20th Biennial Symposium of the Northern Wild Sheep and Goat Council

9-12 May 2016
Moscow, Idaho
Pullman, Washington

Program and Abstracts

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Meeting Introduction and Host Cities

Meeting Introduction

The 20th biennial symposium of the Northern Wild Sheep and Goat Council will take place 9-12 May, 2016 in Moscow, Idaho and Pullman, Washington. This year's meeting offers an extensive selection of contributed oral and poster presentations, social activities and the annual Council business meeting. The symposium field trip will be an all day jet boat tour of Hells Canyon.

Host Cities

Welcome to Moscow, Idaho and Pullman, Washington!

Settlers were first drawn to the area in 1871, with abundant grassland and available timber for building. The area was first named "Hog Heaven" which was later changed to "Palouse Valley." In 1877, Samuel Neff filed for a postal permit under the name of Moscow because the area reminded him of his hometown of Moscow, Pennsylvania. In 1875, the city's first store was opened on what is now Main Street. Moscow grew with the arrival of the railroad in 1885. The town became incorporated in 1887 and was chosen as the site for a land-grant institution, the University of Idaho, in 1889. Idaho achieved statehood in 1890. Today Moscow is home to over 23,000 residents and students. The area boasts a highly skilled and educated work force employed by Moscow's many thriving businesses and the University of Idaho.

Pullman, with its historical roots in agriculture, was incorporated on April 11, 1888. It has matured into a community with small-town comforts and cosmopolitan amenities. Home to world class Washington State University, Pullman benefits from a diverse and international student population, PAC 12 sporting events as well as cultural and entertainment programs

Conference Venues

Conference activities will be held at the University Inn, Moscow, ID and Washington State University, Pullman, WA.

Registration and Logistics

Registration fees include admission to all oral sessions, breaks, social activities, barbeque, and the program.

Registration Fees:

$ 150 Full registration (includes jet boat tour)
$ 100 Full registration (without the jet boat tour)
$ 100 Student/retiree registration (includes jet boat tour)
$ 50 Student/retiree registration (without jet boat tour)
Add $75 late registration fee after April 15th.

The registration desk will be open at the following times:

Monday	May 9	1500 — 1900
Tuesday	May 10	0700 — 1700

*Locate David Smith at the conference if you need to register after the designated times.

Conference Contact

David Smith - david.smith@idfg.idaho.gov; 208-514-6373

Symposium Organizing Committee

Hollie Miyasaki	Co-chair, Idaho Department Fish and Game
Rich Harris	Co-chair, Washington Department Fish and Wildlife
David Smith	Logistics Coordinator, Idaho Department Fish and Game
Kevin Hurley	Executive Director, Northern Wild Sheep and Goat Council

Conference and Logistical Support

WSU liaison and field trip – Tom Besser, WSU and Frances Cassirer, IDFG
Jet Boat Tour – Frances Cassirer, IDFG and Paul Wik, WDFW
Sponsors – Nathan Borg, IDFG
AV – Jake Powell, IDFG

We would like to thank the session chairs and volunteers that are helping with AV, registration desk, and other logistics during the conference.

Sponsors

Sponsors attending the symposium will have displays at all breaks, lunches, and the Monday and Tuesday evening socials.

Symposium Sponsors

We would like to thank the following sponsors of the 2016 Northern Wild Sheep and Goat Council Symposium. Please support those that support us!

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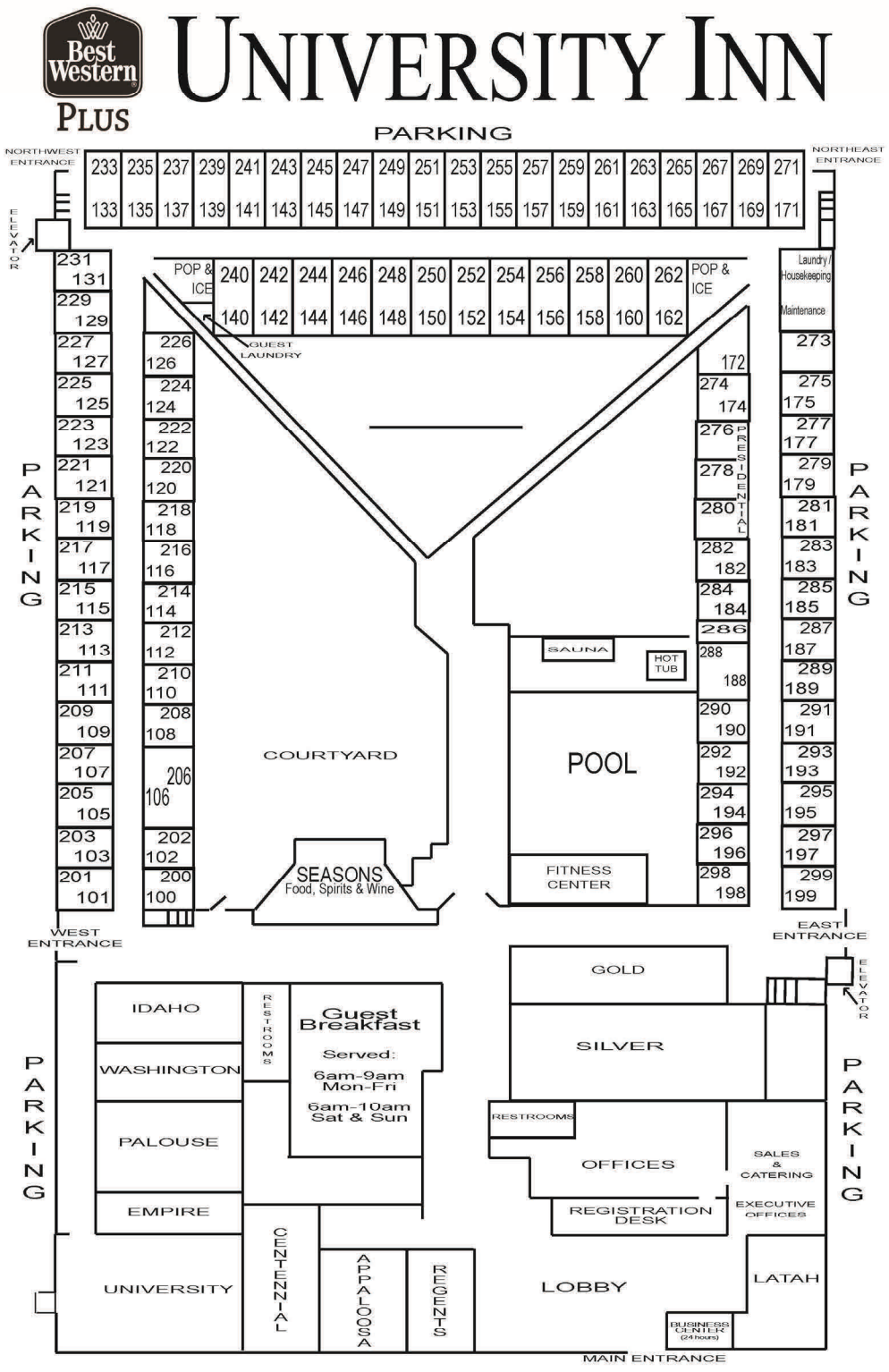

1516 W Pullman Road, Moscow, Idaho 83843
208 / 882-0550 800 / 325-8765 www.uinnmoscow.com

Program At a Glance

Monday 9 May 2016	**University Inn**
Time	University Room
1500-1900	Arrival and Registration—West Lobby
1830-2100	Social (appetizers) and Poster Session - Sponsored by the Upper Columbia United Tribes
Tuesday 10 May 2016	**University Inn**
Time	Idaho, Washington, Palouse Rooms
0700-1700	Registration—West Lobby
0810-0820	Symposium Introduction - Hollie Miyasaki & Rich Harris
0820-0830	Welcome - Kevin Hurley
0830-0900	Invited Speaker— Dr. Jim Unsworth, Director Washington Department Fish and Wildlife Perspectives on Bighorn Sheep Policies and Biology
0910-1200	Papers
1200-1330	Lunch (included with registration) and NWSGC Business Meeting - Kevin Hurley
1330-1640	Papers
1730-2100	Social and Poster Session Sponsored by Wild Sheep Foundation and Rocky Mountain Goat Alliance University Room
Wednesday 11 May 2016	**Hells Canyon Jet Boat Tour**
Time	
0705	Busses leave for Hells Canyon Jet Boat Tour
	Lunch Included with paid jet boat tour
1800	Busses arrive at University Inn
1830-2100	BBQ at University Inn Courtyard Sponsored by Idaho WSF, Washington WSF, and Oregon FNAWS
Thursday 12 May 2016	**Washington State University**
Time	**CUB Junior Ballroom**
0810	Busses depart University Inn
0840-1200	Papers
1200-1300	Lunch provided with registration
1300-1540	Papers
1600-1730	WSU tours (must sign up in advance)
1600	Busses depart for University Inn for those NOT participating in the WSU tour
1745	Busses depart for University Inn for those participating in the WSU tour
	Visit with our sponsors during the breaks, lunch, and the Monday and Tuesday Socials.

Attendee and Presenter Information

Locations
Conference activities will be held at the University Inn, Moscow, ID and Washington State University, Pullman, WA. The field trip will be a jet boat tour of Hells Canyon.

