DEsert Bighorn Council Officers

2015 Program Committee
BEN GONZALES, CHAIR
California Department of Fish and Wildlife
STEVE TORRES, VICE CHAIR
California Department of Fish and Wildlife
REGINA ABELLA, CO-CHAIR
California Department of Fish and Wildlife
LORA KONDE, ARRANGEMENTS
California Department of Fish and Wildlife
MARK JORGENSEN, ARRANGEMENTS
Anza-Borrego Desert State Park (Retired)

Technical Staff
CLAY BREWER, CHAIR
Texas Department of Park and Wildlife
RAY LEE
Ray Lee, LLC
MARA WEISENBERGER
U. S. Fish and Wildlife Service
ELISE GOLDSTEIN
New Mexico Department of Game and Fish
MARK JORGENSEN
Anza-Borrego Desert State Park (Retired)
PAT CUMMINGS
Nevada Department of Wildlife
BRIAN WAKELING
Nevada Department of Wildlife

Secretary
AMBER MUNIG
Arizona Game and Fish Department

Treasurer
KATHY LONGSHORE
U. S. Geological Survey

Transactions Editor
JAMES W. CAIN III
New Mexico Cooperative Fish and Wildlife Research Unit

2015 Desert Bighorn Council Meeting Host
CALIFORNIA DEPARTMENT OF FISH AND WILDLIFE
# SCHEDULE OF EVENTS

## Tuesday, April 14, 2015

<table>
<thead>
<tr>
<th>Location</th>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lobby</td>
<td>6:00 p.m.</td>
<td>Registration</td>
</tr>
<tr>
<td>Citrus Room</td>
<td>4:00 – 7:00 p.m.</td>
<td>Technical Staff Meeting (Invitational Meeting)</td>
</tr>
<tr>
<td>Ballroom</td>
<td>7:00 – 9:00 p.m.</td>
<td>Poster Session and Evening Social</td>
</tr>
</tbody>
</table>

## Wednesday, April 15, 2015

<table>
<thead>
<tr>
<th>Location</th>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ballroom</td>
<td>7:00 a.m.</td>
<td>Registration, Merchandise, Silent Auction</td>
</tr>
</tbody>
</table>
|          | 8:30 – 8:45 a.m. | Welcome and Opening Remarks  
  Ben Gonzales, Chair                           |
|          | 8:45 – 9:15 a.m. | Keynote Speaker  
  Dave Jessup, Executive Manager, Wildlife Disease Association        |
|          | 9:15 – 9:55 a.m. | The Role of Mycoplasma ovin pneumonae in Epizootic Pneumonia of Bighorn Sheep  
  Tom Besser                                                                 |
|          | 9:55 –10:30 a.m. | Pneumonia in Bighorn Sheep  
  Subramaniam Srikumaran                                                               |
|          | 10:30 – 11:00 a.m. | Break                                                                 |
11:00 – 12:00 p.m.  Disease Session 1  
Ben Gonzales, Moderator

11:00 – 11:20 a.m.  Defining Herd Health: A Key Factor of Bighorn Sheep Management  
Peregrine Wolff

11:20 a.m. – 11:40 a.m. Desert Bighorn Sheep Immunity During a Mycoplasma ovipneumoniae Outbreak  
Brian Dugovich

11:40 a.m. – 12:00 p.m. Pneumonia in Bighorn Sheep: Testing the Super-Spreader Hypothesis  
Frances Cassirer

12:00 – 1:30 p.m. Lunch (on your own)

1:30 – 2:30 p.m. Disease Session 2  
Steve Torres, Moderator

1:30 – 1:50 p.m. Respiratory Disease and Mycoplasma ovipneumoniae in Desert Bighorn Sheep of California, Nevada and Utah  
Annette Roug

1:50 – 2:10 p.m. Adaptive Management of Bighorn Herds at Risk to Disease Transmission  
Mike Cox

2:10 – 2:50 p.m. Panel Discussion  
Tom Besser, Srikumaran Subramaniam, Ben Gonzales, Peregrine Wolff, Clint Epps

2:50 – 3:20 p.m. Break

3:20 – 5:00 p.m. Genetics Session  
Alex Few, Moderator

Walter Boyce

3:40 – 4:00 p.m. Range-Wide Population Genetic Structure and Phylogenetics of Desert Bighorn Sheep: Implications for Conservation  
Michael R. Buchalski

4:00 – 4:20 p.m. Preliminary Estimation of Changes in Genetic Structure of a Desert Bighorn Sheep Metapopulation Over Two Generations  
Clinton W. Epps
4:20 – 4:40 p.m.  | Changes in genetic variation over time and merging desert bighorn populations
Phil Hedrick

4:40 – 5:00 p.m.  | Genetics and the Management of Sierra Nevada Bighorn Sheep
John Wehausen

UC Irvine Steele/Burnand Anza-Borrego Research Facility
6:00 p.m.  | BBQ Dinner

**Thursday, April 16, 2015**

*Ballroom*

| 8:00 a.m. – 10:00 a.m. | State Status Report Session  
Regina Abella, Moderator |
|------------------------|---------------------------------------------------------------------|
| 8:00 – 8:15 a.m.       | Arizona Game and Fish (Statewide)  
Amber Munig |
| 8:15 – 8:30 a.m.       | Santa Catalina Mountains, Arizona Game and Fish  
Ben Brochu |
| 8:30 – 8:45 a.m.       | Grand Canyon, National Park Service  
Brandon Holton |
| 8:45 – 9:00 a.m.       | California Department of Fish and Wildlife  
Regina Abella |
| 9:00 – 9:15 a.m.       | Colorado Division of Wildlife  
Brad Banulis |
| 9:15 – 9:30 a.m.       | Nevada Division of Wildlife  
Brian Wakeling |
| 9:30 – 9:45 a.m.       | New Mexico Game and Fish  
Caitlin Ruhl |
| 9:45 – 10:00 a.m.      | Texas Parks and Wildlife  
Froylan Hernandez |
| 10:00 – 10:15 a.m.     | Utah Division of Wildlife  
Annette Roug |
| 10:15 – 10:35 a.m.     | Break |
10:35 a.m. – 12:15 p.m. Applied Management Session
   Jeffrey T. Villepique, Moderator

10:35 – 10:55 a.m. Demographic Responses of Bighorn Sheep to Recreational Activities:
   A Trial of a Trail
   Vernon C. Bleich

10:55 – 11:15 a.m. A Desert Bighorn Population’s Struggle and Recovery at an Urban Interface
   James R. Deforge

11:15 – 11:35 a.m. International Cooperation Vital to Bighorn Restoration
   Thomas S. Janke

11:35 – 11:55 a.m. Linking Nutritional Condition to Population Performance in Bighorn Sheep
   Thomas R. Stephenson

11:55 – 12:15 p.m. Survival Assessment of Desert Bighorn Translocations in Texas
   Carlos Gonzalez

12:15 – 1:30 p.m. Lunch (on your own)

1:30 – 2:50 p.m. Habitat Session
   Christine Thompson, Moderator

1:30 – 1:50 p.m. Resource Selection Functions in Conservation Planning for Endangered Sierra Nevada Bighorn Sheep
   Alex Few

1:50 – 2:10 p.m. GPS Collars – How Much Data is Enough?
   David German

2:10 – 2:30 p.m. Desert Bighorn Lambing Habitat Revisited: Environmental Characteristics at Female Parturition Sites
   James Cain

2:30 – 2:50 p.m. Desert Bighorn Escape Terrain: Novel Approach to Determining the Importance of Slope and Ruggedness within and Across Mountain Ranges
   Chris Lowrey

2:50 – 3:20 p.m. Break

3:20 – 5:00 p.m. Predator Session
   Vernon C. Bleich, Moderator

3:20 – 3:40 p.m. Spatially Explicit Population Structure Analyses Reveal Barriers to Gene Flow Among Mountain Lions in Southwestern United States
   John Clemens

3:40 – 4:00 p.m. Desert Lion Movement Rates and Ungulate Kill Rates Related to Ambient Temperature
   David M. Conrad

4:00 – 4:20 p.m. Disentangling Population Drivers to Understand Causes of the Bighorn Sheep Decline in the Desert National Wildlife Refuge
   Kathleen Longshore
4:20 – 4:40 p.m. The Paradox of North American Ungulate Density in Predator-Free Enclosures and on Predator-Free Islands
Eric M. Rominger

4:40 – 5:00 p.m. Responses by Bighorn Sheep to Risk of Predation: Are Movements Proportional to Risk and Reward?
Jeffrey T. Villepique

5:00 – 6:00 p.m. Business Meeting
The Arches

6:30 p.m. Awards Banquet

Friday, April 17, 2015

Lobby
8:00 a.m. Depart for Field Tour to Palm Canyon
3 mile hike with the likelihood of seeing bighorn

8:00 a.m. Depart for Field Tour to Archeological Site
Native American bighorn hunting blind
ABSTRACTS

THE ROLE OF MYCOPLASMA OVIPNEUMONIAE IN EPIZOOTIC PNEUMONIA OF BIGHORN SHEEP

TOM BESSER, Dept. of Veterinary Microbiology & Pathology, Washington State University, PO Box 647040, Pullman WA 99164-7040.

