

Abstract list (in alphabetical order)

NILS ANDERSON¹: Developing a size-at-age relationship from hunter harvested bighorn sheep to support management relevant population models

ABSTRACT: Ram harvest is commonly constrained by a minimum size restriction to target mature males (e.g. 4/5 curl in Alberta). However, Alberta has lacked robust, data-driven tools to describe how rams grow to achieve this size, and therefore become legal for harvest. From a dataset of hunter harvested rams we used the age-specific cumulative length and the diameter of the circle described by the horn to back-cast the angular size-class of each sheep in each year of its life. The resulting size-at-age relationship can be used to distribute harvest across cohorts in an age-structured simulation model (e.g. assessing relative consequences of alternate management strategies) or to advance post-season survey results to determine pre-season availability of legal rams (e.g. setting tag numbers for a limited entry hunt).

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Laura Balyx¹ : Conflict and Coexistence with Mountain Goats in a Protected Alpine Landscape

Of the North American ungulates, mountain goats (*Oreamnos americanus*) are among the most sensitive to human disturbance. In British Columbia, one vulnerable population is found in Cathedral Provincial Park (CPP), where, mountain goats are subject to year-round disturbance from human recreation and helicopters. This dynamic has led to a number of mountain goat management issues, including, habituation and human-mountain goat conflict. Past research has documented altered foraging behaviour, movement patterns, and population dynamics in mountain goat populations affected by anthropogenic disturbance; however, the knowledge needed to create adequate management is often site- and context-specific. The goal of my research is to better understand the spatial ecology of human-mountain goat interactions within CPP. I will use GPS location data from 10 collared mountain goats to: 1) quantify mountain goat spatial ecology and map seasonal habitat use; 2) determine how helicopter use influences mountain goat movements and habitat use; 3) create a multi-species analysis template for future work in areas where human-ungulate conflict exists. The results of this study will improve mountain goat management within CPP – making it safer for both humans and wildlife – through the development of best management practices for recreation in sensitive mountain goat habitat.

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TOM BESSER¹ Mycoplasma ovipneumoniae in bighorn sheep epizootic pneumonia: Updating the conceptual model

ABSTRACT: *Mycoplasma ovipneumoniae* was initially recognized as a pathogen in wild sheep after an outbreak of fatal pneumonia in Dall's sheep that occurred in the Toronto zoo. Subsequently, it was first sporadically, then strongly and consistently detected in association with epizootic pneumonia in wild bighorn sheep populations across western North America. In this presentation, some of the key observations and research data that have provided evidence in support of this association will be reviewed, and the role of *M. ovipneumoniae* strain typing in addressing epidemiologic questions will be highlighted. Finally, some observations that lead to confusing or contradictory interpretations will be briefly discussed. The presentation will conclude with a short list of outstanding issues and research questions.

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KEVIN A. BLECHA¹ and Karen A. Fox²: Bighorn movement and domestic sheep presence surrounding a case of acute fatal pneumonia in a bighorn sheep

ABSTRACT: Mortality of bighorn sheep (*Ovis Canadensis*) after contact with domestic sheep (*Ovis aries*) has been documented in controlled pen studies, and through anecdotal observations in the wild. As a result, euthanasia of bighorns in contact with domestic sheep has become a routine management strategy for controlling introduction of pathogens to bighorn herds. Information regarding bighorn behavior before, during, and after contact with domestics may help further guide management practices. While studying the movements of a bighorn meta-population, we detected an acute pneumonia fatality of a GPS telemetered bighorn after contact with a recently introduced pen containing three hobby domestic sheep, immediately adjacent to a bighorn sub-herd's home range. GPS data on this and other telemetered bighorn in the vicinity revealed a variety of interesting movements temporally proximate to the contact event. Respiratory disease was not identified in any of the domestic sheep by routine veterinary exam. However, nasal and pharyngeal swabs confirmed the presence of respiratory disease-associated pathogens in all three domestic sheep. One domestic sheep was culled and necropsied revealing chronic upper respiratory disease. Coincidentally, in the years leading up to this event, this small bighorn sub-herd was already trending toward extirpation due to an aging herd and near-zero recruitment, possibly facilitated by chronic disease presence in certain bighorn individuals. Although various factors prevented euthanasia as a management strategy for the in-contact bighorn, the GPS telemetry data from this herd provides insights as to how pathogens could be contracted and subsequently spread to other bighorn.