Oral Presenters
Please take note of your presentation date and time. Please note that all **general session** talks should be limited to 20 minutes total (including time for questions). It is extremely important that we maintain this schedule. For **general session** talks, a brief (5 minute) period post-presentation should be left so members of the audience can ask a few questions. Take the time to practice so your delivery fits into the scheduled interval. Check with your session chair well in advance of the start of your session to make sure that you know where the tools are that you need for your talk (e.g., remote control, laser pointer) and how to use them. This is also the time to check and see if your PowerPoint presentation (ideally saved in Microsoft Office PowerPoint Show [.pps] format) runs properly on the projector and projection computer. Presentations should be uploaded no later than the break preceding your talk. David Smith at the registration desk, Jake Powell, or your session chair can help you upload your presentation.

Posters
The poster session will be held during the Socials on both Monday May 9th and Tuesday, May 10th in the University room. Poster displays should be set up between 1500 and 1800 Monday, prior to the first social. Material to secure posters to the wall will be provided. All authors should be at their posters and prepared to discuss their work from 1830 to 1930 on Monday and Tuesday evening. Posters must be removed after the social Tuesday evening.

<u>Notice to all attendees</u>: As a courtesy to all presenters, we request that you turn off your cellular phones while attending sessions and meetings.

Monday—University Inn
WELCOME!!

Registration is available in the West Lobby from 1500 — 1900

Social

Sponsored by Upper Columbia United Tribes

University Room, 1830 — 2100

Posters Presentations 1830— 1930

Sponsors and Vendors attending

Appetizers, complimentary keg, no-host bar

James Unsworth, Director

Dr. Jim Unsworth is the Director of the Washington Department of Fish and Wildlife (WDFW). He was appointed to his position in February 2015.

Prior to becoming the Director of WDFW, he spent more than 30 years in wildlife management with the Idaho Department of Fish and Game. Jim held several management positions for the department, including deputy director, state big game manager and wildlife bureau chief.

He holds a bachelor's degree in wildlife management from the University of Idaho, a master's degree in fish and wildlife management from Montana State University and a doctorate in forestry, wildlife and range sciences from the University of Idaho. Jim and his wife Michele have four adult children. He is an avid hunter and angler.

Tuesday Morning—University Inn Idaho, Washington, Palouse Rooms

0700 1700 **Registration - West Lobby**

0810 0820 **Symposium Introduction and House Keeping**

Hollie Miyasaki and Rich Harris, NWSGC Symposium Co-chairs

0820 0830 **Welcome:** Kevin Hurley, Executive Director NWSGC

0830 0900 **Invited Speaker:**
Dr. Jim Unsworth, Director Washington Department Fish and Wildlife

Perspectives on Bighorn Sheep Policies and Biology

Session Chair: Jon Rachael, IDFG

0910 0930 **The Montana-Wyoming Collaborative Bighorn Sheep Research Program**

Robert Garrott

0930 0950 **An Initial Assessment of the Potential of Genomic Analysis to Help Inform Bighorn Sheep Management**

Elizabeth Flesch

0950 1010 **Population Genetics of the World's Thinhorn Sheep (*Ovis dalli*)**

Zijian Sim

1010 1040 **BREAK** (Exhibitors and Posters) University Room

Session Chair: Jeff Heinlen, WDFW

1040 1100 **Pregnancy Rates, Metabolites, Metabolic Hormones, and Application of Nuclear Magnetic Resonance Spectroscopy of Metabolic Profiles for Assessing Physiological Status in Bighorn Sheep (*Ovis canadensis*)**

Rashelle Herrygers

1100 1120 **Management Responses to Pneumonia Outbreaks in 3 Washington State Bighorn Herds: Lessons Learned and Questions Yet Unanswered.**

Rich Harris

1120 1140 **Status of Western Montana Bighorn Sheep Herds and Discussion of Control Efforts After All-age Die-offs**

Keri Carson

1140 1200 **Seasonal Variation in Behavioral Connectivity Among Groups of Bighorn Sheep: Implications for Disease Transmission**

Nathan Borg

Tuesday Afternoon— University Inn Idaho, Washington and Palouse Rooms

1200 1330 **NWSGC Business Meeting / Working Lunch—Kevin Hurley**
Lunch provided with registration. Baked Potato and Chili Bar. University Room

Session Chair: Ruth Milner, WDFW

1330 1350 **Seasonal Resource Selection by Introduced Mountain Goats in the Southwest Greater Yellowstone Area**

Blake Lowrey

1350 1410 **Nuclear Magnetic Resonance Spectroscopy Metabolic Profiles Distinguish Geographically Isolated Populations of Mountain Goats (*Oreamnos americanus*)**

Rashelle Herrygers

1410 1430 **Spatial Responses of Bighorn Sheep to Forest Canopy in North-central Washington**

Tiffany Baker

1430 1450 **Vegetation Change, Production, and Nutrient Content, Middle Fork Salmon River, Idaho**

James Peek

1450 1520 **BREAK** (Exhibitors and Posters) University Room

Session Chair: Regan Berkley, IDFG

1520 1540 **Rocky Mountain Bighorn Sheep in the Beaverhead and Lemhi Mountains of Idaho. A Management Information Project.**

Josh Rydalch

1540 1600 **Delineating and Estimating Seasonal Migration Patterns of Rocky Mountain Bighorn Sheep in the Mountain Valley Complex of South Central Idaho**

Scott Bergen

1600 1620 **Bighorn Sheep Movements and Mineral Lick Use in Waterton-Glacier International Peace Park**

Tabitha Graves

1620 1640 **Populist Influences on Dall Sheep Management and Allocation in Alaska**

Wayne Heimer

1730 2100 **SOCIAL AND POSTER SESSION—Sponsored by WSF and RMGA**— University Room
Taco and Fajita Bar, Complimentary Keg, No-host Bar

Wednesday - Hells Canyon Jet Boat Tour

0650	Busses Arrive at University Inn
0705	Busses Depart University Inn
0800	Jet Boats depart Clarkston
1200	Lunch provided with paid jet boat tour
1645	Jet Boats arrive Clarkston
1700	Busses Depart Clarkston
1800	Busses Arrive University Inn
1830	**BBQ—University Inn Courtyard**
	Complimentary keg, No-host bar
	BBQ sponsored by Idaho WSF, Washington WSF, and Oregon FNAWS

Hollie Miyasaki

Thursday Morning—Washington State University CUB Junior Ballroom

0810		Busses leave the University Inn
0825		Busses arrive WSU
		Session Chair: Carrie Lowe, WDFW
0840	0900	**Strain-type Matters: Mortality in a *M. ovipneumoniae*-positive Herd in Association with the Detection of a Different Strain of *M. ovipneumoniae*** Anne Justice- Allen
0900	0920	**Retrospective Survival and Force-of-Infection Modeling Following a Cross-Strain *Mycoplasma ovipneumoniae* Epidemic in Bighorn Sheep** Brandi Felts
0920	0940	**Evidence for Strain-specific Immunity to Pneumonia in Bighorn Sheep** Frances Cassirer
0940	1000	**Genetic Linkages Among *Mycoplasma ovipneumoniae* Outbreaks in Wild and Domestic Sheep and Goats** Pauline Kamath
1000	1020	**BREAK** (Exhibitors)
		Session Chair:: Mark Penninger, USFS
1020	1040	***Mycoplasma ovipneumoniae* Originating from Domestic Goats Triggers Mild Bronchopneumonia in Experimentally Exposed Naïve Bighorn Sheep (and Domestic Goats)** Thomas Besser
1040	1100	**Disease Agents in Domestic Goats in Idaho and Oregon and Relevance to Bighorn Sheep Management** Mark Drew
1100	1120	**Reaching Domestic Sheep and Goat Owners to Mitigate Pneumonia Transmission Risk to Bighorn Sheep**
1120	1140	Laura Heinse
1140	1200	**Bighorn Sheep Sinus Tumors, an Update** Peregrine Wolff

Thursday Afternoon—Washington State University CUB Junior Ballroom

1200	1300	**Lunch Provided with Registration**
		Session Chair: Dana Base, WDFW
1300	1320	**Disease Transmission between Sympatric Mountain Goats and Bighorn Sheep** Peregrine Wolff
1320	1340	***M. ovipneumoniae* Detection in Pneumonic Mountain Goat Kids** Danielle Nelson
1340	1400	**Understanding the Dynamics of *Mycoplasma ovipneumoniae* Carriers in a Bighorn Sheep Population** Frances Cassirer
1400	1420	**BREAK** (Exhibitors)
		Session Chair: Toby Boudreau, IDFG
1420	1440	**Persistent Pneumonia Drives Long-term Bighorn Population Dynamics in Hells Canyon** Kezia Manlove
1440	1500	**Modeling Management Strategies for the Control of Bighorn Sheep Respiratory Disease** Emily Almberg
1500	1520	**An Improved Method for Culturing *Mycoplasma ovipneumoniae* from Field Samples** Jessica Jennings-Gaines
1520	1540	**What Does It All Mean? Interpreting Respiratory Pathogen Survey Results for Bighorn Sheep Management** Carson Butler
1600	1730	**WSU Tour**—meet at Animal and Disease Biotechnology Facility, first floor lobby
*1600		Busses depart for University Inn for those ***NOT** participating in the WSU tour
1745		Busses depart for University Inn for those participating in the WSU tour.

