



# Bleats and Blats

Official Newsletter of the Desert Bighorn  
Council



AUGUST 2007

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*Hello DBC members!*

*I hope you're all having a good summer. Although it may feel like a quiet mid-summer time for some of you, there are some important dates and meetings just around the corner. Please read on for more information!*

*The next newsletter is scheduled for early November so if you have updates or announcements to share, please send them to me by October 20th. I hope to hear from you!*

*For more information about the Desert Bighorn Council, or to download a membership form, please visit our website at [www.desertbighornCouncil.org](http://www.desertbighornCouncil.org)*

*All the best to you,*

*Esther Rubin*

*DBC Secretary ([esrubin@consbio.org](mailto:esrubin@consbio.org))*

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## **DBC TRANSACTIONS**

We invite and encourage you to publish your work in the DBC Transactions, and are still waiting on submissions for the 2007 Transactions. Brian Wakeling, DBC Editor, has extended the deadline for submission to September 1, 2007. If you would like to submit a paper or if you are working on a 2007 state report, this is the time to get materials prepared and sent to Brian. So far, Brian only has reports from two states (Arizona and Texas) so we hope the rest of the states complete their reports soon!

Please remember that any manuscript addressing the ecology, biology, management, and conservation of desert bighorn sheep, even if not presented at a Desert Bighorn Council meeting, may be submitted for publication in the Transactions. For more information, please email Brian Wakeling at [BWakeling@azgfd.gov](mailto:BWakeling@azgfd.gov)

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## **NEW DBC HISTORIAN**

As many of you know, Rick Brigham has stepped down from his position of DBC Historian. Thanks, Rick, for all of your work! The role of historian has been accepted by Don Armentrout. If any of you have historical information or photos to share, or are looking for information on the long and productive history of the DBC (now 50 years!!!), please contact Don at [armentrouts@citlink.net](mailto:armentrouts@citlink.net) or at 530-251-0560. Thanks, Don, for accepting this role!

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## **BIGHORN SHEEP MANAGEMENT: RESPIRATORY DISEASES**

A great deal of effort and expertise has gone into two recent workshops and a working group project to deal with the important issue of respiratory disease in bighorn sheep and related management implications.

One workshop addressed the risk of disease transmission between domestic sheep and bighorn sheep on the Payette National Forest. The complete report “Risk Analysis of Disease Transmission Between Domestic Sheep and Bighorn Sheep on the Payette National Forest” and a summary of a science panel discussion can be obtained at:

[http://www.fs.fed.us/r4/payette/publications/big\\_horn/bighorn%20sheep%20index\\_2007.shtml](http://www.fs.fed.us/r4/payette/publications/big_horn/bighorn%20sheep%20index_2007.shtml)

In April, a second workshop, entitled “Respiratory Disease in Mountain Sheep: Knowledge Gaps and Future Research”, was held in Davis, California. A summary of the workshop can temporarily be found on the website of the American Association of Wildlife Veterinarians, at <http://www.aawv.net/> (see link on their front page).

In January 2007, the Western Association of Fish and Wildlife Agencies’ (WAFWA) Directors unanimously decided to create a west-wide, multi-faceted, comprehensive Wild Sheep Working Group. The first task undertaken was to form Wild Sheep Working Group #1, tasked with the job of developing a framework of recommendations on the management of domestic sheep and goats in wild sheep habitat. Kevin Hurley, Wyoming Game and Fish Department was named chair of the working group, and the group consisted of wild sheep managers, wildlife veterinarians, and federal agency (e.g., BLM, USFS) personnel. A 27-page report was completed on June 21, 2007, and the WAFWA Directors unanimously

endorsed this report on July 12<sup>th</sup> at their Flagstaff, AZ Business Meeting, agreeing that this report now formed the official WAFWA position on this topic. The report will be sent to the BLM, USFS, and other federal land management agencies, to serve as the basis for revision of their policies related to this topic. The report, entitled "Management of Domestic Sheep and Domestic Goats in Wild Sheep Habitat", will soon be posted to an internet link. You may also contact Kevin Hurley (Kevin.Hurley@wgf.state.wy.us) for a digital copy.