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FRANCES CASSIRER¹, Tom Besser², Raina Plowright³, Kezia Manlove⁴, Brandi Felts⁵, Tyler Garwood⁵, Jon Jenks⁵, Mike Cox⁶, Paul Cross⁷, Andy Dobson⁸, Jack Hogg⁹, Pete Hudson¹⁰, Matt Jeffress¹¹, Chad Lehman¹², Amy Lisk¹³, Pat Matthews¹⁴, Logan Weyand², Paul Wik¹⁵, Peri Wolff⁶, and Dan Walsh¹⁶: The Role of Bighorn Ewe Infection Status in Managing Pneumonia in Lambs

ABSTRACT: Spillover of the bacterium *Mycoplasma ovipneumoniae* (Movi), can have long term negative demographic impacts on bighorn sheep (*Ovis canadensis*) populations, principally through chronically low lamb recruitment associated with pneumonia-induced mortality. Despite the devastating respiratory disease epidemics often observed in all age classes on first exposure to Movi, most survivors eventually clear infection. Some individuals do not however, and they can become persistent carriers. We conducted experiments in free-ranging and captive bighorn sheep to test the hypothesis that recurring pneumonia epidemics in lambs are triggered when persistent carrier dams transmit Movi to lamb nursery groups. We tested individual sheep repeatedly over at least two consecutive years in two captive research facilities and four free-ranging populations presenting lethal pneumonia in lambs to identify intermittent and persistent carriers of Movi. We then moved persistent carriers from free-ranging populations to captivity and conducted lamb survival trials in pens with and without persistent carriers. We observed no Movi, no respiratory disease, and increased lamb survival in populations and pens without carrier ewes, whereas high rates of lamb morbidity, Movi infection, and low survival were observed in populations and pens with carrier ewes. We also identified cofactors that may contribute to variation in shedding prevalence and persistence. The results of these experiments support the hypothesis that persistent carriers maintain Movi infection in bighorn sheep populations and are the cause of recurring pneumonia epidemics in bighorn lambs. These results have important implications for the epidemiology and management of pneumonia epidemics in wild sheep populations.

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GRANT CHAPMAN¹, Scott Jevons², Layne Seely², Kim Poole³, Rob Serrouya⁴, Irene Teske⁵, Anne Hubbs⁶, John T.Hogg⁷, Kathreen E. Ruckstuhl⁸, Dale Paton⁹: Mapping Alberta Bighorn Sheep Winter Range - RSF validation and inter-jurisdictional collaboration.

ABSTRACT: Poole et al., 2016 derived a winter range Resource Selection Function (RSF) for Bighorn Sheep Populations in the Elk Valley of BC which are contiguous with those in south west Alberta. Alberta Environment and Parks staff and collaborators utilized an Alberta updated 2020 Earth Observation for Sustainable Development of Forests (ESOD) spatial dataset and are validating this RSF (Chapman et al 2020 in progress) using additional gps collar data collected during 2002-2020 (by Hogg,

Paton, Ruckstuhl and Parks Canada). Albertan RSF values are being derived and validated using 95% kernel home ranges and methods similar to k-fold cross validation (Boyce et al 2002). A Spearman's rank correlation coefficient is being calculated between the area-adjusted frequency for each class and the class rank (1-10). Preliminary results of the Spearman correlation using a sample of collar data indicate a significant positive association between the RSF values and winter habitat use (P=0.005). These results are in progress and being completed in October 2020 and demonstrate the utility of RSF's in describing sheep habitat use at the inter-provincial scale and highlights the benefits of multi-agency collaboration and data sharing, and have already been used to efficiently inform prescribed burning planning in the Canmore, AB area. Additional efforts are underway to further extend these maps to northern Alberta sheep ranges where a Northern RSF had been developed. The supporting geographical information system products and methods may enable efficient creation of similar products for adjoining agencies.

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[SAMUEL DEAKIN¹, Jamieson C. Gorrell², Jeffery Kneteman³, David S. Hik^{1,4}, Richard M. Jobin⁵, and David W. Coltman¹: Spatial genetic structure of Rocky Mountain bighorn sheep *Ovis canadensis canadensis* at the northern limit of their native range](#)

ABSTRACT: The Canadian Rocky Mountains are one of the few places on Earth where the spatial genetic structure of wide-ranging species have been relatively unaffected by anthropogenic disturbance. We characterised the spatial genetic structure of Rocky Mountain bighorn sheep (*Ovis canadensis canadensis* (Shaw, 1804)) in the northern portion of their range. Using microsatellites from 1495 individuals and mitochondrial DNA sequences from 188 individuals, we examined both broad and fine scale spatial genetic structure, assessed sex-biased gene flow within the northern portion of the species range, and identified geographic patterns of genetic diversity. We found that broad-scale spatial genetic structure was consistent with barriers to movement created by major river valleys. The fine-scale spatial genetic structure was characterized by a strong pattern of isolation-by-distance, and analysis of neighborhood size using spatial autocorrelation indicated gene flow frequently occurred over distances of up to 100 km. However, analysis of sex specific spatial autocorrelation and analysis of mitochondrial haplotype distributions failed to detect any evidence of sex-biased gene flow. Finally, our analyses reveal decreasing genetic diversity with increasing latitude, consistent with patterns of post-glacial recolonization of the Rocky Mountains.