The increasing body of evidence that supports a key role for Mycoplasma ovipneumoniae (Movi) in the epidemiology and pathophysiology of pneumonia of bighorn sheep will be summarized. A causal role for Movi is supported by a strong statistical association between its detection in a population and the occurrence of the disease (with an odds ratio >40), by observational and experimental evidence satisfying Koch's postulates and by stronger support than competing hypothesized agents under Bradford Hill’s criteria. Ongoing studies are investigating the role chronic carrier ewes, animals that survived pneumonia and recovered but continue to shed Movi in nasal secretions. Chronic carriers appear to play a key epidemiologic role in the transmission of Movi to susceptible lambs and the persistence of the agent in the population. Other ongoing studies to be described include 1) comparison of domestic sheep and goats Movi strains as agents of bighorn sheep pneumonia; 2) the impact of introduction of a second Movi strain to a previously Movi-exposed population; and 3) a method to document the specific source of Movi that trigger bighorn sheep pneumonia outbreaks. Finally, differences between desert bighorn sheep and other sub-species that may affect the transmission and persistence of Movi will be discussed.

PNEUMONIA IN BIGHORN SHEEP

SUBRAMANIAM (SRI) SRIKUMARAN, Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University, Pullman, WA 99164-7040 ssrikumaran@vetmed.wsu.edu.

Pneumonia is the primary disease that has been responsible for the drastic decline of bighorn sheep (BHS) populations in North America. Several die-offs of BHS have been attributed to pneumonia following contact with domestic sheep (DS). Experimental commingling of BHS and DS also results in death of BHS. Mannheimia haemolytica and Mycoplasma ovipneumoniae are important pathogens of BHS pneumonia. Studies in our laboratory with green fluorescent protein-tagged M. haemolytica irrefutably proved transmission of this bacterium from DS to BHS. DS can also transmit M. ovipneumoniae which predisposes BHS to infection by M. haemolytica and other pathogens. M. haemolytica produces a toxin known as leukotoxin that kills the white blood cells, causes lung damage, and death of BHS. Our earlier studies in BHS with M. haemolytica wild-type and leukotoxin-deletion mutant have revealed that leukotoxin-deletion mutant causes only mild lesions, but does not cause death of BHS. Studies conducted by our laboratory involving transmission of passive immunity from ewes to lambs, bacterial clearance from the lungs, and experimental immunization, have clearly indicated that if BHS develop antibodies against leukotoxin and surface antigens of M. haemolytica, they will be protected against pneumonia caused by this organism. Needle immunization of wildlife is not easy. Administering booster doses is even more difficult. Therefore, it is logical to develop a vaccine that does not require needle-inoculation and booster doses. This vaccine can be easily administered to BHS prior to transplanting them to a new habitat. Progress with the development of such a vaccine will be discussed.
Bacterial pneumonia is recognized as one of the primary challenges facing conservation of bighorn sheep in many areas of the western United States, thus a comprehensive wildlife health plan should be a core component of bighorn sheep management programs. The plan should be based on the management goals identified for each herd or metapopulation and should include establishing baseline herd health status and specific protocols for disease surveillance and investigation. In 2013, a bighorn sheep disease sampling workshop comprised of wildlife health professionals from nine western states and two Canadian provinces was conducted to review and update the testing protocols established in the 2009 WAFWA WHC Sheep Sampling Guidelines for respiratory pathogens of bighorn sheep as well as to standardize sample collection and testing protocols.

Products from the workshop include:

- Testing recommendations based on the herd management plan: baseline herd health, source stock or recipient herd, and disease investigation and follow up surveillance and the laboratories that conduct each test.
- Standardized definitions for key terms involving herd health status
- Standardized protocols for sampling for: Pastuerellaceae spp. and Mycoplasma ovipneumoniae
- Standardized necropsy protocol

The standardization of testing protocols across agencies allows for consistent data collection and interpretation of results and will support recommendations across agencies for different management practices providing a valuable resource and reference for all wildlife health and management professionals.
Infectious diseases have been suggested to be key drivers in the extinction vortex of small, isolated wildlife populations due to the loss of immunogenetic variability. In 2013 an epizootic of *Mycoplasma ovipneumoniae* caused high mortality in desert bighorn sheep (DBH) at Old Dad Peak in the Mojave National Preserve and spread to neighboring populations. Genetic diversity is known to vary widely among populations in this system, including genetic diversity of microsatellite loci linked to immune-system genes, but the consequences of that variation in diversity during an epizootic are unclear. We used blood samples (n=72) from DBH subsequently captured in 9 populations in this region to measure individual DBH immunity using a variety of immunoenzyme assays (hematology, bacterial killing, lymphocyte proliferation, and mRNA isolation). We evaluated whether those measures of individual immune function were correlated with individual characteristics (e.g. disease status) or population-level characteristics such as population connectivity and genetic diversity at neutral or adaptive-linked markers. At the population level, decreased genetic diversity of microsatellites linked to immune genes was correlated with increased disease prevalence, although interpretation is complicated by the spatial progression of the disease. Also, individual immune measures appeared to vary. Finally, using next generation sequencing technologies, we have identified a subset of DQB MHC class II genes expressed in DBH.
Following introduction of pneumonia, disease can persist in bighorn sheep (*Ovis canadensis*) populations for decades as annual or sporadic pneumonia epidemics in lambs. Recurring years of depressed recruitment due to high rates of pneumonia-induced mortality in juveniles is a major obstacle to population recovery. Management strategies for resolving this problem have so far been elusive. We are investigating the feasibility of removing individual “super-spreaders” to improve lamb survival. Individual variation in infection and transmission is well documented in human diseases (e.g. “Typhoid Mary”). We are testing the hypothesis that pneumonia epidemics in lambs are initiated by transmission of pathogens from a few “chronic-shedder” ewes. We have completed the first year of a 5-year project in the Hells Canyon region of Idaho, Oregon, and Washington, and in a captive population at South Dakota State University. Through repeated testing of free-ranging individuals in Hells Canyon, we have identified individual differences in shedding of *Mycoplasma ovipneumoniae*, a primary pathogen in the bighorn sheep respiratory disease complex. We also found that when penned separately in captivity, lambs of ewes that consistently tested positive (chronic shedders) were infected and died of pneumonia, whereas lambs born to ewes from an infected population that tested negative (non-shedders), were not infected and survived. Over the next 4 years we plan to 1) continue and expand testing of free-ranging and captive animals, 2) determine whether removal of chronic-shedder ewes improves lamb survival in free-ranging populations, 3) expand and replicate chronic-shedder commingling experiments in captivity, and 4) establish and monitor a new population founded with non-shedders from an infected population.

