

**EVOLUTIONARY GENETICS OF *PASTEURELLA* ISOLATED FROM WILD
AND DOMESTIC SHEEP AND DOMESTIC GOATS.**

SCOTT T. KELLEY, Biology Department., San Diego State University, San Diego, CA
E. FRANCES CASSIRER, Idaho Department of Fish and Game, 1540 Warner Ave.,
Lewiston ID

GLEN C. WEISER, Univ. of Idaho, Caine Veterinary Teaching Center, Caldwell, ID
ALTON C. S. WARD, Univ. of Idaho, Caine Veterinary Teaching Center, Caldwell, ID

Abstract: Phylogenetic analysis of molecular sequences is commonly used to determine the source of infectious diseases, including diseases such as Hanta virus, HIV, and SARS. This approach has also been useful for determining the source of many bacterial infections, for example distinguishing Pasteurella bacteria from domestic sheep and cattle. We used phylogenetic analysis of two structural genes to classify Pasteurella samples collected from healthy Alaska Dall's sheep; from healthy and pneumonic bighorn sheep; from healthy and pneumonic and domestic sheep; and healthy domestic goats. Phylogenetic analysis successfully grouped bacteria isolated from bighorn, and Dall's sheep, and domestic sheep and goats. The significant correlation between host species and phylogeny of Pasteurella isolates suggests that there are host specific lineages of Pasteurella and/or that transfer of bacteria between species is relatively rare and short lived. The existence of host-specific lineages is not surprising but is significant in that it could help determine the host source of bacteria responsible for bighorn sheep pneumonia epizootics. The biogrouping classification scheme used to type Pasteurella bacteria was also generally supported by phylogenetic analysis. The phylogeny of the virulence-associated leukotoxin gene did not correspond to that of the structural genes, suggesting it evolves more rapidly, recombines, and may transfer among strains.