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JESSE DEVOE¹, Blake Lowrey¹, Kelly Proffitt², Robert Garrott¹: A Home on the Prairie? Restoration Potential of Bighorn Sheep in Montana's Prairie Region

ABSTRACT: Efforts to recover Montana's bighorn sheep (*Ovis canadensis*) have focused primarily in the mountainous western region; however, rugged areas in the eastern prairie region were historically occupied by bighorn sheep. Currently, only 4 populations exist in this region and are some of the state's most abundant and stable populations. We predicted that potential habitat and restoration opportunity likely exists in the prairie. We used GPS collar data collected during 2014–2018 from 2 bighorn sheep populations located along the Missouri River in Montana to estimate a resource selection model. We first extrapolated model predictions across Montana's prairie region to understand the spatial distribution of predicted habitat and restoration potential of bighorn sheep. Second, within an estimate of bighorn sheep historic range, we estimated the abundance of bighorn sheep that the predicted habitat could potentially support. Resource selection was most strongly associated with terrain slope and ruggedness, canopy cover, and an NDVI metric. Within currently unoccupied areas of the historic range, the model predicted 7,211 km² of habitat, with about half (55%) managed by public land agencies. We estimated that these unoccupied areas of habitat could support 1,327–3,457 bighorn sheep, an increase in the abundance of Montana's prairie bighorn sheep of 1.9–3.2 times. Our results demonstrate substantial potential for restoration opportunities of bighorn sheep in eastern Montana. Broad restoration of bighorn sheep across the prairie region would likely require strong collaboration among and between public resource managers and private landowners given the heterogeneous landownership patterns.

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GRACE ENNS¹, Bill Jex² and Mark S. Boyce¹: Stone's sheep lambing habitat selection in the Cassiar Mountains, British Columbia

ABSTRACT: Parturient wild sheep are known to use steep, rugged terrain at high elevations during parturition events to avoid predation on newborn lambs. Lambing habitat selection studies in North America have largely focused on bighorn sheep, and this is the first study of its kind on Stone's sheep (*Ovis dalli stonei*), a subspecies of thinhorn sheep residing predominately in British Columbia. Our study focuses on a Stone's sheep population in the Cassiar Mountains, a relatively remote area with varying levels of landscape disturbance. Recent increases in human activity, including mining, snowmobiling, ATV use and highway traffic could threaten recruitment, creating a need for identifying critical lambing habitat. We equipped ewes in 2018 ($n=8$) and 2019 ($n=10$) with GPS radio-collars collecting relocations every 2hrs (2018) and 1hr (2019). Ewes confirmed pregnant ($n=17$) were outfitted with a vaginal implant transmitter. We estimated parturition events using step lengths from GPS relocations and information obtained from the vaginal implant transmitters. We found that timing and synchronicity of parturition events varied annually. We used resource selection functions to identify significant variables influencing habitat selection during the periods of parturition and lactation. Understanding lambing habitat selection will help wildlife managers to identify and conserve critical habitats for Stone's sheep recruitment in the Cassiar Mountains.

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MARCO FESTA-BIANCHET¹ and Michael B. Morrissey²: Despite denials, persistent harvest-based selection leads to the evolution of smaller horns in mountain sheep.

ABSTRACT: Multiple lines of evidence in the scientific literature show that when phenotype-based harvest of North American mountain sheep (*Ovis canadensis* and *O. dalli*) rams is intense, persistent for decades, over a large area, with no or limited possibility of rescue from protected areas, it will lead to evolutionary shrinkage of horns. Two recent papers that claim that evolutionary change is unlikely, irrelevant or rare, in fact show that such change is highly likely and has occurred under the management regime of bighorn sheep in Alberta. A model commissioned by the Journal Wildlife Management to show that evolutionary horn shrinkage is unlikely, when fitted with published values of additive and phenotypic variance for bighorn sheep horns predicts a decline in size consistent with empirical results from the Ram Mountain population. A broad analysis of temporal change in bighorn sheep horns in multiple jurisdiction, that concluded that there was no decline in most 'hunt units' in Alberta is based upon a questionable approach to statistical analyses and a biased technique to adjust horn size to 7 years of age. A meta-analysis of data presented in that paper reveals that horn size is likely declining in 93% of hunt units in Alberta and in 57% of units in the USA, confirming that the very liberal and highly selective management regime in Alberta has led to a decrease in horn size greater than those seen in most US jurisdictions, where bighorn sheep management is more conservative. Harvest-induced evolutionary change is a serious concern for harvest management of several mountain ungulates. It can be avoided by evolutionarily enlightened management strategies, particularly those that direct the harvest to rams aged 8 years and older.

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ELIZABETH P. FLESCH¹, Tabitha A. Graves², Jennifer M. Thomson³, Kelly M. Proffitt⁴, P.J. White⁵, Thomas R. Stephenson⁶, Robert A. Garrott¹: Evaluating Bighorn Sheep Restoration Using Genomics