RESPIRATORY DISEASE AND MYCOPLASMA OVIPNEUMONIAE IN DESERT BIGHORN SHEEP OF CALIFORNIA, NEVADA, UTAH

BEN GONZALES, STEVE TORRES, REGINA ABELLA, California Department of Fish and Wildlife
PEREGRINE WOLFF, MIKE COX, Nevada Department of Wildlife
ANNETTE ROUG, DUSTIN SCHAIBLE, Utah Division of Wildlife Resources
CLINTON EPPS, DANIELLA DEKELAITA, Oregon State University
CHRISTINE KREUDER JOHNSON, University of California, Davis

Respiratory disease is one of the most important factors limiting the recovery of bighorn sheep (*Ovis canadensis*). In 2013, a pneumonia outbreak with high mortality occurred in desert bighorn sheep (*Ovis canadensis nelsoni*) populations in the Mojave Desert of California. *Mycoplasma ovipneumoniae*, which is considered a primary pathogen in the bighorn sheep respiratory disease complex, was detected with ELISA and PCR from the Mojave bighorn sheep populations. Concurrent disease surveys in neighboring Nevada identified one identical and one distinct strain of *Mycoplasma ovipneumoniae*. In 2014, additional disease surveys were conducted across a wider area, and populations as far as the Orocopia Mountains were found seropositive and PCR positive. We report findings from the 2013 disease outbreak and 2014 disease surveys and provide an overview of historical and current data on the distribution of *Mycoplasma ovipneumoniae* in desert bighorn sheep populations in California, Nevada and Utah.
ADAPTIVE MANAGEMENT OF BIGHORN HERDS AT RISK TO DISEASE TRANSMISSION

MIKE COX, Nevada Department of Wildlife, 1100 Valley Road, Reno, NV  89512
PEREGRINE L. WOLFF, Nevada Department of Wildlife, 1100 Valley Road, Reno, NV  89512

In Nevada, the core mission of our bighorn management program for decades focused on restoration of sheep through translocations and water developments; in essence “putting sheep on the mountain”. Unprecedented success (3,000 wild sheep in 1980 to 11,000 in 2013) fostered a cavalier attitude toward disease risks which was supported by disease surveillance of growing source stock herds showing most harbored “bugs”, specifically Mannheimia hemolytica, which should have caused deadly die-offs. After successfully creating metapopulations of interconnected herds, we experienced disease events of varying severity. The confidence and excitement of herd expansions and high lambdas turned to concern over reports of sick sheep and poor lamb recruitment. Improved pathogen diagnostics, realization of how rapid the spread of disease can occur between herds, the unknown severity of the next disease event, and variation in herd responses to disease led to a paradigm shift of increasing emphasis on “keeping sheep on the mountain”. Several new tenets to Nevada’s bighorn management program are:

- Don’t cause a disease event through management actions; make informed decisions;
- Polymicrobial pneumonia may cause severe and long-lasting herd impacts;
- Public land sheep allotments and private flocks should be mapped and monitored;
- Pathogens spread by bighorns are equally as devastating as the initial transmission from domestics;
- Conduct active and passive disease surveillance on all herds but prioritize healthy herds at high risk to exposure;
- Attempt to define lamb mortality caused by drought vs. disease;
- Presample source and recipient herds prior to translocations;
- Conduct low risk translocations but commit to intensive monitoring as if they were experiments;
- Collaborate to stratify and replicate the varying conditions that bighorns are exposed to in understanding the variable population responses to pathogens;
- Educate NGO’s, sportsmen, wildlife commissions, policy makers, and general public;

GENETIC POPULATION STRUCTURE OF PENINSULAR BIGHORN SHEEP (OVIS CANADENSIS NELSONI) INDICATES SUBSTANTIAL GENE FLOW ACROSS THE US-MEXICO BORDER

MICHAEL R. BUCHALSKI, Wildlife Health Center, University of California, Davis, CA
ASAKA Y. NAVARRO, San Diego Zoo Institute for Conservation Research, San Diego, CA
WALTER M. BOYCE, Wildlife Health Center, University of California, Davis, CA
T. WINSTON VICKERS, Wildlife Health Center, University of California, Davis, CA
MATHIAS W. TOBLER, San Diego Zoo Institute for Conservation Research, San Diego, CA
LISA A. NORDSTROM, San Diego Zoo Institute for Conservation Research, San Diego, CA
JORGE ALANIZ GARCIA, Universidad Autónoma de Baja California
DAPHNE A. GILLE, Wildlife and Ecology Unit, Veterinary Genetics Laboratory, University of California, Davis, CA
MARIA CECILIA T. PENEDO, Veterinary Genetics Laboratory, University of California, Davis, CA
OLIVER A. RYDER, San Diego Zoo Institute for Conservation Research, San Diego, CA
HOLLY B. ERNEST, Department of Veterinary Sciences, University of Wyoming Laramie, WY
Within the United States (US), Peninsular bighorn sheep (*Ovis canadensis nelsoni*, PBS) are listed as federally endangered. Despite known metapopulation structure, little is known regarding functional connectivity across the international border with Mexico. Increasing threats to connectivity associated with highway expansion, renewable energy development, and completion of the US-Mexico border fence, led us to conduct a study of genetic variation and spatial structure. Blood and fecal samples were collected (n = 224) on both sides of the border from 1992 to 2013. Genetic data was obtained for 25 microsatellite loci and 515 base pairs of the mitochondrial DNA control region. Microsatellite diversity (observed heterozygosity = 0.56; allelic richness = 4.1; inbreeding coefficient = 0.01) was substantial despite past demographic declines. STRUCTURE analysis indicated the presence of three genetic populations, one of which spanned the international border. This pattern of genetic structure was supported by analysis of molecular variance for both microsatellites and mitochondrial DNA (P < 0.01), and low-moderate pairwise fixation indices (FST = 0.09—0.15; ΦST = 0.18—0.27) indicated substantial gene flow among populations. Migrant detection tests indicated natal dispersal occurred within both sexes, with no evidence of sex bias. Despite the severe reductions in population abundance which led to federal listing in the US, these data suggest PBS have retained substantial genetic variation and show little evidence of a recent genetic bottleneck. Patterns of genetic spatial structure suggest gene flow throughout the ranges is common, and construction of a US-Mexico border fence or wind energy infrastructure would disrupt connectivity of the metapopulation. Future conservation efforts should focus on identifying dispersal corridors and maintaining functional connectivity to facilitate recolonization of unoccupied habitat. (*Buchalski et al. 2015 Biological Conservation*).

### RANGE-WIDE POPULATION GENETIC STRUCTURE AND PHYLOGENETICS OF DESERT BIGHORN SHEEP: IMPLICATIONS FOR CONSERVATION

**MICHAEL R. BUCHALSKI**, Wildlife Health Center, University of California, Davis, CA

**BENJAMIN N. SACKS**, Mammalian Ecology and Conservation Unit, Veterinary Genetics Laboratory, University of California, Davis, CA

**DAPHNE A. GILLE**, Wildlife and Ecology Unit, Veterinary Genetics Laboratory, University of California, Davis, CA

**MARIA CECILIA T. PENEDO**, Veterinary Genetics Laboratory, University of California, Davis, CA

**HOLLY B. ERNEST**, Department of Veterinary Sciences, University of Wyoming Laramie, WY

**WALTER M. BOYCE**, Wildlife Health Center, University of California, Davis, CA

Though often well characterized at the regional level, few studies have examined the genetic structure or phylogeography of desert bighorn sheep range-wide. We examined genetic variation of 672 desert bighorn sheep (*Ovis canadensis* spp.) across 53 sites throughout their range in the southwestern US and northern Mexico, and an additional 52 Sierra (*O. c. sierrae*) and 70 Rocky Mountain bighorn (*O. c. canadensis*) from adjacent populations. Variation at 39 microsatellites and a 515 bp portion of the mitochondrial D-loop was analyzed. Using microsatellite data, a discriminant analysis of principle components differentiated the three recognized taxa (Sierra, Rocky Mountain, and desert), and provided evidence of substructure (5 groups) within desert bighorn. Genetic differentiation among desert bighorn herds appears largely due to isolation-by-distance, though discrete barriers within the central Mojave and Transverse Ranges were identified. Concordantly, network and maximum-likelihood analysis of the mitochondrial D-loop revealed three distinct clades (≥ 72% bootstrap support) that conformed to the three major groups. Our microsatellite and mitochondrial data suggest strong divergence of desert bighorn from other subspecies in North America, with no statistical support for recognition of multiple subspecies within the taxon. Although desert bighorn appear connected by gene flow as a single evolutionary unit, future analyses are needed to investigate potential for local selection to structure functional genes. Regardless, conservation of localized genetic variation remains necessary for maximizing diversity.
PRELIMINARY ESTIMATION OF CHANGES IN GENETIC STRUCTURE OF A DESERT BIGHORN SHEEP METAPOPULATION OVER TWO GENERATIONS

