Imperfect Tests, Pervasive Pathogens, and Variable Demographic Performance: Thoughts on Managing Bighorn Sheep Respiratory Disease

Carson J. Butler, Ecology Department, Montana State University, Bozeman

W. Hank Edwards, Wyoming Game and Fish Department, Laramie

Jessica Jennings-Gaines, Wyoming Game and Fish Department, Laramie

Halcyon J. Killion, Wyoming Game and Fish Department, Laramie

Mary E. Wood, Wyoming Game and Fish Department, Laramie

J. Terrill Paterson, Ecology Department, Montana State University, Bozeman

Kelly M. Proffitt, Montana Fish Wildlife and Parks, Bozeman

Emily S. Almberg, Montana Fish Wildlife and Parks, Bozeman

P.J. White, Yellowstone National Park, Mammoth, WY

Douglas E. McWhirter, Wyoming Game and Fish Department, Cody

Jay J. Rotella, Ecology Department, Montana State University, Bozeman

Robert A. Garrott*, Ecology Department, Montana State University, Bozeman

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 17 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. Seventy-six percent of study populations hosted both Mycoplasma ovipneumoniae and *Pasteurellaceae* pathogens, yet a number of these populations were estimated to have positive population growth rates and recruitment rates greater than 30%. Overall, the results of this work suggest that bighorn sheep respiratory disease may be mitigated by manipulating population characteristics and respiratory disease epizootics could be caused by pathogens already resident in bighorn sheep population.