ABSTRACT: Wildlife restoration often involves translocation efforts to reintroduce species and enhance genetic diversity of small, fragmented populations. We examined the genomic consequences of bighorn sheep (*Ovis canadensis*) translocations and population isolation, to enhance understanding of evolutionary processes that affect population genetics and inform future restoration strategies. We conducted a population genomic analysis of 511 bighorn sheep from 17 areas, including native and reintroduced populations with contrasting translocation histories. Our analyses determined that most examined populations were isolated from recent, unassisted gene flow, including two pairs of native herds that had past connectivity but were recently fragmented. To identify which augmentation and

reintroduction efforts made a genetic contribution, we synthesized genomic evidence across three analyses to evaluate 24 different translocation events. We detected five successful augmentations and eight successful reintroductions based on genetic similarity with the source populations. A single native population founded most of the reintroduced herds, suggesting that genetic diversity of founders may have been more important to successful reintroduction than matching environmental conditions. We looked for genetic signatures of adaptation to pathogen presence by comparing herds that recovered after respiratory disease die-off events to those that did not, to identify candidate genes important to the disease process in bighorn sheep. Finally, we examined the relationship between herd inbreeding and recruitment rates. Our results provide insight on genomic distinctiveness of native and reintroduced herds, the relative success of reintroduction/augmentation efforts and their associated attributes, and guidance for genetic rescue augmentations and reintroductions to aid in bighorn sheep restoration.

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EMMA C. GRUSING¹, Blake H. Lowrey¹, Jesse DeVoe¹, Robert A. Garrott¹: Evaluating Characteristics of Mineral Licks used by Two Mountain Ungulates

ABSTRACT A deficiency in trace minerals is a common cause of impairment to an organism's physiological functions which can negatively affect the demographic vigor of populations. Bighorn sheep (*Ovis canadensis*) and mountain goats (*Oreamnos americanus*) ingest soil at areas called "licks" to obtain trace minerals that are lacking in their diets. However, the mineral composition of licks the two mountains ungulates are seeking is not well documented. The purpose of this research was to gain insight into the chemical composition of licks used by bighorn sheep and mountain goats, as well as to characterize movements to lick sites by bighorn sheep. To accomplish this, we obtained soil samples from 17 lick sites used by bighorn sheep and mountain goats throughout Montana and Wyoming in autumn 2019. Samples were analyzed for the concentrations of 7 essential trace minerals: calcium, sodium, magnesium, sulfur, copper, selenium, and zinc. We combined these analyses with similar published data to characterize general patterns of trace minerals obtained by the two species. To characterize movement behavior likely associated with use of lick sites, we analyzed a large dataset of GPS radio-collar locations from 5 bighorn sheep herds throughout Montana. Many of the instrumented individuals made short-duration, and in some cases long distance, movements to low elevation sites in the summer months. We hypothesize that these elevational movements were the result of ewes, likely accompanied by lambs, travelling to licks to avoid deficiencies possibly caused by lactation and the switch from dry to succulent forage in the spring.

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N. JANE HARMS¹, Kristenn Magnusson¹, Meghan Larivee¹, Maud Henaff¹, Mary Vanderkop¹:
Mycoplasma ovipneumoniae surveillance in Yukon wildlife

ABSTRACT: The bacterium *Mycoplasma ovipneumoniae* (*M. ovi*) has been implicated in outbreaks of pneumonia in bighorn sheep in British Columbia, Canada and the western United States. In Yukon, *M. ovi* has been identified as a pathogen of potential health concern for thinhorn sheep and mountain goats, although no outbreaks of pneumonia have been detected to date. Since 2015, over 450 nasal swabs samples have been collected from harvested thinhorn sheep and mountain goats throughout Yukon and tested for *M. ovi*. Given the recent detection of *M. ovi* in caribou, moose and thinhorn sheep in Alaska, USA, over 160 caribou, moose, deer, elk and muskox samples from Yukon have also been tested for *M. ovi* since 2018. To date, *M. ovi* has not been detected in any wildlife samples. Increased surveillance efforts in wild species is occurring by providing hunters with sample kits in order to collect higher quality samples. *M. ovi* is carried by domestic sheep and goats, and contact between wild sheep or goats and domestic small ruminants is implicated in the transmission of the pathogen and initiation of outbreaks. On January 1, 2020, a control order under the *Animal Health Act* came into effect in Yukon, intended to reduce the risk of transmission of respiratory pathogens, including *M. ovi*, from domestic animals to wildlife.

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WAYNE E. HEIMER¹: Management Update and Summary: Alaskan Dall Sheep 2020

ABSTRACT: The Dall sheep (*Ovis dalli dalli*) management scene in Alaska has been vibrant in recent years. Major events resulting from the “resident preference revolt” (Heimer 2012) included re-discovery of existing management plans and formation of a resident-preference special interest group. Additionally, challenges to the age-based harvest rate calculation (*ibid*) have been addressed. Continent-wide interest in *Mycoplasma ovipneumoniae* (*M. ovi*.) drove the Alaska Department of Fish and Game to conduct a wide-spread *M. ovi* survey. An apparent *M. ovi* DNA has been found throughout Alaska’s Dall sheep ranges, in mountain goats (*Oreamnos americanus*), and caribou (*Rangifer tarandus*). Speculation on the origin of this *M. ovi* DNA sparked a review of past domestic sheep imports to Alaska. Results will be included. Alaska has never experienced a typical bighorn pneumonia dieoff. The Alaska Wild Sheep Foundation’s aggressive advocacy of an *M. ovi*-free domestic sheep and goat population in Alaska has driven negotiations that appear poised to require testing of domestics for *M. ovi* prior to Alaskan import. An unexpected domestic-owner willingness to implement lethal farmstead-level separation of wild sheep from domestic sheep and goats makes

separation of species a more likely prospect than formerly appreciated. Although the management scene in Alaska will always be volatile, Alaska's Dall ram harvest management program appears stable at this time.