CLINTON W. EPPS, Oregon State University, Dept. of Fisheries and Wildlife, Nash Hall Room 104, Corvallis, OR 97331. Clinton.Epps@oregonstate.edu

RACHEL S. CROWHURST, Oregon State University, Dept. of Fisheries and Wildlife, Nash Hall Room 104, Corvallis, OR 97331. Rachel.Crowhurst@oregonstate.edu

Investigations of genetic structure within a metapopulation of desert bighorn sheep in the central Mojave Desert of California conducted from 2000-2004 revealed a highly fragmented system where genetic structure was strongly influenced by connectivity and isolation, barriers such as interstate highways, and habitat. Genetic structure also appeared to be influenced by extinction-colonization dynamics, which are often obscure. Since that time, several apparent recolonizations of little-used habitat patches have been observed. Moreover, a recent outbreak of respiratory disease within the system apparently spread rapidly among populations, even across barriers such as Interstate 40, suggesting that gene flow and genetic structure may have changed significantly. We present a preliminary recharacterization of genetic structure within this system using samples collected approximately two generations (12 years) after the first systematic genetic sampling, using 14-16 putatively neutral microsatellite loci. We observed dramatic changes in genetic structure, including shifts in genetic diversity and genetic distance across barriers. The most significant changes appear to have resulted from establishment of inter-population connectivity following natural recolonization or population expansion in previously underutilized habitat patches. Overall levels of connectivity and gene flow in the system appear higher than observed previously, likely due to increases in population size and occupied areas. Thus, potential for disease spread among populations may have increased as well. Overall, genetic structure within this metapopulation of desert bighorn sheep appears to be more dynamic than previously assumed.

CHANGES IN GENETIC VARIATION OVER TIME AND Merging DESERT BIGHORN POPULATIONS

PHIL HEDRICK, School of Life Sciences, Arizona State University, Tempe, AZ 85287. philip.hedrick@asu.edu

JOHN WEHAUSEN, University of California, White Mountain Research Station, 3000 E. Line Street, Bishop, CA 93514. wehausen@qnet.com

Measuring the amount of genetic change over generations provides a way to evaluate past management and the theoretical effect of management provides an approach to predict future genetic variation. Founder effects and genetic bottlenecks in general can lead to low levels of genetic diversity, which can influence the persistence of populations. We examined genetic variation in two captive populations of desert bighorn sheep (Ovis canadensis) to measure change over time and evaluate the impact of introducing individuals from one into the other. Over about three generations, the amount of genetic variation in the Red Rock, New Mexico population increased. In contrast, over about two generations the amount of genetic variation in the Pilares, Coahuila population decreased significantly compared to its ancestral Tiburon Island, Sonora population. In addition, although both populations have low genetic variation, it is predicted that the introduction of Pilares rams into the Red Rock population in 2011 might increase the amount of genetic variation in the Red Rock population.
GENETICS AND THE MANAGEMENT OF SIERRA NEVADA BIGHORN SHEEP

JOHN WEHAUSEN, University of California, White Mountain Research Center, 3000 East Line St., Bishop, CA 93514; wehausen@qnet.com

DAVID GERMAN, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; David.German@wildlife.ca.gov

ALEXANDRA FEW, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; Alexandra.Few@wildlife.ca.gov

THOMAS STEPHENSON, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; Tom.Stephenson@wildlife.ca.gov

About thirty years ago it became evident that bighorn sheep exist as metapopulations where migration between subpopulations is critical for genetic and demographic integrity. Since then, metapopulation considerations have been incorporated into conservation planning for this species in hopes that resulting gene flow will be sufficient to maintain genetic diversity. Where might it be important to give genetics additional consideration in conservation planning? Bighorn sheep in the southern and central Sierra Nevada appear to be one such situation for multiple reasons. They occur in a separate and largely linear metapopulation in a single mountain range at the western edge of bighorn sheep distribution in the region. Most native subpopulations were extirpated, and the few that survived exhibit a genetic signature of severe past bottlenecks. Consistent with that history, Sierra bighorn have the lowest genetic diversity measured for non-captive bighorn sheep in the desert region. These findings suggest that these sheep could be vulnerable to inbreeding problems and potentially near a genetic tipping point. This talk will present results of some genetic analyses within the Sierra Nevada at metapopulation, subpopulation, and individual sheep levels. There is evidence that gene flow is occurring among many subpopulations in the Sierra, but not all. Subpopulations at the northern end of the current distribution are small with mostly inadequate gene flow. One of those has notably lower genetic diversity and a long history of inconsistent lamb production, which is consistent with the finding of a heterozygosity-fitness correlation throughout the Sierra involving lamb production. That subpopulation recently became the focus of a genetic rescue experiment, but simultaneously experienced an apparent natural genetic rescue. A strategy has been developed for the restoration of subpopulations to vacant habitat that attempts to produce founding gene pools that will produce offspring with higher heterozygosity levels.

DEMOGRAPHIC RESPONSES OF BIGHORN SHEEP TO RECREATIONAL ACTIVITIES: A TRIAL OF A TRAIL

VERNON C. BLEICH, Wildlife Branch, California Department of Fish and Wildlife, 1812 9th Street, Sacramento, CA 95811; vern.bleich@wildlife.ca.gov

BRETT P. WIEDMANN, North Dakota Game and Fish Department, 225 30th Avenue SW, Dickinson, ND 58601; bwiedmann@nd.gov

Long-term effects of anthropogenic disturbance to wildlife, and whether such effects have population-level consequences, are often difficult to determine. In 1996, a recreational hiking trail (Maah Daah Hey Trail) was constructed by the U.S. Forest Service through 4 geographic areas, each occupied by a distinct subpopulation of bighorn sheep (Ovis canadensis), in western North Dakota, USA. From 2001 to 2012, we monitored distribution, recruitment rates, and abundance of female bighorn sheep to investigate responses to activities associated with unhindered use of that trail and subsequent free access to an important lambing area. To investigate whether demographic consequences occurred, we compared those data to identical information from 3 reference populations of bighorn sheep that were not exposed to unhindered public use of the trail. Female bighorn sheep were displaced from, and eventually abandoned, lambing habitat subjected to intensive, erratic, and unpredictable recreational use. Those females had lower fidelity to lambing areas than the reference populations, all of which realized 100% fidelity. Further, the females exposed to unhindered dis-
turbance achieved lower recruitment of young, exhibited a substantial downward trend in recruitment rate, and a decline in the number of females in that population compared with the others, for which perturbation was less severe and human activities were consistent and predictable, and public use of lambing habitat was not unhindered. Metapopulations of bighorn sheep occurring in fragmented habitat having minimal vertical relief may be especially susceptible to sources of disturbance, which should be a consideration when recreational facilities are developed.

Peninsular bighorn sheep (Ovis canadensis nelsoni) in the northern Santa Rosa Mountains (NSRM) of southern California regularly utilized residential and urban areas that were constructed within their habitat beginning in the early 1950s. In 1998, bighorn sheep in the Peninsular Ranges were federally listed as endangered. From 1985-2002, the NSRM population averaged 34 adult bighorn with 19 adult ewes and the herd experienced chronic low lamb recruitment averaging 14 lambs/100 ewes. We conducted cause-specific mortality studies of adult radio-collared bighorn from 1991-1996 and of radio-collared lambs from 1998-2001. We found that urbanization accounted for 34% of the adult bighorn deaths and 43% of the lamb deaths during these studies with 56% of the adult and 93% of the lamb mortalities within 300 meters of the urban interface. Urban deaths included auto collisions, ingestion of toxic, non-native plants and drowning in swimming pools. As a result of these findings, a 4 mile, 8 feet high exclusionary fence was constructed around the NSRM urban interface in Rancho Mirage, California and was completed in 2002. The bighorn exclusion fence has completely eliminated urban-related bighorn deaths in the NSRM. Post-fence (2003-2014) the NSRM population has averaged 58 adult bighorn and 31 adult ewes and lamb recruitment has averaged 26 lambs/100 ewes. Within 2 years of the completion of the bighorn exclusion fence, the NSRM ewe group reached its recovery goal of 25 adult ewes.