Modeling Management Strategies for the Control of Bighorn Sheep Respiratory Disease
EMILY ALMBERG, Montana Fish, Wildlife, and Parks, 1400 S. 19th Avenue, Bozeman, MT 59718
KEZIA MANLOVE, Center for Infectious Disease Dynamics, Penn State University, University Park, PA
FRANCES CASSIRER, Idaho Department of Fish and Game, Lewiston, ID 83501
JENNIFER RAMSEY, Montana Fish, Wildlife, and Parks, 1400 S. 19th Avenue, Bozeman, MT 59718
KERI CARSON, Montana Fish, Wildlife, and Parks, 1400 S. 19th Avenue, Bozeman, MT 59718
JUSTIN GUDE, Montana Fish, Wildlife, and Parks, 1420 East 6th Avenue, Helena, MT 59620
RAINA PLOWRIGHT, Department of Microbiology & Immunology, Montana State University, Bozeman, MT 59718

Infectious pneumonia has plagued bighorn sheep populations and stymied recovery efforts across the western United States for decades. Management efforts aimed at controlling the disease have met limited success. Here we present a simple, a-spatial, stochastic, discrete-time model that captures basic bighorn demographics and in which we simulate the dynamics of Mycoplasma ovipneumoniae, the suspected primary causative agent in bighorn sheep respiratory disease, based on our current working knowledge of pathogen transmission and impacts. We then use the model to explore an ensemble of proposed management techniques, including augmentation, depopulation and reintroduction, density reduction, and test and cull, aimed at reducing or eliminating the pathogen, its transmission, or associated infection costs. We will describe preliminary model results, and discuss the implications of these results on long-term strategies for controlling disease and inciting long-term bighorn population recovery.

Spatial Responses of Bighorn Sheep to Forest Canopy in North-central Washington
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MARK E. SWANSON, *School of the Environment, Washington State University,* P.O. Box 646410, Pullman, WA 99164-6410, USA
LISA A. SHIPLEY, *School of the Environment, Washington State University,* P.O. Box 646410, Pullman, WA 99164-6410, USA
JANET L. RACHLOW, *Department of Fish and Wildlife Sciences, University of Idaho,* 6875 Perimeter Drive MS 1136, Moscow, ID 83844-1136, USA

Fire suppression has allowed conifers to encroach into historically open grasslands and shrublands. Woody encroachment may reduce habitat quantity and quality for bighorn sheep (*Ovis canadensis*), which rely on open escape terrain. We examined the influence of conifer canopy cover, along with topography and forage resources, on habitat selection by bighorns in north-central Washington, where thinning and prescribed fire treatments have been applied to encroaching forest to restore historic landscape conditions. To model habitat selection of bighorns using Resource Selection Functions (RSFs), we estimated Utilization Distributions (UDs) from GPS (Global Positioning System) locations of 21 radiocollared bighorns using the Brownian bridge movement model. After creating annual, lambing, summer, and winter 99% home ranges from UDs, we generated random points within each 99% home range to represent available habitat. We then used logistic regression to compare bighorn GPS locations (i.e., "use") to random points (i.e., "available") after assigning them to habitat variables that we created in a geographic information system. As we predicted, bighorn sheep selected areas with lower tree canopy cover, and also consistently selected for steeper slopes. Restoring or maintaining open habitat in areas with woody encroachment may influence movements and increase the value of habitat for bighorn sheep.

Delineating and Estimating Seasonal Migration patterns of Rocky Mountain Bighorn Sheep in the Mountain Valley Complex of South Central Idaho.
Scott Bergen, IDFG, 1345 Barton Road, Pocatello, ID 83204
Hollie Miyasaki, IDFG, 4279 Commerce Circle, Idaho Falls, ID 83401
Mark Hurley, IDFG, 600 South Walnut Street, Boise, ID 83707

Fifty-two Rocky Mountain Bighorn Sheep were fitted with GPS collars from January 2013 to July of 2015 from four herds across the Lemhi and Beaverhead Ranges. Net-Squared Displacement (NSD) is investigated and modified for the purposes

of identifying when and where individual sheep initiated their spring and fall migrations between seasonal ranges. This population of Rocky Mountain Bighorn Sheep has a spatiotemporal behavior, forays into winter range for short periods (1-3 days) and returning to summer range that complicated the interpretation of seasonal migration movements, as well as the spatial delineation of summer range. Once this foray behavior is accounted for methodologically, more accurate estimates are calculated and reported. On average, spring migration commences in late April to mid-May, where an individual will have increased rates of movement for 12 days over a distance of 12.8 kilometers (3 annual migrations). Fall migration starts at the end of October to Early November, where increased movements occur over a period of 8 days, returning to winter range over a distance of 11.5 Km. Inter-annual and intergroup differences are observed in the data and reported. As an example of how this analysis is relevant to this species management, seasonal movement patterns will be compared to domestic sheep allotments as well as intergroup movement patterns to infer best management practices for the long–term.

***Mycoplasma ovipneumoniae* originating from domestic goats triggers mild bronchopneumonia in experimentally exposed naïve bighorn sheep (and domestic goats)**

THOMAS E. BESSER, *Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University, Pullman WA 99163, USA*
E. FRANCES CASSIRER, *Idaho Department of Fish and Game, 3316 16th St., Lewiston, ID 83501, USA*

A series of experimental exposure studies were conducted to investigate the virulence of *Mycoplasma ovipneumoniae* carried by domestic goats (*Capra aegagrus hirca*) for naïve bighorn sheep (*Ovis canadensis*). Bighorn sheep (N=6) from an *M. ovipneumoniae*-free population were transported to WSU and divided into two groups of three animals held each in isolated pens. Following comingling of naturally *M. ovipneumoniae*-colonized domestic goats (N=3) in one of the pens, all the bighorn sheep developed symptoms of chronic respiratory disease and at necropsy 100 days later, all exhibited focal bronchopneumoniae, while the isolated, non-comingled bighorn sheep in the second pen remained healthy. We then comingled *M. ovipneumoniae*-free domestic goats with the bighorn sheep in the second pen but observed no evidence of respiratory disease in either bighorn sheep or goats during the subsequent 100 day period. Two of comingled domestic goats were then removed, inoculated with a goat-origin *M. ovipneumoniae* strain and again comingled with the third goat and the three bighorn sheep in the second pen. During the subsequent 100 days, all domestic goats and bighorn sheep in the pen exhibited signs of chronic respiratory disease, and at necropsy all of the animals exhibited focal bronchopneumonia. The results indicate that the goat-origin *M. ovipneumoniae* strains used in these experiments were capable of causing respiratory disease symptoms and pneumonia lesions in susceptible bighorn sheep and domestic goats. However, the disease observed was notably milder than that reported in previous experiments conducted with domestic sheep-origin strains of *M. ovipneumoniae*.

Seasonal variation in behavioral connectivity among groups of bighorn sheep: implications for disease transmission

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MICHAEL S. MITCHELL, *US Geological Survey, Montana Cooperative Wildlife Research Unit, 205 Natural Science Building, University of Montana, Missoula, MT 59812, USA*
PAUL M. LUKACS, *Wildlife Biology Program, 32 Campus Drive, University of Montana, Missoula, MT 59812, USA*
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PAUL R. KRAUSMAN, *Wildlife Biology Program, 32 Campus Drive, University of Montana, Missoula, MT 59812, USA*

Connectivity is important for population persistence and can reduce the potential for inbreeding depression. Connectivity between populations can also facilitate disease transmission; respiratory diseases are one of the most important factors affecting populations of bighorn sheep (*Ovis canadensis*). The mechanisms of connectivity in populations of bighorn sheep likely have implications for spread of disease, but the behavioral drivers of connectivity between bighorn sheep groups are not well understood. From 2007-2012, we radio collared and monitored 56 bighorn sheep in the Salmon River canyon in central Idaho. We used cluster analysis to define social groups of bighorn sheep and then estimated connectivity between these groups using a multi-state mark-recapture model. Social groups of bighorn sheep were spatially segregated and linearly distributed along the Salmon River canyon. Monthly probabilities of movement between adjacent ram and ewe groups ranged from 0.08 (+/- 0.00) to 0.76 (+/- 0.01) for rams and 0.05 (+/- 0.02) to 0.24 (+/- 0.00) for ewes. Movements of rams were extensive and probabilities of movement were considerably higher during the rut. Probabilities of movement for ewes were lower than those of rams and did not change seasonally. Whereas adjacent groups of bighorn sheep along the

Salmon River canyon were well connected, connectivity between groups north and south of the Salmon River was limited. The novel application of a multi-state model to a population of bighorn sheep allowed us to estimate the probability of movement between adjacent social groups and approximate the level of connectivity across the population. Our results suggest high movement rates of rams during the rut have the most potential to result in transmission of pathogens among both ram and ewe groups. Potential for disease spread due to movement among ewe groups was smaller but non-trivial.

What Does It All Mean? Interpreting Respiratory Pathogen Survey Results for Bighorn Sheep Management
CARSON J. BUTLER, *Ecology Department, Montana State University, Bozeman, Montana, USA 59717*
ROBERT A. GARROTT, *Ecology Department, Montana State University, Bozeman, Montana, USA 59717*

Respiratory disease has been a major challenge for bighorn sheep conservation and is a dominant factor influencing management decisions of bighorn sheep. However, much about the disease process remains unknown. Decades of research have compiled considerable evidence that domestic sheep and goats transmit the disease to bighorn sheep as well as strong evidence for several bacterial organisms commonly carried by domestic sheep and goats as causative agents for the disease. However, there are examples of bighorn populations hosting the agents linked to respiratory disease with little demographic side-effects. Further, the immediate cause of disease events often remains undetermined. Two general hypotheses exist to explain observed disease events in wildlife populations: 1) A disease event is caused by introduction of a novel pathogen from neighboring or sympatric host populations or; 2) A disease event is caused by certain conditions which trigger resident pathogens to increase in virulence or transmissibility. While the extent to which these competing hypotheses explain observed respiratory disease events in bighorn sheep is unknown, the appropriate management actions to address disease events caused by these processes are very different. This presentation discusses respiratory pathogen sampling in light of these hypotheses, highlighting both the challenges and recent advances.