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PAMELA E. HENGEVELD¹, J. Clint Cubberley¹: Looking Forward: Insight from 20 Years of Wild Sheep and Goat Research in British Columbia

ABSTRACT: The last 20 years have spanned a period of social and technological change in professional biology, with notable influences on scientific research and management of wild sheep and goats. I discuss these influences in the context of 5 academic and applied research projects that I have led or contributed to in British Columbia (BC) over the last 20 years. These projects include: (1) the first forest industry partnerships to test adaptive management of mountain goat access to low-elevation mineral licks; (2) the first provincial assessment of horn growth trends in 2 bighorn sheep ecotypes; (3) assessment of meta-population recovery following BC's first bighorn sheep die-off attributed to pneumonia; (4) the first large-scale telemetry-based habitat use and demography study of thinhorn sheep, including the first radio-collaring of male sheep in a BC wild sheep research project; and (5) the emergence of psoroptic mange in BC bighorn sheep. I highlight results of scientific and management interest, and discuss professional challenges encountered in implementing these projects. I conclude by reflecting on lessons learned, and provide advice for improvements in wild sheep research and management.

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ADAM M. HERING¹, Neil B. Chilton², Tasha Y. Epp¹, Murray R. Woodbury¹: Determining the source of the *Psoroptes* outbreak in British Columbian bighorn sheep

Psoroptes mites have been documented in American bighorn sheep (*Ovis canadensis*) populations throughout the 19th and 20th centuries however they were not reported in Canadian populations until 2011. Determining the source of the outbreak is necessary to understand the risk to other naïve populations and of re-exposure following disease eradication efforts. We hypothesized that rabbits known to be infested in the area were the source of infestation in the Canadian herd. *Psoroptes* mites recovered from bighorn sheep in British Columbia and northern Washington were compared to those found on pet rabbits and on historically infested bighorn sheep in Nevada, Oregon and Idaho using morphologic and molecular methods. Measurement of outer opisthosomal setae lengths of mature male mites and sequencing of mitochondrial genes Cytochrome B and Cytochrome C oxidase subunit I was performed to compare the relatedness of mites collected from these different hosts. *Psoroptes* mites acquired from BC and northern Washington bighorn sheep were more morphologically and genetically similar to those collected from rabbits than those of bighorn origin collected south of Washington state. This is the first report of *Psoroptes* mites matching the rabbit ecotype (previously

called *P. cuniculi*) parasitizing bighorn sheep in a natural setting. This information suggests that the source of *Psoroptes* introduction into Canadian bighorn populations was through a disease spillover event from rabbits rather than from spread of the parasite through bighorn movements. *Psoroptes* susceptible hosts such as rabbits and horses should be considered when managing *Psoroptes* in bighorn sheep.

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ADAM HERING¹, Andrew Walker², Helen Schwantje², Tasha Epp¹, Craig McLean², Aaron Reid², Sean O'Donovan², James Pepper³, Cailyn Glasser⁴, Murray Woodbury¹: testing of new options for the treatment of *Psoroptes ovis* in bighorn sheep

Bighorn sheep (*Ovis canadensis*) in North America have shown significant declines after the outbreak of *Psoroptes*; a highly pruritic skin mite. Current treatment options have limited residual effects necessitating multiple drug applications, thereby limiting their value in free-ranging wildlife situations. This study aimed to identify a treatment for *Psoroptes* that is effective and appropriate for use in free-ranging bighorn sheep. A randomized, controlled, treatment trial was performed to test the efficacy of two different anti-parasitic drugs: eprinomectin and fluralaner, using injectable, oral, and topical routes of administration. Twenty naturally infected bighorn sheep were captured and housed in two purpose-built 5-acre enclosures. Animals were monitored daily and sampled monthly to assess disease resolution following treatment through evaluation of clinical signs, microscopic skin crust analysis, and antibody titer testing. Eprinomectin and the topical form of fluralaner were ineffective at the dosages used. The oral formulation of fluralaner showed encouraging results when administered at either 5 or 25mg/kg dosages. All orally treated individuals showed resolution of clinical signs lasting for one to four months following treatment despite cohabitation with other persistently infected individuals. Due to a lack of host immunity, the treatment of entire herds is essential for disease eradication. Residual effects of orally administered fluralaner present a new management option for the treatment of psoroptic mange in free-ranging bighorn sheep and the potential exists for remote application using medicated feeds, enabling a cost-effective, low-stress option for the management of this disease in affected free-ranging bighorn sheep herds.