In the late 1800s, there were believed to be 1,500 desert bighorn roaming throughout 16 mountain ranges in the Trans-Pecos region of Texas. By the early 1960s, the last of the native bighorn were believed to be extirpated from the state. Just across the border, Chihuahua, Mexico, also lost the last of their native bighorn around the same time. Starting in 1957, restoration efforts began in Texas with the capture and transport of desert bighorn from Arizona back into Texas. Since that time, more than 700 bighorn have been captured and transplanted to historic mountain ranges in Texas from in-state and out-of-state translocation efforts. In December of 2010 and 2011, 141 desert bighorn were transplanted to Big Bend Ranch State Park (BBRSP). Data from
54 collared bighorn have produced >100,000 GPS points for analysis. Movements have been documented in all directions of the release site at BBRSP. More than 1.25 million acres of habitat were explored and used by the translocated bighorn. Forty percent of the collared bighorn were documented crossing into Chihuahua, Mexico. The natural movements of the bighorn from BBRSP/Texas into Mexico are the first instance of bighorn ranging freely in the mountains of Chihuahua. The recorded movements and range sizes ultimately show that our restoration undertakings are on a scale more grand than previously imagined. When dealing with a species that requires vast, continuous landscapes, the necessity and benefits of cooperation on all levels: public, private, state, federal, and international, is exemplified.

**LINKING NUTRITIONAL CONDITION TO POPULATION PERFORMANCE IN BIGHORN SHEEP: APPROACHING THE HOLY GRAIL**

THOMAS R. STEPHENSON, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Game, 407 West Line St., Bishop, CA 93514
KEVIN L. MONTEITH, Wyoming Cooperative Fish and Wildlife Research Unit, Department of Zoology and Physiology, University of Wyoming, Laramie, WY 82071
ALEXANDRA P. FEW, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Game, 407 West Line St., Bishop, CA 93514
D. W. GERMAN, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Game, 407 West Line St., Bishop, CA 93514
J. D. WEHAUSEN, White Mountain Research Center, University of California, Bishop, CA 93514

We developed a unique approach to quantify nutritional status in free-ranging ungulates that establishes a direct link between populations and their habitats. Body fat integrates caloric gain and loss as determined by factors such as forage supply, competition for food among conspecifics, winter severity, and reproductive costs. Consequently, body fat in free-ranging animals is an integrated measure of nutritional status and represents how animals balance the energetics of their environment. Energy from forage and fat, in conjunction with protein, is the currency that ultimately underpins growth and reproduction in animals. We present data from bighorn sheep that couples life-history traits with nutrition. We used ultrasonography and a palpation score to estimate body fat. We then analyzed relationships between body condition and vital rates estimated from radio-collared individuals. We also estimated population size and the finite rate of population growth (λ). The physiological limits of total body fat varied between 0.5 and 26%. Mean pre-winter body fat among 8 herds was 8.2 – 15.1% and 14.8 – 23.7% for lactating and non-lactating females, respectively. Mean body fat of females in late winter ranged from 10.1 – 13.6%. Nutritional condition of adult females was positively related to survival and pregnancy. Population growth rate varied between 0.6 and 1.3 and was positive for populations that exhibited mean body fat for lactating females >10.4% in October. The relationship between body fat and population growth rate supports the notion that nutritional status can represent the proximity of a population to animal-indicated nutritional carrying capacity.

**SURVIVAL ASSESSMENT OF DESERT BIGHORN TRANSLOCATIONS IN TEXAS**

CARLOS GONZALEZ, Borderlands Research Institute, Sul Ross State University, Alpine, TX, 79832, USA
Dr. LOUIS A. HARVESON, Borderlands Research Institute, Sul Ross State University, Alpine, TX, 79832, USA
THOMAS S. JANKE, Borderlands Research Institute, Sul Ross State University, Alpine, TX, 79832, USA
JOSHUA CROSS, Borderlands Research Institute, Sul Ross State University, Alpine, TX, 79832, USA
FROYLAN HERNÁNDEZ, Texas Bighorn Project Leader, Texas Parks and Wildlife Department, Alpine, TX, 79830, USA
Beginning in 1959, translocation efforts initiated in Texas to restore desert bighorn (Ovis canadensis mexicana) to their historic habitats. Partnering with the Texas Parks and Wildlife Department, the Borderlands Research Institute has been at the forefront of desert bighorn sheep research in Texas. Since 2010, 172 bighorn (63 rams and 109 ewes), of 246 captured and released, have been fitted with GPS radio collars for research purposes. So far, we have recovered more than 100 collars from our study, producing nearly 200,000 GPS points for our analyses. Over the last 4 years, we have investigated 53 bighorn mortalities in the Big Bend area and Mexico. Of those mortalities, 19 were killed by mountain lions, 1 fell from a cliff, 1 was poached in Mexico, 2 died in a pile, 1 ewe died from birth complications, 1 ram died from eating toxic vegetation, 1 ram died from a fight injury, and 21 deaths were from unknown causes. There were also 6 documented mortalities of bighorn rams with skin conditions that we believe to be associated with the parapox virus. Five of the 6 cases consisted of mature rams and we are in the process of trying to determine why this virus is primarily being found on mature rams. The knowledge gained will continue bettering our understanding of bighorn restoration and conservation efforts in Texas, and in the Chihuahuan Desert. Without collaborative conservation, the desert bighorn sheep restoration program would not be where it is today.

**RESOURCE SELECTION FUNCTIONS IN CONSERVATION PLANNING FOR ENDANGERED SIERRA NEVADA BIGHORN SHEEP**

ALEXANDRA FEW, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; Alexandra.Few@wildlife.ca.gov

BRIAN HATFIELD, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; Brian.Hatfield@wildlife.ca.gov

DEREK SPITZ, College of Forestry and Conservation, University of Montana, 32 Campus Drive, Missoula, MT 59812; derekspitz@gmail.com

ROB KLINGER, U.S. Geological Survey, Western Ecological Research Center, Yosemite Field Station, 40298 Junction Drive, Suite A, Oakhurst, CA 93644; rcklinger@usgs.gov

KATHLEEN KNOX, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; Kathleen.Knox@wildlife.ca.gov

DAVID GERMAN, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; David.German@wildlife.ca.gov

THOMAS STEPHENSON, Sierra Nevada bighorn sheep recovery program, California Department of Fish and Wildlife, 407 W Line St., Bishop, CA 93514; Tom.Stephenson@wildlife.ca.gov

Species distribution models (SDMs) provide a measure of the importance of ecological variables that correlate with species occurrence. These models can provide a framework in which to implement adaptive management in the recovery of federally endangered Sierra Nevada bighorn sheep (Ovis canadensis sierra; SNBS) and reoccupy historic habitat. Model results can be applied to spatial data to produce maps representing the likelihood of species occurrence. We use one type of SDM, a resource selection function (RSF), generated by logistic regression to examine how species rarity affects model predictions of the likelihood of occurrence. We present RSFs constructed with a use-availability design based on summer ewe occurrences or ram locations between May and December. Using k-fold cross validation and leave-one-out validation which includes locations from newly reintroduced bighorn, we show that a ewe summer RSF has higher predictive power interpolating between than extrapolating outside of patches of occupied habitat. This model and a winter RSF that accounts for altitudinal migration identified two large patches of bighorn habitat unrecognized by the Recovery Plan in remote geographic areas where there is a paucity of historic occurrence data. We combined an RSF based on ram occurrences with a cost distance analysis to quantify the proximity of domestic sheep grazing relative to bighorn sheep core home range. We ask how robust this model is to the expanding distribution of SNBS. By quantifying habitat quality and disease risk, these models will directly inform translocation efforts, allowing managers to identify suitable areas for future Sierra sheep reintroductions.
With the use of modern high fix-rate GPS collars, it is now possible to perform a wide variety of analyses that were formerly difficult. In deploying GPS collars, a critical question is: “What fix-rate is suitable to investigate our particular question?” Since battery life is a trade-off with study duration and sampling rate, ideally researchers would collect the minimum amount of data needed per unit time in order to maximize the study duration while minimizing the use of scarce resources. We analyze GPS data collected from Sierra Nevada bighorn sheep to explore how much information is contained in various fix rates and times with respect to a number of different analytic parameters: home-range size, slope, elevation, aspect, forage and cover type. We use high fix-rate data collected at 1 point per hour as the standard for comparison. We compare the high fix-rate data to the permutations of data collected at lower rates using subsampling, looking at all of the time and fix-rate permutations. We compare the values of each subsample to the true values to determine what minimum fix-rate substantially describes the target parameter. The results suggest that researchers can employ relatively low fix-rates (<<24/day) and still adequately assess many spatial variables. Our analysis may help reduce oversampling of spatial data. However, since the list of variables we analyzed is not exhaustive, it is possible that other variables may be more nuanced and require higher fix-rates so some caution in implementation is advised.