Status of western Montana bighorn sheep herds and discussion of control efforts after all-age die-offs
MIKE THOMPSON, Montana Fish, Wildlife and Parks, 3201 Spurgin Road, Missoula, MT 59804
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EMILY ALMBERG, Montana Fish, Wildlife and Parks, 1400 S. 19th Avenue, Bozeman, MT 59718

During the winter of 2009-2010, four of nine bighorn sheep (*Ovis canadensis*) herds in a western Montana (Region 2) metapopulation experienced pneumonia-related all-age die-offs. Montana Fish, Wildlife, and Parks personnel attempted to prevent the spread of the disease to healthy herd segments and neighboring populations by aggressively culling bighorns in two of the herd units based on symptoms (East Fork of the Bitterroot) and in an effort to depopulate sheep within a containment zone (Bonner). The pneumonia outbreaks were allowed to run their course in the other two herds (Lower and Upper Rock Creek), although both experienced some lethal sampling for diagnostic purposes. Now, five years later, we report on the fate of these four treated and untreated herds, as well as that of the other five monitored herds within the metapopulation, in terms of demographic performance, pathogen community, and disease history. Despite initial optimism, the data suggests that culling did little to affect the 5-year post-outbreak population trajectories or pathogen communities for the affected herds. Furthermore, three additional herds within the metapopulation have since experienced all-age die-offs, followed by chronically reduced lamb recruitment. We will discuss the overall lessons from these management interventions.

Evidence for strain-specific immunity to pneumonia in bighorn sheep
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versity, Pullman WA 99163, USA
We used multi-locus sequence typing to document the introduction of a novel strain of *Mycoplasma ovipneumoniae* into a free-ranging bighorn sheep population. Despite preexisting serologic antibodies and asymptomatic carriage of *M. ovipneumoniae*, adult morbidity (100%) and pneumonia-induced mortality (33%) were within the range observed in epizootics following exposure of naïve bighorn sheep. During the outbreak the new strain apparently replaced the original strain in the population. Retrospective analysis of 100 lung and upper respiratory samples in 14 Hells Canyon bighorn sheep populations revealed 5 strain types of *M. ovipneumoniae* associated with pneumonia outbreaks over nearly 3 decades, consistent with repeated spillover from reservoir hosts. Some strains persisted and spread to adjacent populations, whereas others apparently faded out or were replaced. Domestic sheep and goat flocks typically carry a wide range of *M. ovipneumoniae* genotypes and provide a constant source of novel strains. Lack of cross-strain immunity could be one explanation for the regular occurrence of disease outbreaks in bighorn sheep despite a century of exposure to domestic *Caprinae*. Our results provide support for intensifying efforts to reduce the risk of *M. ovipneumoniae* transmission from domestic small ruminant hosts and from bighorn sheep carrying different strain types as strategies for managing disease in bighorn sheep.

Understanding the dynamics of *Mycoplasma ovipneumoniae* carriers in a bighorn sheep population
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We tested the hypothesis that pneumonia is maintained in bighorn sheep populations by asymptomatic carriers of the pathogen *Mycoplasma ovipneumoniae*. Our objectives were to (i) estimate the variation among individuals in the extent and duration of *M. ovipneumoniae* shedding, (ii) estimate the prevalence of chronic carriage, (iii) identify attributes that can be used to predict carriage, and (iv) determine whether a relationship exists between maternal chronic carriage and lamb survival. We collected upper respiratory samples and serum from over 80 individuals in the Lostine population in northeastern Oregon multiple times between 2009 and 2015. We report on patterns of *M. ovipneumoniae* shedding and exposure in adults, lambs, and yearlings relative to health, survival, and lamb recruitment.

Disease agents in domestic goats in Idaho and Oregon and relevance to Bighorn sheep management

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This study was designed to be a survey with the objectives of 1) to evaluate the health status and disease exposure of pack and herd domestic goats and 2) to use this information to develop risk management criteria for situations in which domestic goats may come into contact with bighorn sheep. Domestic goats are raised for meat, milk and hair production and are also used as herd goats for rangeland weed control and as pack animals. Domestic sheep, goats and wild bighorn sheep are all susceptible to a multifactorial pneumonia. We sampled 43 herd goats from 7 herds and 48 pack goats from 11 groups for viral and bacterial serology, parasitology, and Pasteurellaceae microbiology. The goats in this study were in generally good health, although most goats did harbor various pathogens and parasites. Several of these, such as bacteria in the family Pasteurellaceae, have been associated with pneumonia in free-ranging bighorn sheep, although it is not generally known that domestic goats will transmit readily to wild sheep. However, due the possibility of transmission, management of domestic goats in areas in or near bighorn sheep habitat should be conducted to minimize the risk of spread of disease agents.

Retrospective Survival and Force-of-Infection Modeling Following a Cross-Strain *Mycoplasma ovipneumoniae* Epidemic in Bighorn Sheep

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Bighorn sheep (*Ovis canadensis*) researchers and managers continually face dynamic challenges associated with population-limiting, bronchopneumonia epizootics. Although the etiology of pneumonia is not completely understood, we consider *Mycoplasma ovipneumoniae* (*M.ovi*) to be a primary pathogen responsible for bighorn sheep respiratory disease. Individuals recovered from initial *M. ovi* disease outbreaks become carriers of the *M. ovi* strain type encountered, and these strains are usually unique in independent outbreaks. Our objectives are to present information resulting from *M. ovi* strain cross-transmission in captive bighorn sheep. Unique *M. ovi* strains detected were 393 (Black Butte herd), 398 (Badlands and Rapid Creek herds), 400 (Snowstorm herd), and 404 (Asotin, Lostine, and Sheep Mountain herds). No earlier than July 2015, a *M. ovi* 400 strain spread across all populations within the South Dakota State University Captive Wildlife Research Facility. Serial samples were collected every 4-6 weeks and we documented exposure to the 400 *M. ovi* strain. Of these, 84% of sheep, at some point, actively shed 400 strain bacteria, which contributed to > 25% all-age-adult mortality from July 2015 to February 2016. Within our herd, we compared pneumonia-related lamb mortality prior to the spread of the 400 strain (2014) versus mortality post 400 strain spread (2015). Mortality increased nearly two-fold after the spread of the pathogen with rates of 40% and 81%, respectively. To examine infection rates among populations, we estimated apparent *M. ovi* prevalence, which ranged from 0.19 to 0.83. We used event-time analyses to retrospectively model lamb and adult survival and determine force-of-infection of the 400 strain, and examined factors influencing the virulence of *M. ovi* strain types. By effectively modeling the response of populations to a novel *M. ovi* strain challenge, we aim to provide insight into the management of *M. ovi* cross-strain transmissions within and among wild bighorn sheep populations.

An Initial Assessment of the Potential of Genomic Analysis to Help Inform Bighorn Sheep Management

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Genetic research may be a useful approach for understanding factors that could impact productivity and restoration of bighorn sheep herds. For example, genetic consequences of inbreeding in small populations can impact recruitment and local adaptations can influence translocation success. This modest pilot study quantified genetic attributes of bighorn sheep populations with a range of different herd histories in Montana and Wyoming to investigate genetic similarity and differences, genetic heterogeneity, and genetic distance. Employing an Ovine array containing about 700,000 single nucleotide polymorphisms (SNPs) with approximately 24,000 markers that are informative for Rocky Mountain bighorn sheep, we used whole genome genotyping to analyze genetic material. This technique represents a significant advancement in genetic analysis of bighorn sheep, as most previous studies have used microsatellites and less than 200 genetic markers. We analyzed approximately fifteen individuals from each of four different populations that we predicted would differ in genetic characteristics, due to population dissimilarities that potentially impacted their genetics, including origin (native/reintroduced), population size, bottleneck history, degree of connectivity, and augmentation history. We selected four populations that provided a spectrum of these herd attributes, including the Tendoys, Stillwater, and Glacier National Park in Montana and the northeastern Greater Yellowstone Area in Wyoming. We present the results of this effort and examine expected and observed heterogeneity and genetic distance estimates to evaluate the potential for links between genetics and herd demography. We discuss the utility of genetic analyses in improving knowledge of bighorn sheep populations and potential implications for bighorn sheep management.

The Montana-Wyoming Collaborative Bighorn Sheep Research Program

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Managers are routinely making decisions on bighorn sheep population augmentation and restoration, harvest, habitat management, disease prevention and response, and other conservation actions without adequate knowledge of the drivers of demographic processes that inform management of many of the more successfully restored ungulate species. Two complementary long-term research programs have been initiated in Montana and Wyoming to help address the need for a better understanding of bighorn sheep ecology. These studies are designed on the premise that research insights that are broadly applicable for management and conservation are best obtained by addressing the same questions in multiple populations representing the range of variation realized by the species of interest. The studies were initiated in the Greater Yellowstone Ecosystem in 2009 and expanded to include bighorn populations throughout Montana in 2014. Twelve bighorn herds are incorporated in the studies which will continue for at least another 3-4 years. Herds were selected to capture a wide range of variability in disease outbreak history, environmental settings, and herd attributes in an effort to maximize realized variation in adult survival, recruitment, and population dynamics among herds. A multi-disciplinary team of agency biologists and academics are conducting the integrated studies that include investigations of health/physiology, spatial ecology, disease, genetics and population dynamics.