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ANNE HUBBS¹, Mark Ball²: Alberta jurisdiction: “Little Bo-Peep, please test your sheep”
Managing disease risk in Alberta

ABSTRACT: Mitigating the risk of *Mycoplasma ovipneumoniae*-associated pneumonia in bighorn sheep from domestic sheep and goats has faced significant challenges. Of particular importance has been the impending risk of disease from domestic sheep and goat that, through current legislation, are permitted to utilize areas proximate to native bighorn home range. These domestic species are known to carry the bacterium *M. ovi.*, There have been localized outbreaks of pneumonia in southwestern Alberta, the most recent being in 2000. In response to this ongoing risk, wildlife managers from the government of Alberta have been working closely with stakeholders and other governmental agencies to develop a comprehensive plan to protect wild sheep populations. Public education and the development of a domestic/wild sheep separation policy are key components under this mandate. Furthermore, a large scale disease surveillance program was initiated in 2017 to determine the disease status of Alberta’s wild sheep populations. This will provide baseline data that will direct adaptive disease and population management in the area. This presentation will detail the collaborative efforts in the development bighorn sheep disease protection plan, the current state of the disease surveillance, and challenges that still require attention to maintain pneumonia free bighorn sheep in Alberta.

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JOSHUA P. JAHNER¹, Marjorie D. Matocq², Mike Cox³, Michael R. Buchalski⁴, Thomas I. Parchman¹:
Characterizing genetic differentiation and hybridization among California, Rocky Mountain, and desert bighorn sheep in Nevada to inform future translocations.

ABSTRACT: Over the past century, dozens of bighorn sheep herds have been reestablished via translocation, representing one of the most noteworthy conservation success stories in the history of North American wildlife management. In Nevada, translocations reestablished three bighorn sheep subspecies in relatively close proximity, allowing for the possibility of hybridization among genetically differentiated populations. Further, the genetic separation between California and Rocky Mountain bighorn sheep has been heavily disputed recently based on morphological variation, and a genetic assessment is needed to determine whether future translocations should either allow for mixing or maintain differentiation between these subspecies. We generated DNA sequencing data for more than 1,100 California, Rocky Mountain, and desert bighorn sheep from across Nevada to ask whether subspecies are genetically differentiated and if hybridization has occurred following the past 50 years of translocations. We find pronounced genetic differentiation among all subspecies and identify putative hybrids between desert and Rocky Mountain bighorn sheep. Our results provide preliminary evidence that reintroduced California and Rocky Mountain bighorn herds in Nevada are strongly differentiated based on genetic data, which could complicate future translocations that plan to mix these subspecies. Nonetheless, a range-wide evaluation of genetic variation across the ranges of

California and Rocky Mountain bighorn sheep populations is needed to further expand upon these results.

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BRIANNA JOHNSON¹, Kezia Manlove¹, Janice Stroud-Settles², Jace Taylor³, Annette Roug³ : Symptom progression and serological dynamics following introduction of a low-virulence *Mycoplasma ovipneumoniae* strain in a desert bighorn herd

ABSTRACT: *Mycoplasma ovipneumoniae* was detected in the previously-unexposed Zion desert bighorn sheep herd in July of 2018. The ensuing disease event produced symptoms similar to those reported during other introductions of *M. ovipneumoniae* into bighorn sheep herds, but without any documented mortality. Thus, the Zion herd provides us a unique opportunity to closely observe disease progression in a desert bighorn system after an apparently low-virulence pathogen introduction event. Animal testing in the 18 months following introduction indicated that *M. ovipneumoniae* continued to circulate in the Zion population, and mild symptoms were observed with some regularity. However, intensive monitoring throughout 2019 revealed a symptom progression in lambs that was substantially delayed from patterns reported in other systems. Additionally, serological patterns deviated from those of other well-studied bighorn populations, with animals producing lower percent inhibition values than is typically expected in infected herds. Taken together, these observations suggest that low-virulence *M. ovipneumoniae* events may exhibit fundamentally different dynamics, requiring a prolonged follow-up monitoring structure compared to that typically required for higher-virulence events. More generally, this work underscores the utility of collecting directly comparable data on disease progressions across a variety of bighorn herds.

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SOFIA KARABATSOS¹, Majid Irvani², Jeff Kneteman³, Anne Hubbs⁴, David S. Hik⁵: Distribution of bighorn sheep in their Alberta Rocky Mountain winter range over half a century

ABSTRACT: Long-term census data over large geographic areas offer an opportunity to track changes in wildlife distribution over time and space, and to detect areas of interest. We used 52 years of annual winter bighorn sheep surveys from the Alberta Rocky Mountains to describe bighorn sheep distribution in the greater part of their northern winter range. We determine (1) where bighorn sheep are distributed across the winter landscape; (2) how distribution changes across three periods from 1967 -

2018; (3) whether these distributions vary between ewes and rams. Lastly, two methods for analyzing spatial patterns were compared: Kernel density and hotspot analyses. Different clustered distributions and trends across time were observed for ewes and rams. Over time, ewe clusters changed from their northern historic range to new southern ranges, while ram clusters consistently occurred in their historic northern range. Ewes seemed to congregate more than rams, but all sheep congregated in larger areas during the recent period compared with earlier periods. In contrast with the hotspot approach, density analyses indicated a larger number of sheep congregations on the landscape, and no change over time. Our study provides the first macroscopic overview of bighorn sheep distribution in their largest and most intact range. These patterns of bighorn use of space over the last half a century add to our understanding of sheep resiliency to stressors and can inform the priorities for bighorn management in the future.

