Mycoplasma ovipneumoniae Cross-strain Transmissions in Captive Bighorn Sheep

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ABSTRACT Bighorn sheep (*Ovis canadensis*) researchers and managers continually face dynamic challenges associated with population-limiting bronchopneumonia epizootics. Although the etiology of pneumonia is not completely understood, we consider *Mycoplasma ovipneumoniae* to be a primary pathogen responsible for bighorn sheep respiratory disease. Some individuals that have recovered from initial *M. ovipneumoniae* disease outbreaks become carriers of the *M. ovipneumoniae* strain type encountered, and these strains are usually unique in independent outbreaks. Our objectives are to present information resulting from accidental *M. ovipneumoniae* cross-strain transmission and explore factors that might influence the rate of individual bighorn sheep transitioning through the disease process. All experiments were conducted at the South Dakota State University Captive Wildlife Research Facility (SDSU CWRF). Free-ranging bighorn sheep used for this study were identified through collaborative efforts during the routine disease surveillance efforts of state wildlife managers and researchers, and selective removal of individuals from the wild to prevent further spillover infections to adjacent bighorn sheep populations (e.g., young rams that come into close proximity to domestic sheep flocks). We obtained adult bighorn sheep from source herds in Asotin, Washington (n = 9); Black Butte, Washington (n = 8); Lostine, Oregon, (n = 5); Sheep Mountain, Idaho (n = 2); Rapid Creek, South Dakota (n = 1); Badlands, South Dakota (n = 2); and Snowstorm Mountains, Nevada (n = 11). We assigned adults to pens based on source herds and sex, which were separated by ≥ 15m in an effort to prevent aerosol pathogen transmission across pens. We anesthetized and sampled all adults at 4-6 week intervals from January to March, and again from October to December or when no dependent lambs were present, annually during 2014–2015. We collected nasal and oropharyngeal swabs at each sampling event. We extracted DNA and used PCR to detect *M. ovipneumoniae* in nasal swabs or lung tissue. We used multi-locus sequence typing of the 16S-23S intergenic transcribed region (IGS) and 3 genes (16S, ryoB, and gyrB) to characterize strain types. We detected 4 strains of *M. ovipneumoniae* and refer to strain types by IGS length: 393 (Black Butte herd), 398 (Badlands and Rapid Creek herds), 400 (Snowstorm herd), and 404 (Asotin, Lostine, and Sheep Mountain herds). After cross-strain exposure, 84% (n = 32) of sheep actively shed 400 strain bacteria, which we infer contributed to high morbidity (100%; n = 38). We documented high adult pneumonia mortality (> 25%; n = 11) attributed to the 400 strain in upper respiratory tracts and in acute lung lesions at necropsy from July 2015 to February 2016. During this time, we documented a 4-fold increase in apparent *M. ovipneumoniae* prevalence (from 0.19 to 0.83), which we infer was the result of unintentional cross-strain transmissions that occurred in our study. We failed to detect more than 1 strain in any sample, and concluded that the 400 strain likely replaced all prior strains. We characterized the dynamics observed at SDSU CWRF using an epidemiological Susceptible-

Infected-Recovered (SIR) compartmental hazard-based model with spatial effects, initial strain type, and immune response as covariates influencing disease dynamics. We found support for models in which response of individual bighorn sheep to cross-strain transmission was a function of previous strain exposure. In general, bighorn sheep previously exposed to the 393 strain were less affected by cross-strain transmission in our study. In contrast, adults previously exposed to 398 and 404 strains were more susceptible to cross-strain infection and associated mortality. Our results underscore the importance of considering strain-specific *M. ovipneumoniae* exposure history when making bighorn sheep management decisions. Previously exposed bighorn sheep populations that experience spillover infections caused by a novel strain challenge may experience high adult morbidity and mortality similar to epidemics recorded in *M. ovipneumoniae* naïve populations upon first introduction of this pathogen. Spillover infections caused by the introduction of novel strains from adjacent free-ranging populations may impede bighorn sheep recovery in some areas.

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