Habitat characteristics at parturition sites may play an influential role in desert bighorn lamb survival, yet little is known about bighorn parturition sites because pregnant females isolate themselves prior to parturition and give birth in seclusion, making them difficult to find. Our goal was to examine habitat characteristics at parturition sites, and lamb nursery group and predation sites. We evaluated elevation, slope, terrain ruggedness and adult female visibility at parturition, nursery, and lamb predation sites by comparing them to paired random sites using conditional logistic regression, and used binary logistic regression to compare parturition sites to nursery sites, and predation sites to nursery sites. When compared to randomly available sites, odds of sites being parturition or nursery sites increased with increasing elevation, slope and ruggedness, but decreased with increasing visibility. Odds of a site being a predation site did not change with elevation, but increased with increasing slope and ruggedness, and decreased with increasing visibility. When compared to
nursery sites, odds of a site being a parturition site decreased with increasing elevation, slope and ruggedness, but visibility was similar between the two. Odds of a site being a predation site increased with increasing elevation, slope and ruggedness, but decreased with increasing visibility when compared to nursery sites. Understanding factors that affect female parturition site selection, and how habitat characteristics at these sites differ from those at predation and nursery sites, can provide insight into strategies female bighorn employ both during and after parturition to promote lamb survival.

**DESERT BIGHORN ESCAPE TERRAIN: NOVEL APPROACH TO DETERMINING THE IMPORTANCE OF SLOPE AND RUGGEDNESS WITHIN AND ACROSS MOUNTAIN RANGES**

CHRIS LOWREY, U.S.G.S. Western Ecological Research Center, Las Vegas Field Station, 160 N. Stephanie St, Henderson, Nevada. clowrey@usgs.gov.

KATHLEEN LONGSHORE, U.S.G.S. Western Ecological Research Center, Las Vegas Field Station, 160 N. Stephanie St, Henderson, Nevada. longshore@usgs.gov.

DANIEL THOMPSON, University of Las Vegas, Nevada. 1201 Maryland parkway, Las Vegas, Nevada.

For desert bighorn sheep, occurrence of escape terrain, usually defined as steepness of slope and ruggedness of terrain, has been demonstrated to be the most important predictor of probability of occurrence. The degree that slope and ruggedness are correlated within a mountain range can vary among ranges due to differences in their physiography. Correlation between slope and ruggedness make it difficult to determine how each variable contributes to animal presence. Many studies use slope and ruggedness as independent variables, which may or may not be a valid approach. This fact may impede managers and scientist alike in their quest to predict the likelihood of animals to occur, cross over into adjoining ranges, or predict areas of critical habitat. In a novel approach, we use principle components analysis, regression residuals, and logistic regression to separate the contributions of slope and ruggedness within bighorn sheep escape terrain. We use female locations during the lambing season in three different mountain ranges as an example to determine how different physiographic regions can alter interpretations of escape terrain for bighorn sheep.

**SPATIALLY EXPLICIT POPULATION STRUCTURE ANALYSES REVEAL BARRIERS TO GENE FLOW AMONG MOUNTAIN LIONS IN SOUTHWESTERN UNITED STATES**

ASHWIN NAIDU, School of Natural Resources and the Environment, University of Arizona, Tucson, Arizona 85721; ashwin@email.arizona.edu

ROBERT R. FITAK, Institut für Populationsgenetik, Veterinärmedizinische Universität Wien, Veterinärplatz 1, 1210 Wien, Austria; robert.fitak@vetmeduni.ac.at

JOHN CLEMONS, Arizona Desert Bighorn Sheep Society Inc., P.O. Box 21705, Mesa, Arizona 85277; clemonsjp@aol.com

SOPHIA S. AMIRSULTAN, School of Natural Resources and the Environment, University of Arizona, Tucson, Arizona 85721;sophiesa@email.arizona.edu

RON W. THOMPSON, Primero Conservation, Box 16106, Portal, Arizona 85632; leoneroronatsulross@gmail.com

ALEXANDER OCHOA, School of Natural Resources and the Environment, University of Arizona, Tucson, Arizona 85721; alexocho@email.arizona.edu

MELANIE CULVER, U.S. Geological Survey – Arizona Cooperative Fish and Wildlife Research Unit, School of Natural Resources and the Environment, University of Arizona, Tucson, Arizona 85721; mcculver@email.arizona.edu
Natural and anthropogenic landscape features that restrict movement of wide-ranging terrestrial species can potentially restrict gene flow among their populations, which may ultimately be detrimental to the persistence of the species and its habitat. We used spatially explicit Bayesian clustering models to investigate contemporary population genetic structure of mountain lions (*Puma concolor*) in southwestern U.S., and to explore the potential impact of landscape features such as rivers and interstate highways. We performed spatial genetic analyses on 401 DNA samples genotyped at 11 well-utilized *Felis catus* (FCA) microsatellite loci. Our analyses revealed a substantial level of genetic structuring among mountain lions with maximum statistical support for the occurrence of four subpopulations. Geographic visualization of the four subpopulations identified based on these data suggested that major highways, specifically Interstate-10 west of the metropolitan area of Phoenix, Interstate-40, and Interstate-17, may be barriers restricting gene flow among mountain lions. We comment on the possibility of combined effects of natural and anthropogenic barriers, and isolation-by-distance, being the underlying cause of observed population genetic structure. These data reveal potential consequences of anthropogenic impacts on mountain lions and their habitat. Wildlife managers, stakeholders, and conservation planners can use this information in guiding management decisions for mountain lion populations, and in prioritizing corridors that may restore habitat connectivity and gene flow for wildlife.

**DESERLION MOVEMENT RATES AND UNGULATE KILL RATES RELATED TO AMBIENT TEMPERATURE**

**DAVID M. CONRAD**, Arizona Game and Fish Department, 9140 East 28th Street, Yuma, AZ 85365 USA, 623-910-7872, dconrad@azgfd.gov

**ESTHER S. RUBIN**, Arizona Game and Fish Department, 5000 W. Carefree Hwy, Phoenix, AZ 85086 USA, 623-236-7379, erubin@azgfd.gov

We examined movement rates of mountain lions (*Puma concolor*) in an arid landscape of west-central Arizona in relation to ambient temperature and season. Seventeen lions were fitted with Global Positioning System (GPS) collars during 2009-2014 for multiple monitoring and research purposes, and collars were programmed to obtain locational fixes at least 4 times per day. We calculated mean hourly movement rates and tested for correlation with ambient high temperature, and compared movement rates among seasons. We also tested if increased movement rates resulted in a corresponding expansion of home range size. We identified GPS-clusters using an automated algorithm, ground-truthed a subset of the identified clusters with field investigations, and estimated ungulate kill rates by season for each lion. Finally, we examined potential relationships between kill rates, ambient temperature, and movement rates. Results of these analyses will be discussed in relation to potential implications to lion predation on desert bighorn sheep (*Ovis canadensis*).

