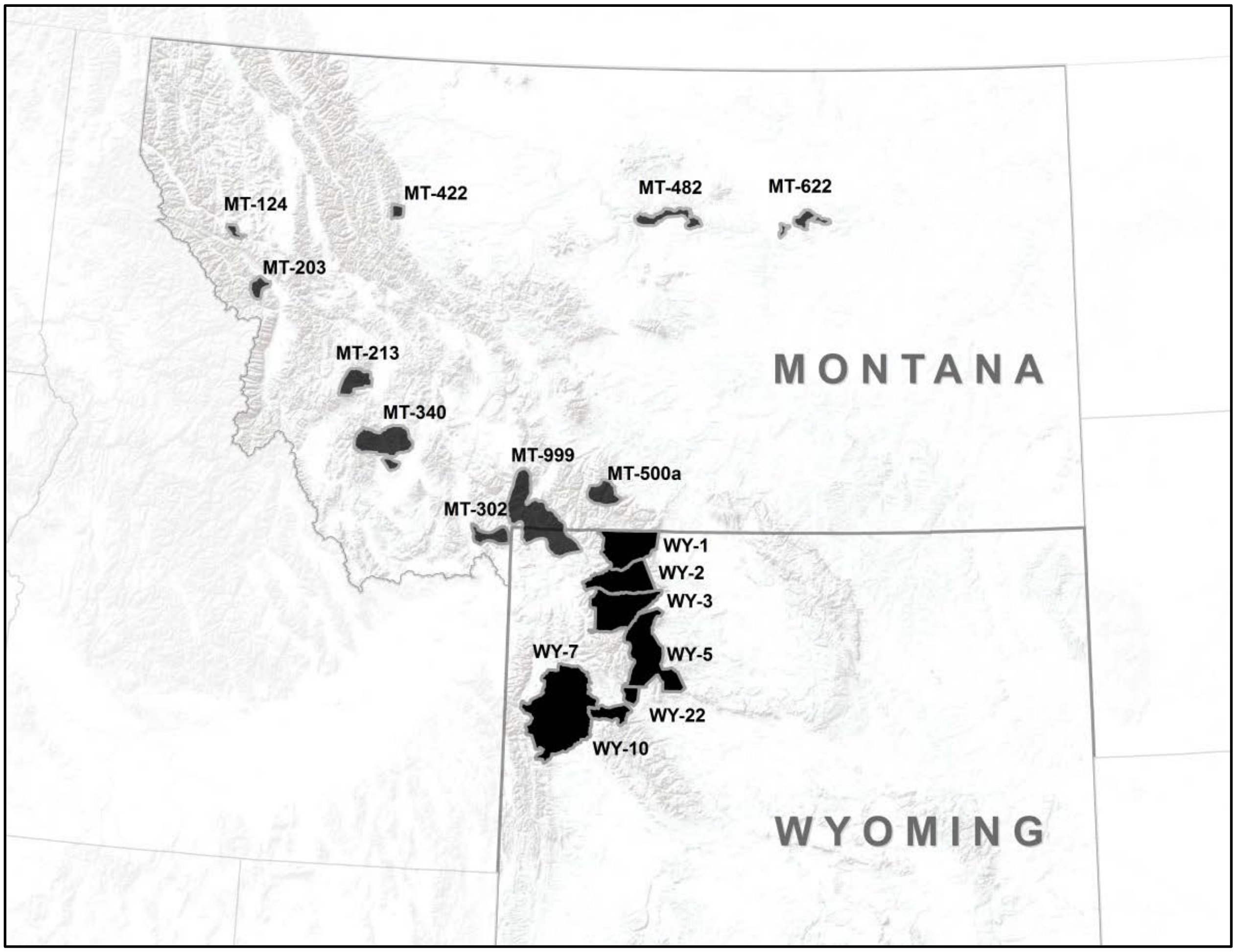

Figure 1. Bighorn sheep study populations in Montana and Wyoming to be collaboratively surveyed for respiratory pathogens. Labels correspond to the respective state’s hunting districts.