BIGHORN SHEEP MOVEMENTS AND MINERAL LICK USE IN WATERTON-GLACIER INTERNATIONAL PEACE PARK

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We used bighorn sheep telemetry data collected in Glacier National Park, Waterton Lakes National Park, and the Blackfeet Reservation to examine bighorn sheep movements and use of known mineral licks. Over 168,400 GPS locations were collected between 2002 and 2011 on 95 bighorn sheep individuals from 17 different social groups. We examined the proximity of bighorn sheep telemetry data to 13 known mineral lick locations to describe timing and frequency of mineral lick use. After estimating bighorn sheep kernel home ranges, we evaluated how movement towards the lick, timing, and frequency of use varied depending on location of the mineral lick relative to bighorn sheep home ranges. Of the 89 sheep with sufficient data to detect mineral lick visits, 76 individuals had locations near known mineral licks, primarily between May and August. We found that social groups consistently used the same mineral lick location and visitation rates were generally influenced by distance between the mineral lick and home range. Duration of mineral lick visits was variable, but ewes generally visited mineral licks more frequently and for a longer duration than rams. We discuss management options for using mineral lick locations to monitor bighorn sheep populations.

Management responses to pneumonia outbreaks in 3 Washington State bighorn herds: Lessons learned and questioned yet unanswered

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Die-offs and subsequent periods of low lamb survival are the single greatest impediment to restoration of historic bighorn sheep abundance in North America, and developing effective responses to disease outbreaks in bighorn sheep has been frustrating for wildlife managers. A difficulty in understanding the phenomena is that no 2 situations seem identical. Thus, careful documentation of individual events is needed to understand common patterns and processes. We provide an update on 3 bighorn herds in Washington State that recently experienced pneumonia-related declines; management responses and outcomes differed in each case. The Yakima Canyon herd experienced an all-age die-off during winter 2009-2010, during which we culled animals showing signs of respiratory disease. In 2011 and 2012, the herd briefly rebounded, but then suffered 3 consecutive years of recruitment less than 0.10 lambs:ewe accompanied by pneumonia (cohorts born in 2013-2015). The Yakima Canyon herd is characterized by considerable spatial structuring that challenges our understanding of internal disease transmission. The Asotin herd suffered an all-age die-off in 2012; we took no management actions during the outbreak. Similar to Yakima Canyon, after 1 year of high lamb mortality, survival returned to normal and we failed to detect evidence of disease. In 2013 and 2014 we removed 3 ewes (~10% of survivors) that tested positive for *Mycoplasma ovipneumoniae* and recruitment has been 0.31 – 0.54 lambs:ewe with no pneumonia detected through the 2015 cohort. The Tieton herd suffered a catastrophic all-age die-off in winter 2013. Due to its proximity to the adjacent Cleman Mountain herd, we lethally removed every Tieton individual. To date, the Cleman herd has shown no evidence of pneumonia. While we do not assert that our management response was the only reason for the differing outcomes we hope that follow-up monitoring will help us to identify which actions are effective at controlling the impacts of disease in bighorn sheep.

POPULIST INFLUENCES ON DALL SHEEP MANAGEMENT AND ALLOCATION IN ALASKA

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Extra-statutory process in pursuit of assuring resident Dall sheep hunter satisfaction is taking Alaska to a new frontier in wildlife management. The Alaska Constitution prescribes management of Alaska's wildlife to provide maximum opportunity for human use consistent with the public interest as well as management on the sustained yield principle. This defines Alaska's management policy for Dall sheep as well as other wildlife. The presently articulated desire of Alaska resident hunter activists is at odds with this policy. The Alaska Statutes give force to the constitution, and define the Commissioner of Fish and Game as "the manager" of the State's fish and wildlife. However, since statehood (57 years ago) the regulatory Boards of Fish and Game have assumed progressively more of the Commissioner's management responsibility. In fisheries, this progression is highly advanced, probably because the entire surplus of returning salmon has been allocated for commercial harvest since statehood. Hence, salmon management is via allocated mortality. On the wildlife side, human-allocated mortality is insignificant for Dall sheep. The "allocation Board as manager" paradigm, which is so practical for fisheries is simply not in accord with constitutional and statutory guidelines. Nevertheless the "allocated mortality" traditions of the fisheries side are seeping into the Board of Game process as resident Dall ram hunter complaints have invited the Board of Game to solve "human conflicts" via allocation shifting which limits maximal opportunity for use. Whether this is in the public interest has not been settled. Recently the tradition of extra-legal transfer of authority from the Commissioner's Office to the Board resulted in a budget request from a fish-experienced administrator requesting funding for the Board of Game to rewrite Dall sheep management plans (as though Dall sheep were salmon). The Board of Game was more than willing to take on this task given its statutory responsibility to factor public desires into wildlife harvesting regulations. In this paper, I shall argue this is a departure from the intent of the Alaska Constitution and Alaska Statutes. This departure not only presages a non-professional, populist management system, which may or may not be responsible to scientific management under the sustained yield principle, it also obviates the need for professional managers, and places laypersons in control of management rather than in their legally-defined advisory capacity. This may or may not benefit conservation of Dall sheep and opportunities for Dall sheep hunters.

Reaching domestic sheep and goat owners to mitigate pneumonia transmission risk to bighorn sheep
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Bighorn sheep (*Ovis canadensis*) across North America have experienced large population losses due to the pneumonia, generally thought to be initiated by the bacteria *Mycoplasma ovipneumoniae*, transmitted from domestic sheep and goats. We surveyed 40 owners of sheep and goats living near wild bighorn sheep herds in central and southeast Washington. Over one-third of sheep and goat owners had no knowledge that their animals could transmit pathogens to bighorns, but all owners were interested in reducing interactions between the wild and domestic species, especially via options that did not restrict their autonomy. *M. ovipneumoniae* was detected in 41% of sheep or goat herds sampled, and animals escaped their enclosures in 78% of these herds. We concluded that physical contact between bighorns and domestics is probable due to the geographic overlap and social nature of both species, and a combination of solutions is necessary to reduce this risk.

Pregnancy Rates, Metabolites, Metabolic Hormones, and Application of Nuclear Magnetic Resonance Spectroscopy of Metabolic Profiles for Assessing Physiological Status in Bighorn Sheep (*Ovis canadensis*)
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The goal of this project is to develop knowledge of factors that influence demographic processes to restore and/or maintain bighorn sheep (*Ovis canadensis*) populations in Montana and Wyoming. Reproductive and physiological processes that affect reproductive health are integral components of population dynamics. Blood samples were collected from 242 adult bighorn ewes from 13 herds between December 2014 to March 2015. Herds represented a wide range of habitat types, disease outbreak history and topography. We evaluated variation in pregnancy rates, energy-related metabolites and hormones using 'traditional' methodologies. Additionally, we examined the utility of nuclear magnetic resonance (NMR) metabolic profiling to gain a better understanding of variation of physiological status. Although, pregnancy rates were generally high, there was variation among herds; probably related to ecological or physiological differences among herds. There was significant variation among herds in patterns of energy-related metabolites and metabolic hormones that might influence reproductive success. We established a NMR database of 54 compounds in large ungulates, and found that significant 'metabolic pathway shifts' occur in bighorn herds under different environmental conditions. During pregnancy, these 'shifts' may have consequences that increase the risks of fetal stress syndrome, lamb mortality, lamb vigor, and later reproductive success, which in turn, may affect population dynamics in bighorn sheep.

Nuclear Magnetic Resonance Spectroscopy Metabolic Profiles Distinguish Geographically Isolated Populations of Mountain Goats (*Oreamnos americanus*)
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Basic physiological studies on mountain goats (*Oreamnos americanus*) are conspicuously lacking in the literature, and the physiology of this species is perhaps the least known of the high mountain ungulates. Fundamental knowledge of physiology, and in particular, metabolism of this species would greatly improve our understanding of how changes in nutrition, reproduction, susceptibility to disease, and survival rates drive population dynamics. The objective of this study was to evaluate metabolite profiles of female mountain goats from two geographically distinct populations using Nuclear Magnetic Resonance (NMR) spectroscopy. Serum samples were collected during the first week of August from nannies located in Alaska (AK; n = 10) and Montana (MT; n = 12). Serum was extracted with acetone, dried and re-suspended in a standard NMR buffer. NMR spectra were analyzed with Chenomix™ software. Metabolites were identified and concentrations determined using the Chenomix™ database and the Human Metabolome Database. We identified 54 metabolites in the serum of mountain goats using this emerging technology. Of these, 28 metabolites differed between AK mountain goats in those from MT. Analyses of these metabolites allowed us to clearly differentiate metabolic profiles in carbohydrate, protein and lipid metabolism in nannies from AK and MT. It is possible that these metabolic shifts are related to specific physiological, genetic or geographical factors or interactions among these variables. The results of this study clearly demonstrate the utility of this technology to contribute to a profound understanding of physiological changes that occur as a result of genetic and environmental interactions in mountain goats. Additionally, this study has the potential to enhance our understanding of factors that drive population dynamics of mountain goats.

An Improved Method for Culturing Mycoplasma ovipneumoniae from Field Samples

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To better understand the distribution, occurrence, and role of Mycoplasma ovipneumoniae in the epidemiology of pneumonia in bighorn sheep, techniques that accurately and consistently detect this organism in wild sheep populations are needed. We reviewed published techniques and compared commercially available growth media to optimize methods for growing M. ovipneumoniae in our laboratory. Using a modified tryptone soya broth (TSB-1) and incubating field samples at 37 C in 10 % CO2, for 48 hours for enrichment, followed by direct plating onto solid media, we improved detection, culture success, and overall agreement between culture and polymerase chain reaction results.