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KYLE H. KNOPFF¹, Meghan M. Beale², Christina Small³: Estimating Nutritional Carrying Capacity of Bighorn Sheep in the Elk Valley

ABSTRACT: Bighorn sheep (*Ovis canadensis*) in British Columbia's Elk Valley utilize high elevation grasslands during winter. Grasslands that serve as winter range are uncommon in the Elk Valley and may contribute to an upper limit to bighorn sheep population size. We developed an approach to estimate the nutritional carrying capacity for bighorn sheep winter range in the Elk Valley to determine whether availability and quality of winter range may limit bighorn sheep populations. Our aim was to produce a tool capable of supporting current and future resource management decisions by permitting bighorn sheep population size to be compared with nutritional carrying capacity of available winter range, including predicted changes in winter range carrying capacity over time. We developed a winter resource selection function using global positioning system telemetry data and mapped bighorn sheep winter ranges to constrain forage availability spatially. Species contributing to bighorn sheep winter diet were identified through a literature review of previous diet composition studies and consultation with experts. We estimated energy available to bighorn sheep at >2,000 vegetation plots using a relationship between the forage biomass of plant species consumed by bighorn sheep and percent cover of that forage species at each plot. Data were used to develop a spatially explicit forage model to estimate the distribution of energy across bighorn sheep winter ranges in the Elk Valley. Finally, we calculated nutritional carrying capacity by summing the energy available across winter ranges, weighted by relative selection, and divided this total by the average winter energetic requirements.

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KYLE H. KNOPFF¹, Aliah R.A. Knopff², Martin G. Jalkotzy¹: Mountain Goat Response to Human Activity in Jasper National Park

ABSTRACT: Mountain goats (*Oreamnos americanus*) typically exhibit low tolerance for human activity, and the degree to which they can adjust their behavior to accommodate human activity is poorly understood. The Glacier Skywalk, an interpretive glass-bottomed viewing platform and tourist attraction, was constructed in Jasper National Park in 2012 and 2013. Mountain goats extensively used the cliffs and other habitats below and adjacent to the Glacier Skywalk, and potential impact to mountain goats was a primary concern associated with the project. We used remote cameras to document seasonal, diel, and demographic use by mountain goats at the Glacier Skywalk over a 9-year period (2011-2019) and conducted focal animal sampling to measure responses to construction in 2013. Unlike most other places where they have been studied, goats at the Glacier Skywalk exhibited high tolerance for human activity. Seasonal and diurnal use by goats in 2012 and 2013 as the Skywalk was being built was like that observed prior to construction in 2011, and amount of use increased in some years during operations (2014-2017). Behavioral observations indicate that goats access the site primarily to obtain minerals. Goats did not abandon the site during construction activities, were observed on the cliff the same day as blasting and were also present during periods of high human visitation during operations. Effects to mountain goats were lower than predicted in an environmental assessment for the Glacier Skywalk, and our results indicate that some mountain goat populations can accommodate high levels of human activity, particularly around mineral licks.

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LAURA KROESEN¹, David Hik¹, Seth Cherry²: Laura Kroesen: Life on the edge: identifying mountain goat habitat hotspots in the high alpine

ABSTRACT:

Understanding where, why and how individual animals move is a fundamental biological question, but directly observing animal behaviour and the habitat they utilize is logistically challenging. Mountain goats (*Oreamnos americanus*) are elusive high alpine ungulates that live in steep and mountainous environments where it is difficult to directly observe and record behaviour. Hidden Markov models (HMM) are emerging as a useful method for predicting the behaviour of animals over space and time. We used HMM to identify hidden behavioural states and predict habitat hotspots of mountain goats. We evaluated how these inferred states can serve as a proxy for identifying habitat hotspots. We explored associated environmental covariates, time of day and distance from escape terrain, to explain these behaviours, and visited field sites selected by mapping fast and slow movements of mountain

goats to look for physical evidence of several behaviours, including foraging, travelling and bedding. We found mountain goats are most likely to forage during daylight hours away from escape terrain, travel within and away from escape terrain during the crepuscular periods and bed nearest to escape terrain in the night-time and afternoon. The inferred behavioural states were validated against the field observations. Our results illustrate that HMMs have the power to predict habitat hotspots of mountain goat and this approach may assist wildlife managers in assessing locations where mountain goats spend most of their time and the movement corridors that connect them.

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Margaret Langley¹: Limiting Factors on a Small Herd of Rocky Mountain Bighorn Sheep Resident in the Kicking Horse Canyon, near Golden, British Columbia.

