

Genetic Linkages Among *Mycoplasma ovipneumoniae* Strains in Wild and Domestic Sheep and Goats

PAULINE L. KAMATH, U.S. Geological Survey, Northern Rocky Mountain Science Center, Bozeman, MT 59715; School of Food and Agriculture, University of Maine, Orono, ME 04469; pauline.kamath@maine.edu

PAUL C. CROSS, U.S. Geological Survey, Northern Rocky Mountain Science Center, Bozeman, MT 59715

E. FRANCES CASSIRER, Idaho Department of Fish and Game, Lewiston, ID 83501

THOMAS E. BESSER, Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164

ABSTRACT Epizootic pneumonia has contributed greatly to historical declines and extirpations of bighorn sheep populations, and is now hampering their re-establishment. We examined the genetic diversity and phylogeographic structure of the bacterium *Mycoplasma ovipneumoniae* in reservoir (domestic sheep and goat) and spillover (bighorn sheep and mountain goat) hosts affected by bronchopneumonia across the western United States. We obtained *M. ovipneumoniae* isolates ($n = 343$) from diverse geographical and host sources and used a multi-locus sequence-based genetic typing (MLST) approach that targeted four polymorphic *M. ovipneumoniae* loci: the 16S-23S intergenic spacer (IGS), the small ribosomal subunit (16S), *gyrB*, and *rpoB*. We integrated pathogen sequence data with host species, location, and sampling year in population genetic and phylogeographic analyses to examine *M. ovipneumoniae* genetic diversity and relatedness among hosts and locations, and to evaluate patterns of pathogen spillover and persistence in bighorn sheep populations. Our preliminary results indicated that genetic diversity of *M. ovipneumoniae* strains was higher in domestic sheep than strains found in bighorn sheep. There was no evidence for geographic clustering of *M. ovipneumoniae* strains from domestic sheep. Instead, these strains were found distributed among strains derived from wildlife throughout the primary *M. ovipneumoniae* phylogenetic clade. Taken together, the genetic diversity and the relationships among strains suggest that there have been repeated *M. ovipneumoniae* spillover events from domestic to bighorn sheep. We also identified genetic linkages within and between neighboring bighorn sheep outbreaks, but because we have limited sampling from domestic sheep (relative to the *M. ovipneumoniae* strain diversity observed in this group), these outbreaks may alternatively be linked through unsampled domestic sheep sources. Domestic goats formed a genetically distinct clade, and there were only three observed instances of *M. ovipneumoniae* spillover from domestic goats into bighorn sheep. These data will enable a broad-scale molecular epidemiologic investigation of *M. ovipneumoniae* transmission dynamics and inform the development of effective management strategies for both controlling the disease and promoting the re-establishment of bighorn sheep.

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