At least 2 additional workshops are coming up (see below), which we hope you can attend.

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## **UPCOMING MEETINGS AND WORKSHOPS**

### **1. Wild Sheep/Domestic Sheep Disease Risk Assessment Workshop**

Information submitted by Dave Jessup, California Department of Fish and Game

**Date:** September 27, 2007 immediately following The Wildlife Society annual meeting. **All attendees must register before September 1, 2007.**

**Location:** Hotel Arizona, in Tucson (one of the designated TWS host hotels), meeting rooms to be determined. Conference/government per diem rates of \$83/night to be honored by the hotel for all attendees to this workshop. Attendees are responsible for making or extending their own hotel reservations and paying for them. Attendees are also responsible for their own travel arrangements.

**Sponsored by:** National Fish and Wildlife Foundation, University of California-Davis Wildlife Health Center, Foundation for North American Wild Sheep, and California Department of Fish and Game. No cost to attendees.

**Audience:** Up to 90 biologists, wildlife and range managers, public land users as well as academics and students are welcome. All attendees must register by contacting Alexis Nakamura at [asnakamura@ucdavis.edu](mailto:asnakamura@ucdavis.edu) or 530-752-4167 before September 1, 2007.

**Topics to be covered:** The most current information on disease believed to be shared by bighorn and domestic sheep, summary of and links to most recent veterinary workshop on bighorn respiratory diseases and historic and foundational documents, examples of qualitative and quantitative disease risk assessment, problems posed to grazers in accommodating separation from bighorn, frameworks for seeking cooperative solutions, best management practices. These topics will be covered in powerpoint discussion and lecture format by 9 biologists, veterinarians, conservationists and grazers.

**History:** A number of catastrophic die offs of bighorn sheep over the last several decades have been associated with contact with domestic sheep and goats. Most frequently the disease process has been pneumonia and in some cases whole herds have been lost. Efforts to enforce separation of bighorn from domestic sheep and goats as a means of disease control on public land have financial and operational implications for grazers and the need for this separation has been questioned. Federal forest and range management actions have been effected and in several cases litigation has occurred. Meetings sponsored by governmental and non-governmental sources have allowed the accumulation of a great deal of pertinent information but it has not been widely disseminated. Risk assessment, particularly quantitative risk assessment, has great promise as a tool for objectifying risk and potentially for guiding management

actions.

**Goal:** To provide biologist, wildlife and wildland managers with the most current available information on the subject, in particular methods for doing quantitative disease risk assessment, background and foundational information, as well as varied perspectives on the subject.

## **2. Wild Sheep/Domestic Sheep Disease Risk Assessment Workshop**

Information submitted by Kevin Hurley, Wyoming Game and Fish Department, and Dave Jessup, California Department of Fish and Game.

A third in this series of workshops sponsored by governmental and non-governmental agencies will be held in Salt Lake City on February 4-6, 2008, immediately prior to the annual convention of the Foundation for North American Wild Sheep. Further details on this workshop will be available in future newsletters, and more information will soon be provided by Dave Jessup, California Department of Fish and Game, or Kevin Hurley, Wyoming Game and Fish Department.

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## **RECENT LITERATURE RELATED TO BIGHORN SHEEP**

**Brewer, C. E. and L. A. Harveson. 2007. Diets of bighorn sheep in the Chihuahuan Desert, Texas Southwestern Naturalist 52:97-103.**

