

Associations Between Allelic Diversity and *Mycoplasma ovipneumoniae* Shedding History in Bighorn Sheep

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ABSTRACT Epizootic bronchopneumonia is a respiratory disease of high morbidity and mortality and is considered one of the most significant limiting factors of bighorn sheep (*Ovis canadensis*) populations. Furthermore, decreasing genetic diversity within bighorn sheep populations also is a concern. Understanding the complex dynamics between disease and genetic diversity in bighorn sheep populations is of growing importance. One primary pathogen under investigation is *Mycoplasma ovipneumoniae*. *M. ovipneumoniae* is a bacterium associated with respiratory disease in sheep and goats worldwide. Polymorphic Major Histocompatibility Complex (MHC) allelic variants have been associated with susceptibility and resistance to infectious diseases in domestic and bighorn sheep (Larruskain et al. 2010, O'Brien and Evermann 1988). Recent studies have found associations between internal parasite loads and genetic diversity (Luikart et al. 2008). However, the association between allelic variation and *M. ovipneumoniae* shedding patterns in bighorn sheep has not been addressed. Our objective was to compare allelic variation from 5 *M. ovipneumoniae*-exposed populations and associate the genetic diversity of individual bighorn sheep within pathogen shedding groups. Shedding status was categorized by repeated monitoring of *M. ovipneumoniae* presence/absence through collection of nasal and oropharyngeal swabs at ≤ 6 week intervals for 8 consecutive months. Individuals testing negative for *M. ovipneumoniae* on PCR in $\geq 75\%$, 74-26%, and $\leq 25\%$ of repeated test samples were categorized as negative, intermittent, and chronic shedder, respectively. We compared loci to determine if heterogeneity was differentially correlated with *M. ovipneumoniae* shedding pattern dynamics. We predicted that individuals with higher heterozygosity and/or unique polymorphisms in MHC alleles would be more resistant to *M. ovipneumoniae* pathogens. We sampled 27 bighorn sheep, and amplified these samples at 3 microsatellite loci in candidate genes (ADCYAP1, TCRG4 and MMP9). We tested associations between microsatellite genotypes and shedding phenotypes using Pearson's χ^2 . We used Kruskal-Wallis one-way analysis of variance to test for significant differences between the 3 shedding statuses and the associated allelic

diversities within those shedding statuses. Preliminary results indicate that allelic diversity among negative ($\bar{x} = 1.00$) and intermittent ($\bar{x} = 1.27$) shedders were similar (average $P = 0.61$); whereas, chronic shedders ($\bar{x} = 2.50$) had higher allelic diversity and differed from negative ($P < 0.01$) and intermittent ($P < 0.01$) shedding genotypes. In future analyses, we will include 15 microsatellites (8 neutral loci, 3 loci in genes and 4 loci in candidate genes) and individual bighorns from 4 additional *M. ovipneumoniae*-exposed populations. By identifying the effect of genetic diversity and specific loci on disease resistance, we hope to provide managers with scientific evidence to sustain successful long-term bighorn sheep translocations and augmentations while decreasing livestock producer-wildlife conflicts.

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