Strain-type Matters: Mortality in a *M. ovipneumoniae*-positive Herd in Association with the Detection of a Different Strain of *M. ovipneumoniae*

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In August 2015 an emaciated ewe was removed from the Colorado River five miles south of Hoover Dam. Severe bacterial pneumonia with *Mycoplasma ovipneumoniae* was diagnosed by necropsy, and molecular testing of samples. During population surveys in late September, nine sheep carcasses, and several sick sheep were observed in the northern portion of the Black Mountains. The bighorn sheep population in areas adjacent to the river was more than 75% below the five year average and the previous 2013 survey. Three ewes were captured just after the surveys in the southern portion of the river units. All were exhibiting signs of respiratory infection and were positive for *M. ovipneumoniae*. When hunters reported coughing bighorns immediately south of the units, three ewes were removed, necropsied, and samples collected according to the Western Association of Fish and Wildlife Agencies Wildlife Health Committee recommended protocol. All three were diagnosed with acute bacterial pneumonia with *M. ovipneumoniae*, *Bibersteinia trehalosi* (moderate to few), and *Fusobacterium necrophorum* (few to very many). Disease testing by the AGFD in these units in 2012 and in adjacent units annually from 2012 to 2014 detected of *M. ovipneumoniae* by PCR in 5% to 10% of tested animals. Strain-typing using the 16S RNA IGS found a single strain in bighorn sheep in southern Nevada and northern Arizona. Strain-typing of the isolate detected in affected bighorns in 2015 matched the strain detected in a mortality event at Old Dad Peak of California in 2013 and during disease sampling efforts in the Spring Mountains (2013), River Mountains (2014) and Eldorado Mountains and McCullough Range (2015) of Nevada. The events documented in this report suggest that strains of *M. ovipneumoniae* vary in pathogenicity, that immunity to one strain does not necessarily prevent morbidity or mortality when another strain is introduced into a population, and *M. ovipneumoniae* can occur over distance and time with natural movement of bighorns.

Genetic linkages among *Mycoplasma ovipneumoniae* outbreaks in wild and domestic sheep and goats

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Epizootic pneumonia has contributed greatly to historical declines and extirpations of bighorn sheep populations, and is now hampering their re-establishment. In this study, we examined the genetic diversity and phylogeographic structure of the bacterium *Mycoplasma ovipneumoniae* (Movi) in reservoir (domestic sheep and goat) and spillover (bighorn sheep and mountain goat) hosts affected by bronchopneumonia across the western United States. We obtained Movi isolates (n = 343) from diverse geographical and host sources and used a multi-locus sequence-based genetic typing (MLST) approach that targeted four polymorphic Movi loci: the 16S-23S intergenic spacer (IGS), the small ribosomal subunit (16S), *gyrB*, and *rpoB*. We integrated pathogen sequence data with host species, location and sampling year in population genetic and phylogeographic analyses to (1) examine Movi genetic diversity and relatedness among hosts and locations, and (2) evaluate patterns of pathogen spillover and persistence in bighorn sheep populations. Our preliminary results indicate higher genetic diversity of Movi strains in domestic sheep, with no evidence for geographic clustering and repeated spillover into bighorn sheep. We also identified genetic linkages within and between neighboring bighorn sheep outbreaks; however, because we have more extensive sampling from bighorn sheep, these outbreaks may alternatively be linked through unsampled domestic sheep sources. Domestic goats formed a genetically distinct clade, and there were only two observed instances of spillover of goat strains into bighorn sheep. These data enable a broad-scale molecular epidemiologic investigation of Movi transmission dynamics and will inform the development of effective management strategies for both controlling the disease and promoting the re-establishment of bighorn sheep.

Seasonal Resource Selection by Introduced Mountain Goats in the Southwest Greater Yellowstone Area

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Mountain ungulates, although regarded as iconic and charismatic wildlife species, are the least studied and understood large mammals in the Greater Yellowstone Area (GYA). Mountain goats (*Oreamnos americanus*) are considered non-native in the GYA according to reviews of historical records, and have been steadily expanding their range since their introduction in the 1940s. Because of the general propensity of mountain goats to inhabit high elevation, mountainous terrain, there is significant potential for range overlap with native bighorn sheep (*Ovis canadensis*) and the possibility that competition and disease transfer will be detrimental to sympatric bighorn populations. We developed resource selection models using GPS data from 16 allopatric mountain goats in the Snake River Range of Idaho and Wyoming, USA, and generated predictive maps for the surrounding region, including Grand Teton National Park where mountain goats are in the early stages of colonization. Our results provide the first spatial predictions of seasonal habitat use by mountain goats in the GYA using GPS data and provide regional managers with insights regarding the current and future distribution of mountain goats. Building seasonal resource selection models for mountain goats in the GYA is the first step needed to better understand their biological needs, ecological role, and potential to negatively impact native communities and species.

Persistent pneumonia drives long-term bighorn population dynamics in Hells Canyon

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Pneumonia-induced die-offs are a widely recognized management challenge for bighorn sheep, but the long-term effects of the poor recruitment that often follows all-age disease events are less understood. Here we study the long-term effects of lamb disease on bighorn population growth rates in 12 Hells Canyon populations. We find that population dynamics are very sensitive to the frequency of pathogen introduction – a strong argument for continuing policies aimed to segregate bighorn and domestic sheep – but we also show that long-term population viability depends critically on the duration over which disease persists in lambs. Lamb survival rates in Hells Canyon varied between different nursery groups within a single population, suggesting relatively localized transmission during summer. Nursery group size, however, remained relatively constant, even as population sizes declined, limiting the likelihood that pathogens fade-out naturally as population decline. Finally, we will present some preliminary evidence that yearlings may play a limited role in transmission of pneumonia-causing agents to lambs. Our results suggest that long-term pathogen persistence may precipitate a phase-transition in bighorn population dynamics, from a period of rapid growth prior to disease onset, to a period of stagnant-to-declining population trajectories.

***M. ovipneumoniae* Detection in Pneumonic Mountain Goat Kids**

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Pneumonia epizootics resulting in all-age die-offs followed by sporadic reoccurring summer lamb mortalities due to polymicrobial pneumonia have been well documented in bighorn sheep. Following a pneumonia epizootic in bighorn sheep (*Ovis canadensis*) and sympatric mountain goats (*Oreamnos americanus*) in Nevada, kid mortalities were documented. We describe seven mountain goat kids with gross and histologic lesions consistent with polymicrobial bronchopneumonia including *Mycoplasma* sp., and *Mycoplasma ovipneumoniae* was detected in the lungs with real-time PCR from all kids. The overall pattern of disease appears similar to that seen with bighorn sheep. Consequently, *Mycoplasma ovipneumoniae* may affect kid recruitment in mountain goats.

VEGETATION CHANGE, PRODUCTION, AND NUTRIENT CONTENT, MIDDLE FORK SALMON RIVER, IDAHO

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Assessment of plant composition inside and outside of exclosures established in the early 1950s indicates changes towards the original bluebunch wheatgrass (*Pseudoroegneria spicata*) dominated communities 40 years later. Biomass and nutrient levels of bluebunch wheatgrass were evaluated over a 20-year period and 10-year period, respectively. April and May precipitation best predicted the biomass variation (range 17.5-73.3 gm m^{-2}). A fire in August 2000 suppressed biomass for the following two years, aided by low precipitation. Combinations of temperature and precipitation predicted Ca, K, N, P, and Zn values while Cu and Fe were predicted with total monthly precipitation and Mg and S were predicted with mean monthly temperature. Values of Cu, Fe, K, N, P, S, and Zn where higher than predicted for one to two years following the fire. Biomass of curlleaf mountain mahogany (*Cercocarpus ledifolius*) was best predicted with October temperature, while nutrients were predicted with combinations of spring temperatures and precipitation. Biomass of mallow ninebark (*Physocarpus malvaceous*) was best predicted with January mean temperature and December precipitation, while spring mean monthly temperatures best predicted nutrient levels. Bluebunch wheatgrass and curlleaf mountain mahogany are important forage plants for ungulates including mountain sheep. Mallow ninebark resprouts following burning and responses to temperature, precipitation, and fire likely represent other sprouting shrubs that are more palatable in the region.

Rocky Mountain Bighorn Sheep in the Beaverhead and Lemhi Mountains of Idaho. A Management Information Project.

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Rocky Mountain Bighorn Sheep were initially reintroduced into the Beaverhead Mountain Range in 1976 and into the Lemhi Mountain Range in 1983 after being eliminated in most of the area in the early 1900's. Limited data indicated populations were small with low lamb to ewe ratios and that they failed to meet population goals. IDFG identified management actions to better our knowledge and management of bighorn sheep in these areas. Additional information was needed to manage for separation between bighorn sheep and domestic sheep and goats which is IDFG policy. We captured and GPS radio-collared 57 bighorn sheep in order to delineate seasonal distributions of populations, document interchange between populations of wild sheep, estimate productivity and lamb survival, collect health data, and validate habitat models. Domestic sheep are present on portions of wild sheep ranges in the Beaverhead and Lemhi Mountains. Health testing has documented exposure of wild sheep to *Mycoplasma ovipneumoniae* and other respiratory pathogens. We also flew helicopter surveys to collect data on detection of radio-collared sheep and improve aerial survey methods. How this data is being used to address management actions identified in the Idaho Bighorn Sheep Management Plan will be discussed.