This case study attempts to identify limiting factors on the herd of about 15 Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*), resident in the Kicking Horse Canyon, near Golden, British Columbia, using noninvasive techniques. These included fecal analysis (genetic variability, diet quality, parasite load and cortisol level), observations, vegetation sampling, habitat evaluation and citizen reporting to inform about herd health, genetic interchange, lambing success and recruitment, habitat quality and usage levels plus possible management options. Herd health results show heterozygosity at over 65% of the loci tested, good protein levels in summer and low levels in spring with low digestible energy, exposure to a range of parasites and baseline cortisol levels similar to those documented in other studies. The widespread presence of a lungworm, possibly *Muellerius sp*, could be of concern as stress levels on this herd potentially increase with upcoming highway widening. Lamb recruitment increased from one in 2018 and 2019 to two in 2020. The TransCanada Highway #1 occupies almost 20 % of the study area and BC Ministry of Transportation WARS data indicates that highway mortality is not uncommon. Seasonal habitat was identified and rated for quality, indicating that the study area contains relatively poor-quality habitat and is currently shared with white-tailed deer, mule deer and mountain goats. Plant species used by the sheep were identified along with usage levels and indicate use of shrubs, forbs, and grasses. Citizen reporting added to location data and effectively engaged the public. The data from this case study suggests that poor diet quality, highway-related mortality, and small amounts of suitable quality habitat play important roles in limiting this group of sheep. Numerous specific actions are recommended that could improve current habitat quality and access, including altering structures intended to keep wildlife off the highway but which have been found to be ineffective. Successful management practices could result from an understanding of population-specific limiting factors which can be determined using noninvasive techniques as highlighted in this case study.

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N. BETH MACCALLUM¹, ALICE C. PAQUET²: Colonization of a Reclaimed Landscape by Bighorn Sheep

ABSTRACT: Bighorn sheep have high fidelity to seasonal ranges and as such are thought to be poor colonizers but under certain conditions are quite capable of invading new habitat. We documented a colonization event of newly available habitat on the Gregg River Mine in west-central Alberta by bighorn sheep from nearby alpine habitat. Wishart et al (1998) described the rapid population increase of the nursery herd during this event. This paper is a companion article that documents and maps the pattern of reclamation and spatial occupation by bighorn sheep through time by sex/age class since the beginning of the life of the mine. Initial colonization was accomplished by ram groups using small amounts of reclamation. Colonization by nursery groups lagged by several years occurring after larger areas of reclamation became available but once established rapidly expanded into new habitat.

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DOUG MACWHIRTER¹, Hank Edwards², Meredith Van Wick³: Bighorn Sheep Disease Management in Wyoming

ABSTRACT: Like most jurisdictions at the turn of the 20th century, Wyoming's bighorn sheep suffered from unregulated take, introduction of novel pathogens, and loss of habitat. Although regulated hunting and translocations into historic habitats substantially increased numbers by the end of the 20th century, impacts from disease persist and statewide populations are currently lower than they have been in several decades. Recent statewide disease surveillance efforts have greatly increased understanding of pneumonia pathogens, while a statewide collaborative group and the actions of numerous non-governmental organizations (NGO's) and federal land management agencies have dramatically reduced the risk of pathogen introduction from domestic sheep to high-priority, core-native herds. Other specific management actions, including lethal removal of wandering bighorns and feral livestock have also reduced pathogen transmission risk in specific situations. Ongoing research efforts are focused on how respiratory pathogens, habitat, and ewe body condition influence lamb survival. Current perspectives and continuing challenges of disease management are also discussed.

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KRISTENN MAGNUSSON¹, N. Jane Harms¹, Mary Vanderkop¹, Jesse Walchuk², Matthew Larsen²: *Mycoplasma ovipneumoniae*: mitigating the risk of transmission in Yukon

ABSTRACT: In fall 2018, under the *Animal Health Act*, the Yukon Government announced a 5-year control order, which specifies fencing and testing requirements for farmers keeping domestic sheep or goats in Yukon. The order is intended to protect wild populations of thornhorn sheep and mountain goats from respiratory pathogens, specifically *Mycoplasma ovipneumoniae* (*M.ovi*), carried by domestic small ruminants. Prior to the order coming into effect on January 1, 2020 the Yukon Government provided compensation for farmers to either depopulate herds or attain compliance with the terms of

the order. We report the success of the government fencing program, summarizing the containment status of sheep and goat farms. We also report results of testing three monthly nasal swabs for *M. ovi*, including prevalence of *M. ovi* at the individual and herd level. Animals with a positive result were removed from the population, and a pilot treatment trail was completed in hopes of providing an alternative to removal. We will share the treatment trial outcome and report trends observed that relate test results with herd dynamics. Annual testing and containment inspections will be ongoing and permits, with conditions, will be required to acquire sheep and goats from outside Yukon. Actions taken under the control order have increased our understanding of the biology of *Mycoplasma ovipneumoniae* in domestic herds and we expect the results from repeat testing in future years to inform control measures.

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KEZIA MANLOVE¹, Kylie Sinclair¹, Lauren Ricci ¹, Brianna Johnson¹, