

Evidence for Strain-specific Immunity to Pneumonia in Bighorn Sheep

E. FRANCES CASSIRER, *Idaho Department of Fish and Game, 3316 16th St., Lewiston, ID 83501, USA; frances.cassirer@idfg.idaho.gov*

KEZIA R. MANLOVE, *Center for Infectious Disease Dynamics, Pennsylvania State University, University Park, PA 16802, USA*

RAINA K. PLOWRIGHT, *Department of Microbiology and Immunology, Montana State University, Bozeman, MT 59717, USA*

THOMAS E. BESSER, *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University, Pullman WA 99163, USA*

ABSTRACT We used multi-locus sequence typing to document the introduction of a novel genotype (strain) of *Mycoplasma ovipneumoniae* into a free-ranging bighorn sheep population. Despite preexisting serologic antibodies and asymptomatic carriage of *M. ovipneumoniae* in this population, introduction of the new strain was accompanied by adult morbidity (100%) and pneumonia-induced mortality (33%) within the range observed in epizootics following exposure of naïve bighorn sheep. During the outbreak the new strain replaced the original strain in the population. To understand the broader context surrounding this strain introduction, we conducted a retrospective analysis of *M. ovipneumoniae* strains in 123 lung and upper respiratory tract samples from 14 interconnected populations within the region over nearly 2 decades. We identified 5 distinct genotypes of *M. ovipneumoniae* associated with all-age disease outbreaks between 1986 and 2014: a pattern consistent with spillover events from reservoir hosts. Some strains persisted and spread across populations, whereas others apparently faded out or were replaced. We use phylogenetic analysis to show that the strain associated with this outbreak was likely of domestic goat origin, whereas strains from other recent disease outbreaks in this metapopulation probably originated in domestic sheep. Lack of cross-strain immunity may account for a significant proportion of the disease outbreaks in bighorn sheep that continue to occur regularly despite over a century of exposure to pathogens carried by domestic sheep and goats. Enhanced efforts are indicated to avoid introducing new strains of *M. ovipneumoniae* into wild sheep populations, even if they have previously been exposed.

Biennial Symposium of the Northern Wild Sheep and Goat Council 20:75.

KEYWORDS bighorn sheep, disease ecology, Hells Canyon, livestock-wildlife interface, molecular epidemiology, multi-locus sequence typing, *Mycoplasma ovipneumoniae*, *Ovis canadensis*

The Journal of Wildlife Management 81(1):133–143 (2017)

©2017 The Wildlife Society

Reprinted with permission