**DISENTANGLING POPULATION DRIVERS TO UNDERSTAND CAUSES OF THE BIGHORN SHEEP DECLINE IN THE DESERT NATIONAL WILDLIFE REFUGE**

**KATHLEEN LONGSHORE**, U.S. Geological Survey, Western Ecological Research Center, Las Vegas, NV 89074

**DAVID CHOATE**, U.S. Geological Survey, Western Ecological Research Center, Las Vegas, NV 89074

**CHRIS LOWREY**, U.S. Geological Survey, Western Ecological Research Center, Las Vegas, NV 89074

**PEREGRINE L. WOLFF**, Nevada Department of Wildlife, Reno, NV 89512, USA

**PATRICK CUMMINGS**, Nevada Department of Wildlife, Las Vegas, NV 89108, USA

**DANIEL B. THOMPSON**, University of Nevada, School of Life Science, Las Vegas 89154, USA

In the late 1980s, bighorn sheep on the Desert National Wildlife Range experienced a severe population decline. Actual causes of the decline were unknown, but it was hypothesized that drought conditions triggered the initial decline in 1987. Additionally, ensuing low recruitment rates in 1988 and 1989 (fall lamb to ewe ratio 12/100) were believed to have been precipitating factors at the onset of the decline. Telemetry data and
other observations strongly indicated that mountain lion (Puma concolor) predation may have been a significant cause of adult mortality. Other potential causes for the decline e.g. disease and poor habitat conditions, were less well understood. Our goal was to assess factors currently affecting sheep demography in order to elucidate those that may have caused the original decline. Specifically, we evaluated population parameters including survivorship, levels of mountain lion predation, and measures of disease. We deployed 5 collars on cougars (4F, 1M), 30 GPS collars on bighorn sheep (15 M, 15 F), and obtained blood and tissue samples for disease testing. Survivorship of radio-collared adult sheep was high (92.9 ± 4.9%, Kaplan-Meier estimate). Mountain lions primarily killed mule deer (Odocoileus hemionus, 65.5%), and less often bighorn sheep (29.3%) and small mammals (4.3%). Based on Elisa testing >90% of bighorn tested had been exposed to Mycoplasma ovis pneumoniae. It appears that the initial population decline in the 1980’s was likely due to disease but drought and predation may have had a synergistic effect.

THE PARADOX OF NORTH AMERICAN UNGULATE DENSITY IN PREDATOR-FREE ENCLOSURES AND ON PREDATOR-FREE ISLANDS

ERIC M. ROMINGER, Wildlife Management Division, New Mexico Department of Game and Fish, Santa Fe, New Mexico, USA

Many species of North American ungulates have been introduced into predator-free enclosures or onto predator-free islands and allowed to increase in the absence of predation. I have looked at maximum ungulate density in these environs ranging in size from 2.6 km2 to ~8,000 km2. Paradoxically, in all systems, maximum densities stabilize between ~20 and 40 deer-size ungulates/km2 regardless of the ecosystem or size of the predator-free habitat. Excluding the most severe North American ecosystems, e.g., Mojave Desert or sub-arctic islands, maximum ungulate density varies less than 2-fold in ecosystems as diverse as the Chihuahuan Desert in New Mexico and mixed-hardwood forests in Michigan. This includes desert bighorn densities of 24/km2 in Red Rock, NM and desert mule deer densities of 34/km2 in Three-bar, AZ. However, more interesting is the fact that these densities are generally 20-100 times higher than those documented in adjacent habitats with top carnivores. Density-dependent induced decline in fecundity and density-dependent associated ‘drag’ on other physiological variables are reported as these predator-free populations increase; however, the asymptote of population growth curves invariably occur at densities almost never observed in populations subjected to predation. Densities of 68 and 105 deer-size ungulates/km2 have been used in experimental research to assess density-dependence. These densities are substantially higher than maximum densities from predator-free populations. I therefore hypothesize, that western North American ungulates rarely, if ever, approach true resource limited carrying capacity while under predation pressure by sympatric carnivores. Recognition of this paradox is fundamental to the understanding of the relationship between ungulate population density and carrying capacity.

RESPONSES BY BIGHORN SHEEP TO RISK OF PREDATION: ARE MOVEMENTS PROPORTIONAL TO RISK AND REWARD?

JEFFREY T. VILLEPIQUE, California Department of Fish and Wildlife, P.O. Box 3222, Big Bear City, CA 92314, USA, jeff.villepique@wildlife.ca.gov.

BECKY M. PIERCE, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Wildlife, 407 West Line Street, Bishop, CA 93514, USA, becky.pierce@wildlife.ca.gov.

VERNON C. BLEICH, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Wildlife, 407 West Line Street, Bishop, CA 93514, USA, vcbleich@gmail.com.

ALEKSANDRA ANDIC, Department of Astronomy, P.O. Box 30001, MSC 4500, Las Cruces, NM 88003-8000, USA, aleksandra.andic@gmail.com.
We are investigating how Sierra Nevada bighorn sheep (Ovis canadensis sierrae) responded to risk of predation by mountain lions (Puma concolor), by evaluating data collected during winters 2002–2007, in the Sierra Nevada, California, USA. We hypothesized that those endangered ungulates would respond to risk of predation by exhibiting fine-scale movements to areas that mitigated risk. Comparisons of movements by bighorn sheep on days when a mountain lion was active within winter range of bighorn sheep, with movements on days when no mountain lion was known to be present, demonstrated responses by female, but not male bighorn sheep. Female bighorn sheep moved to higher elevations ($\bar{x} = 123$ m), and to areas where an index to mountain lion activity was significantly less than the average for areas used by bighorn sheep on that date, whereas males demonstrated no significant movements in response to proximity of a mountain lion. During above-average precipitation years, both sexes demonstrated use of significantly lower elevations, characterized by a higher index of risk compared with those areas used by bighorn sheep in dry years, with males using areas of greater risk than females during wet years. Bighorn sheep used those areas where mountain lions were most active during wet years, likely because mountain lions were most active in those areas of bighorn winter ranges overlapping ranges of mule deer (Odocoileus hemionus), where both ungulates accrued forage benefits. We present additional results from an ongoing investigation of temporal and spatial scales of risk avoidance by Sierra Nevada bighorn sheep.
POSTER SESSION ABSTRACTS

MOVEMENTS OF DESERT BIGHORN TRANSLOCATED TO NINE POINT MESA

JOSHUA CROSS, Borderlands Research Institute, Sul Ross State University, P.O. Box C-21, Alpine, TX, 79832, USA
LOUIS A. HARVESON, Borderlands Research Institute, Sul Ross State University, P.O. Box C-21, Alpine, TX, 79832, USA
THOMAS S. JANKE, Borderlands Research Institute, Sul Ross State University, P.O. Box C-21, Alpine, TX, 79832, USA
CARLOS GONZALEZ, Borderlands Research Institute, Sul Ross State University, P.O. Box C-21, Alpine, TX, 79832, USA
FROYLAN HERNANDEZ, Texas Parks and Wildlife Department, 109 South Cockrell, Alpine, TX, 79830, USA

Desert bighorn sheep (*Ovis canadensis mexicana*) restoration efforts began in Texas in 1957. A primary tool in these efforts has been translocations of bighorn into viable historic habitat. One of the recent translocations occurred in December 2012 when 44 (22 M, 22 F) bighorn were captured off of the Elephant Mountain Wildlife Management Area and transported to Nine Point Mesa. Forty (18 M, 22 F) bighorn were equipped with Satellite and GPS radio collars to aid in our monitoring and research efforts. After 2 years, data from 36 (90%) of the collars were recovered. Post-release movements and range sizes (core and general use) were analyzed and compared between sexes. The influence of slope on movements and habitat selection was also reviewed. The information gained will aid Texas Parks and Wildlife Department and others in habitat evaluation and restoration efforts.

WATER DRAWDOWN FROM TWO BIGHORN SHEEP WATER DEVELOPMENTS

NEAL DARBY, Mojave National Preserve; 2701 Barstow Road, Barstow, CA, 92311; (760) 252-6146; neal_darby@nps.gov
DEBRA HUGHSON, Mojave National Preserve; 2701 Barstow Road, Barstow, CA, 92311; (760) 252-6146; neal_darby@nps.gov

Water developments in desert areas are an important wildlife management tool. However, their construction and maintenance on federal lands can lead to controversy due to agency policies concerning natural resource management or legislative laws such as the Wilderness Act. The key to minimizing this controversy rests in identifying the appropriate number and distribution of such developments so as to best benefit wildlife populations and distribution while adhering to the law. In an attempt to resolve this controversy, we monitored two water developments constructed specifically for Desert bighorn sheep (*Ovis canadensis nelsoni*) in the Old Dad/Kelso Mountains in Mojave National Preserve. We tracked water drawdown from storage tanks via remote pressure transducer dataloggers maintained by the Society for the Conservation of Bighorn Sheep and used remote cameras to record bighorn use of the drinker box from 2012 through 2014. Overall, water consumption varied temporally and spatially. Maximum water drawdown and wildlife use occurred from June through September while very little use occurred during the winter months of December through February. Maximum water drawdown exceeded 70 gallons per day and certain periods averaged over 40 gallons per day during summer months. Is this a sufficient number of developments to support these bighorn?
INTEGRATING RADIO-COLLAR AND CAMERA DATA TO ASSESS IMPACTS OF PNEUMONIA IN THE MOJAVE DESERT: A
STUDY DESIGN