BIGHORN SHEEP SINUS TUMORS, AN UPDATE

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In 2009, bighorn sheep sinus tumors were discovered within a herd of seven Rocky Mountain bighorn ewes in Colorado, USA that were culled due to a history of at least 10 years of failed lamb recruitment. Since discovery, at least 38 cases of sinus tumors have been identified in at least 10 free ranging bighorn herds in Colorado. Additional cases have been identified in Rocky Mountain bighorns from Wyoming, Nevada, and Nebraska, as well as one herd of California bighorn sheep in Nevada. The disease has been shown to be infectious experimentally and likely has moved across the landscape through natural and artificial movements of bighorn sheep. While sinus tumors alone do not appear to affect adult survival or lamb recruitment, sinus tumors in combination with other typical respiratory pathogens have been consistently identified in Colorado bighorn herds that are struggling with dismal lamb recruitment. Theoretically, sinus tumors may affect the susceptibility of adult bighorns to pneumonia through interference with normal clearance mechanisms of the upper respiratory tract.

Disease Transmission between Sympatric Mountain Goats and Bighorn Sheep

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In 2009-10, Rocky Mountain bighorn (*Ovis c. canadensis*) herds in the adjacent East Humboldt Range (EHR) and Ruby Mountains (RM) in Elko County, NV suffered an all-age pneumonia die-off with an estimated loss of 90% in each herd. Sympatric mountain goats (*Oreamnos americanus*) also experienced pneumonia with an estimated 10-20% loss in both herds. *Mycoplasma ovipneumoniae* (M. ovi) was confirmed as a contributing pathogen in both bighorns and mountain goats and the same strain was identified between both species and ranges. In 2013 after removal of the remaining 15 bighorns from the EHR, 20 bighorns from Alberta, Canada were translocated to this range to assess whether surviving mountain goats would pose a threat to naïve sympatric bighorns. At the time of translocation (n=20), and during subsequent sampling events in 2014 (n=7) and 2015 (n=13) all sheep sampled were negative for M. ovi by both ELISA and RT-PCR on nasal swabs. Concurrent sampling of the EHR goats for M. ovi by RT-PCR between 2013 and 2015 indicated a prevalence of 6% (n=15), 12% (n=16) and 18% (n=11), respectively. From 2010-15 winter aerial surveys, annual mountain goat kid ratios ranged from 17 to 0 per 100 adults ($\bar{x}$ = 7) with an estimated λ of 0.60 for the herd over the same time period. From 2013-15, summer ground observations were conducted on both species. In 2014 and 2015, association of mountain goats with bighorns was observed within a minimum distance of 2 meters. Between September and December 2015, clinical signs of respiratory disease were noted in the bighorns and multiple mortalities observed. *Mycoplasma ovipneumoniae* was identified in pneumonic lungs and 16S RNA IGS sequencing confirmed a match to the strain isolated from the mountain goats. These findings suggest that potential disease transmission between mountain goats and bighorn sheep should be considered where range overlap occurs.

Population genetics of the world's thinhorn sheep (*Ovis dalli*)

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Thinhorn sheep (*Ovis* dalli) populations throughout northwestern North America are managed to maximize hunting, viewing and sustenance opportunities. Central to the effective conservation management is the identification of biologically relevant conservation units from which game management units can be derived. The identification of genetically discrete population units is essential for the delineation of true population boundaries, which can then form the basis for monitoring and the development of specific conservation action. In this study, we investigated the world-wide population genetics of thinhorn sheep. We genetically profiled ~2000 harvested thinhorn ram from across the species' range using 153 single-nucleotide polymorphism (SNP) markers. We used the genetic profiles to characterize the distribution of genetic variation and identify population boundaries across the entire geographic range of thinhorn sheep. We were also able to re-examine the current subspecies (Dall's and Stone's sheep) boundaries for thinhorn sheep and found that current boundaries likely do not reflect the evolutionary history of the species. Results from this study will be used to update the thinhorn management and harvest policies in British Columbia and Yukon, Canada.

Do differences in neutralizing antibody explain the differing susceptibility of neonatal domestic and bighorn sheep lambs to *Mycoplasma ovipneumoniae* infection?

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Mycoplasma ovipneumoniae (Movi) in bighorn sheep (*Ovis canadensis*) causes all-ages pneumonia epizootics upon its initial introduction into a population. The subsequent recurrent lamb pneumonia outbreaks that may persist for years or decades afterwards are the most important factor that limits growth of these populations. Bighorn lambs of Movi-immune ewes may become Movi-infected at less than 1 week of age and develop pneumonia by 2 weeks of age, suggesting that passive maternal antibody is not protective. In contrast, domestic sheep (*Ovis aries*) lambs may remain Movi-free up to 8 weeks of age or older and suffer lamb pneumonia losses less than 2% annually, suggesting passive maternal antibody is protective. We hypothesized that bighorn sheep humoral immune responses against Movi are less effective than those of domestic sheep. We developed a flow cytometry assay to test the ability of domestic and bighorn sheep serum antibodies to neutralize Movi in vitro. Sera from cELISA seropositive and seronegative bighorn sheep and domestic sheep were incubated with Movi for 30 minutes at 35C in 5% CO_2. The mixture was added to SP4 mycoplasma broth media and incubated for 48 hrs at 37C on an orbital shaker. A nucleic acid stain was used to label Movi and flow cytometry was used to measure and compare Movi concentrations over time to produce growth curves. A polyclonal rabbit anti-Movi antisera, known to impair Movi growth in an agar diffusion assay, was used as a positive (growth-inhibiting) control. No Movi growth inhibition was observed using serum from either cELISA seronegative or seropositive domestic or bighorn sheep. This data suggests that neither domestic nor bighorn sheep mount humoral immune responses that neutralize Movi growth, and therefore that the observed resistance of neonatal domestic lambs to Movi infection likely results from a different mechanism.

Maternal Investment Partitioning of Bighorn Sheep: Do Chronic *Mycoplasma* Shedders Exhibit a Superiority Complex?

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Life history theory predicts how natural selection should shape the way iteroparous individuals, such as bighorn sheep (*Ovis canadensis*), should partition resources to optimize their survival and reproductive success. Reproduction is energetically costly due to maternal care and includes provisioning milk intake and vigilance. Maternal care results in a fitness deficit for the dam causing a maternal investment trade-off between current reproduction and the long-term survival of the dam. In species in which male reproductive success exceeds that of females, extra parental investment would favor sons over daughters. The Trivers-Willard hypothesis predicts that dams in superior health invest more heavily in the progeny sex with greater expected lifetime reproductive success. Our research objective is to compare offspring investment, survival, and progeny sex ratios for bighorn sheep relative to the pneumonic pathogen shedding status of females. We predicted (1) bighorn sheep dams will differentially partition parental investment based on the female's current pathogen shedding status with negative ewes investing greater in offspring compared to positive ewes which conserve resources for subsequent reproduction; and (2) negative females differentially partition greater resources to male lambs to increase reproductive

payoff; whereas, positive ewes produce more female lambs that are less costly to raise than males. Our preliminary findings, however, suggest maternal investment was similar ($P = 0.402$) among shedding groups, indicating that pneumonic ewes exhibit more fitness plasticity than previously supported in the literature by exhibiting the ability to invest in offspring as much as ewes in superior health. Our preliminary results do not support the Trivers-Willard hypothesis ($P_{negative} = 0.527$, male:female = 0.6:0.4; $P_{positive} = 1$, male:female = 1:1) suggesting that positive ewes may favor current reproduction over long-term survival. Identifying life history trade-offs between pathogen shedding dams and their offspring provides information critical to management of declining bighorn sheep populations.

Dynamics of a Recolonizing Thinhorn Sheep Population in Southwest Yukon

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Dall's sheep (*Ovis dalli dalli*) numbers on Caribou and Nares Mountains in southwest Yukon were reduced at the turn of the century likely due to commercial harvest and increased access to previously remote areas, following the Klondike gold rush. During the 1970s and 1980s, small, transient groups (~10) were occasionally present. In 1990 a larger group (n = 23) recolonized the area and sheep have since remained on these mountains. Minimum population counts, obtained via helicopter surveys, were periodically collected in the summer from 1990 to 2015. This recolonization event provides a unique opportunity to examine the dynamics of an establishing thinhorn sheep population. Using a data-cloning framework with Markov chain Monte Carlo sampling, adult (i.e., non-lamb) population counts were fitted to a logistic growth model accounting for log-normally distributed observation error. Carrying capacity (K) and r_{max} were estimated as 64.5 (SE = 1.3) and 0.44 (SE = 0.02), respectively. Observation (tau) and process (sigma) errors were estimated as 0.035 (SE = 0.011) and 0.007 (SE = 0.012), respectively. During this period there was no detectable trend in lamb productivity. Further investigation into the mechanisms governing this population's apparent regulation around K will provide greater insight regarding thinhorn sheep carrying capacity.