Abstract: Desert bighorn sheep (*Ovis canadensis*) have been extirpated from much of their historical range in the Chihuahuan Desert. Understanding their dietary preferences in the Chihuahuan Desert is integral to their successful restoration. We evaluated differences (sexual, temporal, and spatial) in the diets of desert bighorn sheep from Elephant Mountain Wildlife Management Area in the Chihuahuan Desert of western Texas by using microhistological analysis of 432 fecal pellet groups (209 rams, 209 ewes, 14 lambs) collected every 2 weeks between September 1998 and August 2000. Ninety-four plant species were identified; bighorn sheep diets consisted of 50% browse, 35% forbs, 11% grasses, and 4% succulents. Diets of rams and ewes did not differ annually. Diets differed seasonally ( $P < 0.05$ ); forbs prevailed in diets of rams during winter. Diets of bighorn sheep from Elephant Mountain were compared to previously determined diets from the Beach, Baylor, and Sierra Diablo mountains. There were significant differences among female diets between Elephant Mountain and Beach Mountain during winter and the Sierra Diablo Mountains in fall, winter, and summer. Dietary overlap was greatest among desert bighorn sheep at Elephant Mountain and the Sierra Diablo Mountain populations (57.6%), followed by Baylor Mountain (55.7%) and Beach Mountain (52.0%). Dietary overlap among all ranges was highest in the browse component (53%), followed by forbs (23%), grasses (16%), and succulents (8%).

**De la Fuente, J., M. W. Atkinson, V. Naranjo, I. G. Fernandez de Mera, A. J. Mangold, K. A. Keating, and K. M. Kocan. 2007. Sequence analysis of the msp4 gene of *Anaplasma ovis* strains. Veterinary Microbiology. 119:375-381.**

Abstract: *Anaplasma ovis* (Rickettsiales: Anaplasmataceae) is a tick-borne pathogen of sheep, goats and wild ruminants. The genetic diversity of *A. ovis* strains has not been well characterized due to the lack of sequence information. In this study, we evaluated bighorn sheep (*Ovis canadensis*) and mule deer (*Odocoileus hemionus*) from Montana for infection with *A. ovis* by serology and sequence analysis of the

msp4 gene. Antibodies to *Anaplasma* spp. were detected in 37% and 39% of bighorn sheep and mule deer analyzed, respectively. Four new msp4 genotypes were identified. The *A. ovis* msp4 sequences identified herein were analyzed together with sequences reported previously for the characterization of the genetic diversity of *A. ovis* strains in comparison with other *Anaplasma* spp. The results of these studies demonstrated that although *A. ovis* msp4 genotypes may vary among geographic regions and between sheep and deer hosts, the variation observed was less than the variation observed between *A. marginale* and *A. phagocytophilum* strains. The results reported herein further confirm that *A. ovis* infection occurs in natural wild ruminant populations in Western United States and that bighorn sheep and mule deer may serve as wildlife reservoirs of *A. ovis*.

**Kelley, S. T., E. F. Cassirer, G. C. Weiser, and S. Safaee. 2007. Phylogenetic diversity of Pasteurellaceae and horizontal gene transfer of leukotoxin in wild and domestic sheep. Infection Genetics and Evolution 7:13-23.**

Abstract: Wild and domestic animal populations are known to be sources and reservoirs of emerging diseases. There is also a growing recognition that horizontal genetic transfer (HGT) plays an important role in bacterial pathogenesis. We used molecular phylogenetic methods to assess diversity and cross-transmission rates of Pasteurellaceae bacteria in populations of bighorn sheep, Dall's sheep, domestic sheep and domestic goats. Members of the Pasteurellaceae cause an array of deadly illnesses including bacterial pneumonia known as "pasteurellosis", a particularly devastating disease for bighorn sheep. A phylogenetic analysis of a combined dataset of two RNA genes (16S ribosomal RNA and RNase P RNA) revealed remarkable evolutionary diversity among *Pasteurella trehalosi* and *Mannheimia (Pasteurella) haemolytica* bacteria isolated from sheep and goats. Several phylotypes appeared to associate with particular host species, though we found numerous instances of apparent cross-transmission among species and populations. Statistical analyses revealed that host species, geographic locale and biovariant classification, but not virulence, correlated strongly with Pasteurellaceae phylogeny. Sheep host species correlated with *P. trehalosi* isolates phylogeny (PTP test;  $P = 0.002$ ), but not with the phylogeny of *M. haemolytica* isolates, suggesting that *P. trehalosi* bacteria may be more host specific. With regards to populations within species, we also discovered a strong correlation between geographic locale and isolate phylogeny in the Rocky Mountain bighorn sheep (PTP test;  $P = 0.001$ ). We also investigated the potential for HGT of the leukotoxin A (lktA) gene, which produces a toxin that plays an integral role in causing disease. Comparative analysis of the combined RNA gene phylogeny and the lktA phylogenies revealed considerable incongruence between the phylogenies, suggestive of HGT. Furthermore, we found identical lktA alleles in unrelated bacterial species, some of which had been isolated from sheep in distantly removed populations. For example, lktA sequences from *P. trehalosi* isolated from remote Alaskan Dall's sheep were 100% identical over a 900-nucleotide stretch to sequences determined from *M. haemolytica* isolated from domestic sheep in the UK. This extremely high degree of sequence similarity of lktA sequences among distinct bacterial species suggests that HGT has played a role in the evolution of lktA in wild hosts.

