

Molecular Identification Of Pasteurella-Related Outbreaks In Bighorn Sheep Using Pulse Field Gel Electrophoresis

TRICIA HOSCH-HEBDON^{1,2}, ¹ Idaho Department of Health and Welfare, Idaho State Health Laboratory, 2220 Old Penitentiary Road, Boise, ID 83712 U.S.A.
² Idaho Fish and Game, Wildlife Health Laboratory, 16569 S. 10th, Caldwell, ID 83705 U.S.A.

Abstract: Bacterial pneumonia-related outbreaks remain a major mortality factor in free ranging bighorn sheep. Current phenotypic (e.g. serotyping, biotyping) analysis of bighorn sheep bacterial pathogens makes it difficult to determine lateral transmission of disease between vectors, individual sheep and even whole populations. Pulse Field Gel Electrophoresis (PFGE), a molecular based subtyping method, is a sensitive and whole genome technique that can detect clonal relationships and determine lateral disease transmission of pathogenic microorganisms. The concept of a clonal relationship between bacterial isolates from a common-source outbreak is important in the epidemiology of infectious diseases and many bacterial outbreaks result from exposure to a common source pathogen. In general, these infectious microorganisms are clonal; that is, they are the progeny of a single cell and thus are genetically identical or nearly so. PFGE is commonly utilized by Federal and State Health agencies to detect outbreaks and conduct epidemiological investigations. It is currently the accepted method for the determination of foodborne disease transmission and outbreak detection throughout the United States and Canada. PFGE was used to determine the clonal relatedness of *Pasteurella multocida* and *Mannheimia haemolytica* isolates that were obtained from healthy free-ranging bighorn sheep, deceased animals from the 1995-1996 Hells Canyon die-off and sick animals that were taken to Idaho Fish and Game's Wildlife Health Laboratory. Identical PFGE restriction products were obtained for *Pasteurella multocida* isolates from 95-96 Hells Canyon die-off but restriction products from free-ranging bighorn sheep and captive sheep from the Wildlife Health Lab differed from the main die-off by a minimum of two mutational events. This suggests that lateral transmission of bacterial isolates occurred during the die-off, but that recolonization or mutation by *Pasteurella multocida* isolates occurred in the free-ranging and captive colonies following the main die-off. In addition, *Mannheimia haemolytica* isolates obtained from a domestic goat and free-ranging bighorn sheep were also found to be identical and support the theory that domestic livestock can infect free ranging wild sheep populations. The direct application of PFGE subtyping in wildlife disease investigation could potentially lead to early detection, tracking and understanding of the spread of pneumonic outbreaks in free-ranging bighorn sheep populations, as well as identifying the source of infection in such outbreaks and the incidence of sporadic disease within these populations.