Social dynamics of bighorn nursery groups

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We provide a detailed analysis of bighorn sheep social dynamics during six lamb pneumonia outbreak seasons, and then assess the role different demographic groups play in disease transmission. We found that dams, dry ewes, and yearlings all followed similar association patterns during summer. Animals of all three reproductive classes resided in large, stable groups prior to the birth pulse. The birth pulse was characterized by ephemeral small groups that stabilized into nursery groups about two weeks after peak lambing. While some of our study populations exhibited complete isolation between nursery groups, others underwent a slow fission-fusion process, facilitated by animals moving between several spatial "hot-spots". While number of associates did not stratify by reproductive or pathogen carriage status, interactions involving direct contact varied substantially between reproductive groups (dams with lambs vs. dry ewes and yearlings). Non-reproductive animals rarely directly contacted their peers, whereas lamb-to-dam and lamb-to-lamb contacts were common. Although yearlings and dry ewes regularly carried *Mycoplasma ovipneumoniae* in our study sites, non-reproductive animals apparently impose much lower forces of infection on lambs than do dams carrying these same pathogens; furthermore, we detect a small but significant protective effect of maternal antibodies on lamb survival.

Movements of a Localized Mountain Goat Herd: Implications for Harvest

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Tribal members of the Muckleshoot Indian Tribe have had a long history of harvesting mountain goats and using their hair, horns, hooves, bones, meat, and other parts for a variety of extremely important cultural purposes. Goat numbers near the Muckleshoot Reservation in the White River watershed have declined and as a consequence harvest opportunity in this area has ended. The Tribe conducts annual helicopter surveys of mountain goats in areas not far from the Reservation. We were interested in assessing if goats found in one area of the White River are migratory and are part of a larger east Cascades sub-population that could be large enough to allow harvest, or if they were a localized isolated herd. We radio-marked 4 male and 1 female goats out of an estimated 10-15 goats to document movements and migrations. We used two types of GPS collars that transmitted locations to satellite and relayed them to us. One type recorded locations at 9 hour intervals, and the other at 23 hour intervals. Both collar types collected adequate data to reveal that goats in this localized area are non-migratory and represent a small herd that would not be sustained if harvest occurred.

Limiting factors of bighorn sheep population performance in central and southwestern Idaho.

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Population and genetic connectivity, dispersal, and habitat preferences of bighorn sheep (*Ovis canadensis*) populations in central and southwestern Idaho is poorly understood. In addition, the health status, risk of disease introduction and transmission, and disease impact on population performance has not been clearly delineated. Answers to these questions are paramount to understanding the limiting factors for these populations and directing effective management programs. In March 2016, we captured 60 bighorn sheep, 30 each in the East Fork of the Salmon River and Owyhee Mountains, and fitted them with GPS collars. Data collected from these individuals will be analyzed to determine seasonal movements and range use, assist current Forest Service/IDFG domestic sheep/goat-wild sheep risk assessments, lamb production and survival, cause specific mortality, and inform potential bighorn sheep habitat models. In addition, samples were collected to measure health status and body condition scores were assigned to each animal. Past aerial survey data and movement data from collared individuals is being gathered and analyzed for inclusion in the dataset. Hunter harvest data are also being incorporated. Additional efforts will be directed in the East Fork of the Salmon River drainage to measure fine-scale habitat characteristics and nutrition.

Investigation of the *Mycoplasma ovipneumoniae* p113 Gene as a Potential Virulence Predictor of Pneumonia Outbreaks in Bighorn Sheep

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When developing solutions for complex and persistent wildlife diseases it is important to understand the virulence mechanisms of causal pathogens. In the case of bighorn sheep (*Ovis canadensis)* pneumonia, there is strong evidence that *Mycoplasma ovipneumoniae* (Movi) is the causal agent, but there is incomplete knowledge about Movi virulence factor(s). One proposed Movi virulence factor is P113, a candidate adhesin (a molecule involved in the binding of a bacterium to the host cilia) encoded by the *p113* gene. In our study we tested the hypothesis that the Movi *p113* DNA sequence is associated with virulence, as reflected in the severity of pneumonia outbreaks in bighorn sheep populations. This hypothesis predicts: a) that *p113* sequences should reflect increased selection (dN/dS ratio) relative to housekeeping genes due to its role in

virulence, b) that *p113* and 'housekeeping' genes may exhibit discordant relationships as a result of that selection and c) that therefore outbreak population mortality rates may be associated with clustering of either *p113* or housekeeping gene sequences. To test our hypothesis we performed a phylogenetic analysis on forty Movi strains isolated from forty pneumonia outbreaks that occurred in bighorn herds in western North America between 1995 and 2015. We amplified and sequenced a 285 bp segment of *p113* for each strain, and obtained the DNA sequences of two housekeeping genes *rpoB* (562 bp) and *gyrB* (400 bp) for the same strains from a pre-existing database. Using these sequences, we constructed phylogenetic trees for *p113*, *rpoB*, and *gyrB* using maximal parsimony and Bayesian approaches. Our data indicate that a) *p113* exhibits higher dN/dS than housekeeping genes, showing greater selection effects, b) *p113* topology exhibits different clustering than the housekeeping genes, consistent with different selection, and c) that neither the *p113* nor the housekeeping sequence clusters are significantly associated with outbreak severity.

ASSOCIATING ALLELIC DIVERSITY AND *MYCOPLASMA OVIPNEUMONIAE* SHEDDING HISTORIES IN BIGHORN SHEEP

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Understanding the complex dynamics between genetic diversity and disease in bighorn sheep (*Ovis canadensis*) populations is of growing importance. Genetic homogenization and infectious bronchopneumonia continue to cause bighorn sheep population declines. Epizootic bronchopneumonia is a respiratory disease of high morbidity and mortality and is considered the most significant limiting factor of bighorn sheep populations. Due to the polymicrobial nature of bronchopneumonia, the etiology of the disease is intensely disputed. One primary pathogen under heavy investigation is *Mycoplasma ovipneumoniae* (*M. ovi*). *M. ovi* is a bacterium that results in respiratory disease in sheep and goats worldwide. Polymorphic MHC allelic variants have been associated with susceptibility and resistance to infectious diseases in domestic and bighorn sheep. Although recent studies have associated genetic diversity to internal parasite loads, the association between heterogeneity and *M. ovi* shedding patterns in multiple populations of bighorn sheep has not been addressed. Our objective is to compare allelic variation among 9 source populations and associate the genetic diversity of individual bighorn sheep within pathogen shedding groups. Individual sheep will be classified in 1 of the 3 shedding status groups: positive, negative, or intermittent. Shedding groups will be determined by collecting nasal and oropharyngeal swabs at ≤6 week intervals. We will compare loci to determine if they differentially affect genetic diversity and *M. ovi* shedding pattern dynamics. We predict that (1) individuals with higher heterozygosity and/or unique polymorphisms in MHC alleles will be more resistant to *M. ovi* pathogens. By identifying the effect of genetic diversity and specific loci have on disease resistance, we will provide critical information regarding the highly argued etiology of this population-limiting disease. Furthermore, we can provide managers with scientific evidence to sustain successful long-term bighorn sheep translocations and augmentations while decreasing livestock producer-wildlife conflicts.

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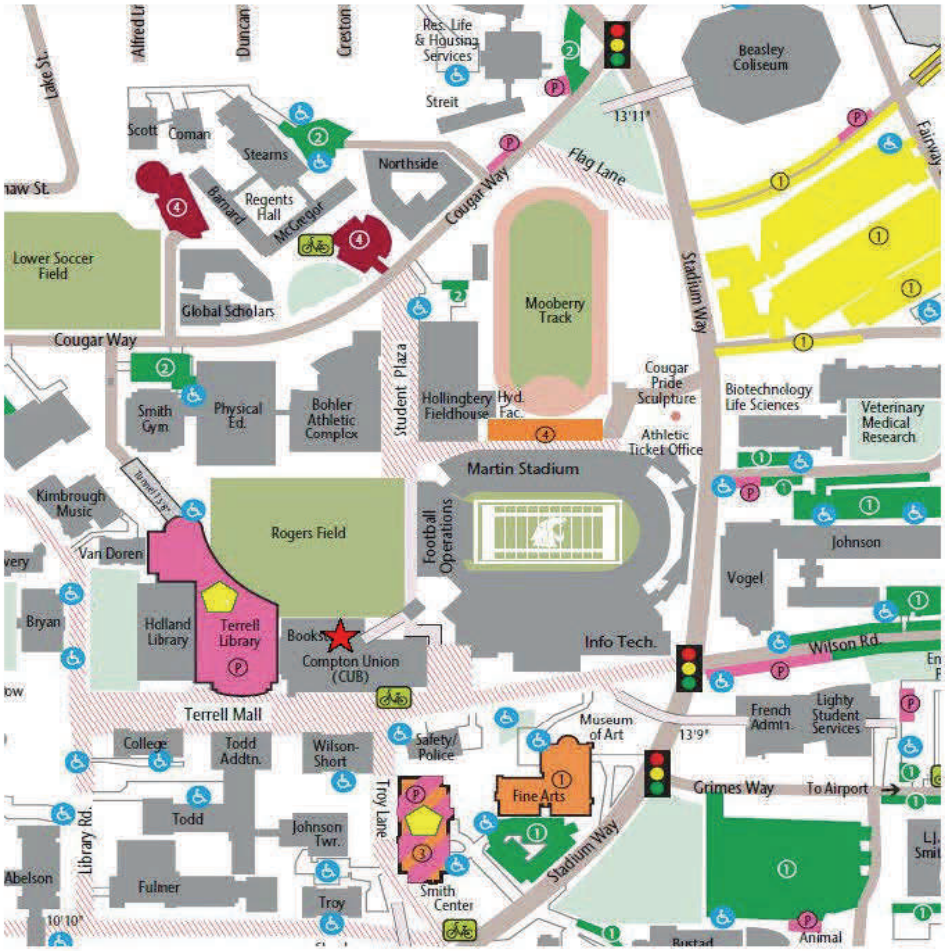

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