DANIELLA J. DEKELAITA, Dept. of Fisheries and Wildlife, Oregon State University, Corvallis, OR 97331
CLINTON W. EPPS, Dept. of Fisheries and Wildlife, Oregon State University, Corvallis, OR 97331
JOHN WEHAUSEN, White Mountain Research Center, University of California, 3000 East Line St.,
Bishop, CA 93514
DEBRA HUGHSON, Chief of Science and Resource Stewardship, Mojave National Preserve,
2701 Barstow Road, CA 92311
NEAL DARBY, Wildlife Biologist, Mojave National Preserve, 2701 Barstow Road, CA 92311
REGINA ABELLA, California Department of Fish and Wildlife, 1812 9th St., Sacramento, CA 95811

In 2013, a pneumonia outbreak in California led to adult-specific sheep die-offs in the Mojave Desert, where
impacts are still being observed. The Mojave Desert system, which is a patchwork of mountain ranges varying
in biotic and abiotic complexity, supports a network of bighorn sheep metapopulations that have become in-
creasingly less connected as a result of anthropogenic development. Previously, bighorn sheep in the Mojave
were believed to be insulated from the threat of pneumonia, due to reduced connectivity with neighboring
systems as well. As of the summer of 2014, outbreak conditions have persisted; lamb recruitment appears
extremely low in some ranges, while remaining steady in at least one, attesting to the variability or possible
asynchrony in disease patterns between populations within the same system. We propose to analyze range-
specific population trends in the Mojave Desert before (prior to 2013) and after (2014-2017) detection of
disease to assess apparent differences in severity of impacts. Our objectives are to quantitatively isolate the
apparent effects of disease given changes in vital rates and population structure. We will proceed by integrat-
ing data from radio-collared animals and camera trap surveys, using a spatially explicit capture-recapture
framework for our analysis. We will present our methodology for obtaining and evaluating these data in 5
ecologically distinct mountain ranges to meet our study objectives. Through this investigation, we seek to
better understand the dynamics of disease and ultimately extrapolate risk factors based on differences in local
environmental factors, which may translate into better management for populations that appear more at risk.

EVALUATING THE FEASIBILITY OF REINTRODUCING DESERT BIGHORN SHEEP INTO THE TAHOE REGION OF THE
NORTHERN SIERRA NEVADA MOUNTAIN RANGE, CALIFORNIA

BREANNA DUPLISEA, California Department of Fish and Wildlife, Wildlife Branch North Central Region,
1701 Nimbus Road Rancho Cordova, CA 95670; 949-878-6907; breanna.duplisea@wildlife.ca.gov
STEVE TORRES, California Department of Fish and Wildlife, Wildlife Investigation Lab, 1701 Nimbus Road
Rancho Cordova, CA 95670; 916-358-1987; steve.torres@wildlife.ca.gov
SARA HOLM, California Department of Fish and Wildlife, Wildlife Branch North Central Region, 1701 Nimbus
Road Rancho Cordova, CA 95670; 530-346-6305; sara.holm@wildlife.ca.gov

Habitat suitability and the risk of disease transmission are vital for evaluating a reintroduction site for desert
bighorn sheep in California. Bighorn sheep were once part of the northern Sierra Nevada ecosystem in 1848,
but were believed to be extirpated due to the gold rush settlers that brought the transmission of disease with
domestic sheep and goats, habitat loss and unregulated hunting. In 2007 to 2008, 6 GPS collared California
bighorn sheep ewes from the Virginia mountain range in Nevada were tracked crossing into the eastern Si-
erra Nevada mountains of California. Although reintroductions have expanded the historical distribution and
population of bighorn sheep in California, a full feasibility is necessary to determine if a bighorn sheep rein-
troduction could be successful.
This study used geographic information system (GIS) habitat suitability models to quantify seasonal home range habitat that could support a viable population of bighorn sheep. A risk analysis was also conducted to evaluate the proximity of active domestic sheep allotments to each potential study plot. Our results found that all six plots exceeded the amount of year round habitat needed to support a herd of 100-125 bighorn sheep. Five out of six plots surpassed 6.25km² of snow-free winter habitat in 2003 and 2011, which may indicate the majority of plots could support a bighorn sheep herd in the harshest of winters. The risk analysis was the limiting factor for this feasibility study as it indicated that only two study plots were greater than 23 km away from an active domestic sheep allotment. The results from this study have provided initial insight into monitoring the possible natural recolonization event of wandering ewes and rams occurring near the Nevada-California border. It also supports recommendations to form a California Bighorn Sheep Technical Working Group (CBST) to further reduce domestic sheep risk in order to reintroduce 10-15 collared bighorn sheep for phase II of the reintroduction plan.

RESOURCE SELECTION BY AN ENDANGERED UNGULATE: A TEST OF PREDATOR-INDUCED RANGE ABANDONMENT

JEFFREY T. VILLEPIQUE, California Department of Fish and Wildlife, P.O. Box 3222, Big Bear City, CA 92314, USA, jeff.villepique@wildlife.ca.gov (presenter).

BECKY M. PIERCE, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Wildlife, 407 West Line Street, Bishop, CA 93514, USA, becky.pierce@wildlife.ca.gov.

VERNON C. BLEICH, Sierra Nevada Bighorn Sheep Recovery Program, California Department of Fish and Wildlife, 407 West Line Street, Bishop, CA 93514, USA, vcbleich@gmail.com.

ALEKSANDRA ANDIC, Department of Astronomy, P.O. Box 30001, MSC 4500, Las Cruces, NM 88003-8000, USA, aleksandra.andic@gmail.com.

R. TERRY BOWYER, Department of Biological Sciences, 921 South 8th Avenue, Stop 8007, Idaho State University, Pocatello, ID 83209, USA, bowyterr@isu.edu.

We investigated influences of risk of predation by mountain lions (*Puma concolor*), topographic metrics at multiple scales, and vegetation, land, and snow cover, on resource selection by Sierra Nevada bighorn sheep (*Ovis canadensis sierrae*), an endangered taxon, during winters 2002–2007, in the Sierra Nevada, California, USA. We hypothesized that those mountain ungulates would trade off rewards accrued from using critical low-elevation habitat in winter for the safety of areas with reduced risk of predation. We also tested the prediction that differences in quality of forage at low-elevations versus high-elevations were reduced in years of below-average precipitation than in wet years, yielding a reduced benefit of migration to low-elevations during drought, compared with years of above-average precipitation. Sierra Nevada bighorn sheep did not trade off benefits of forage for reduced risk of predation, but selected areas of high solar radiation, a correlate of vegetation productivity, where risk of predation by mountain lions was greatest, while mitigating indirect risk of predation by selecting for steep, rugged terrain. Bighorn sheep selected more strongly for areas where mountain lions were active, than for low elevation habitat in winter, likely because mountain lions were most active in those areas of bighorn winter ranges overlapping ranges of mule deer (*Odocoileus hemionus*), where both ungulates accrued forage benefits. We demonstrated reduced benefit of migration to low elevation during drought years, providing an alternative explanation to the predator-induced abandonment hypothesis for the disuse of low-elevation winter range observed during drought years.
Achievements in restoring desert bighorn sheep (*Ovis canadensis*) populations throughout the western United States and Mexico are associated with our ability to transplant animals to new or historical habitats. We designed an aluminum transport crate after years of capturing desert bighorn with safety, mobility, and expense in mind. Given the remote, rugged nature of desert bighorn habitat, the decision to release animals in roadless areas is often preferred. Thus, many areas with Wilderness designation are also habitat for wild sheep. Moreover, the remote release approach with transport crates is generally the best or only method under the current Minimum Requirements Decision Guide for areas with Wilderness designation. Specifications to the crates were designed so they may be loaded into the back of a pickup, on a trailer, or slung under a helicopter. Spinning issues related to helicopter transport and ventilation were addressed, as was the concern for ambient temperatures inside the crates. Dimensions for the crates can be modified for use with other species such as pronghorn (*Antilocapra americana*). These crates have been successfully used in New Mexico, Nevada, and Utah for transporting desert ungulates. This abstract is submitted for an oral presentation.