**Liu, W., K. A. Brayton, W. C. Davis, K. Mansfield, J. Lagerquist, W. Foreyt, and S. Srikumaran. 2007. Mannheimia (Pasteurella) haemolytica leukotoxin utilizes CD18 as its receptor on bighorn sheep leukocytes. Journal of Wildlife Disease 43:75-81.**

Abstract: Pneumonia caused by *Mannheimia (Pasteurella) haemolytica* is a highly fatal disease of bighorn sheep (*Ovis canadensis*). Leukotoxin (Lkt), secreted by *M. haemolytica*, is an important virulence factor of this organism, and is cytolytic to bighorn sheep leukocytes. Previously, we have shown that CD18, the beta subunit of beta 2 integrins, serves as the receptor for Lkt on bovine leukocytes. Furthermore, anti-CD18 antibodies inhibit Lkt-induced cytotoxicity of bighorn sheep leukocytes.

Therefore, we hypothesized that Lkt utilizes CD18 as its receptor on bighorn sheep leukocytes. Confirmation of bighorn sheep CD18 as a receptor for Lkt requires the demonstration that the recombinant expression of bighorn sheep CD18 in Lkt-nonsusceptible cells renders them susceptible to Lkt. Therefore, we transfected cDNA encoding CD18 of bighorn sheep into a Lkt-nonsusceptible murine cell line. Cell surface expression of bighorn sheep CD18 on the transfectants was tested by flow cytometry with anti-CD18 antibodies. Transfectants stably expressing bighorn sheep CD18 on their surface were subjected to flow cytometric analysis for detection of Lkt binding, and cytotoxicity assays for detection of Lkt-induced cytotoxicity. Leukotoxin bound to the transfectants. More importantly, the transfectants were effectively lysed by Lkt in a concentration-dependent manner, whereas the parent cells were not. These results clearly indicate that *M. haemolytica* Lkt utilizes CD18 as a receptor on bighorn sheep leukocytes. Identification of CD18 as a receptor for Lkt on bighorn sheep leukocytes should enhance our understanding of the pathogenesis of pneumonia, which in turn should help in the development of control measures against this fatal disease of bighorn sheep.

**Meadows, J. R. S., O. Hanotte, C. Drogemuller, J. Calvo, R. Godfrey, D. Coltman, J. F. Maddox, N. Marzanov, J. Kantanen, and J. W. Kijas. 2006. Globally dispersed Y chromosomal haplotypes in wild and domestic sheep. *Animal Genetics* 37:444-453.**

Abstract: To date, investigations of genetic diversity and the origins of domestication in sheep have utilised autosomal microsatellites and variation in the mitochondrial genome. We present the first analysis of both domestic and wild sheep using genetic markers residing on the ovine Y chromosome. Analysis of a single nucleotide polymorphism (oY1) in the SRY promoter region revealed that allele A-oY1 was present in all wild bighorn sheep (*Ovis canadensis*), two subspecies of thinhorn sheep (*Ovis dalli*), European Mouflon (*Ovis musimon*) and the Barbary (*Ammonragis lervia*). A-oY1 also had the highest frequency (71.4%) within 458 domestic sheep drawn from 65 breeds sampled from Africa, Asia, Australia, the Caribbean, Europe, the Middle East and Central Asia. Sequence analysis of a second locus, microsatellite SRYM18, revealed a compound repeat array displaying fixed differences, which identified bighorn and thinhorn sheep as distinct from the European Mouflon and domestic animals. Combined genotypic data identified 11 male-specific haplotypes that represented at least two separate lineages. Investigation of the geographical distribution of each haplotype revealed that one (H6) was both very common and widespread in the global sample of domestic breeds. The remaining haplotypes each displayed more restricted and informative distributions. For example, H5 was likely founded following the domestication of European breeds and was used to trace the recent transportation of animals to both the Caribbean and Australia. A high rate of Y chromosomal dispersal appears to have taken place during the development of domestic sheep as only 12.9% of the total observed variation was partitioned between major geographical regions.

**Milner, J. M., E. B. Nilsen, and H. P. Andreassen. 2007. Demographic side effects of selective hunting in ungulates and carnivores. *Conservation Biology* 21:36-47.**

Abstract: Selective harvesting regimes are often implemented because age and sex classes contribute differently to population dynamics and hunters show preferences associated with body size and trophy value. We reviewed the literature on how such cropping regimes affect the demography of the remaining population (here termed demographic side effects). First, we examined the implications of removing a large proportion of a specific age or sex class. Such harvesting strategies often bias the population sex ratio toward females and reduce the mean age of males, which may consequently delay birth dates, reduce birth synchrony, delay body mass development, and alter offspring sex ratios. Second, we reviewed the side effects associated with the selective removal of relatively few specific individuals, often large trophy males. Such selective harvesting can destabilize social structures and the dominance hierarchy and may

cause loss of social knowledge, sexually selected infanticide, habitat changes among reproductive females, and changes in offspring sex ratio. A common feature of many of the reported mechanisms is that they ultimately depress recruitment and in some extreme cases even cause total reproductive collapse. These effects could act additively and destabilize the dynamics of populations, thus having a stronger effect on population growth rate than first anticipated. Although more experimental than observational studies reported demographic side effects, we argue that this may reflect the quite subtle mechanisms involved, which are unlikely to be detected in observational studies without rigorous monitoring regimes. We call for more detailed studies of hunted populations with marked individuals that address how the expression of these effects varies across mating systems, habitats, and with population density. Theoretical models investigating how strongly these effects influence population growth rates are also required.

**Sappington, J. M., K. M. Longshore, and D. B. Thompson. 2007. Quantifying landscape ruggedness for animal habitat analysis: a case study using bighorn sheep in the Mojave Desert. *Journal of Wildlife Management* 71:1419-1426.**

Abstract: Terrain ruggedness is often an important variable in wildlife habitat models. Most methods used to quantify ruggedness are indices derived from measures of slope and, as a result, are strongly correlated with slope. Using a Geographic Information System, we developed a vector ruggedness measure (VRM) of terrain based on a geomorphological method for measuring vector dispersion that is less correlated with slope. We examined the relationship of VRM to slope and to 2 commonly used indices of ruggedness in 3 physiographically different mountain ranges within the Mojave Desert of the southwestern United States. We used VRM, slope, distance to water, and springtime bighorn sheep (*Ovis canadensis nelsoni*) adult female locations to model sheep habitat in the 3 ranges. Using logistic regression, we determined that the importance of ruggedness in habitat selection remained consistent across mountain ranges, whereas the relative importance of slope varied according to the characteristic physiography of each range. Our results indicate that the VRM quantifies local variation in terrain more independently of slope than other methods tested, and that VRM and slope distinguish 2 different components of bighorn sheep habitat.

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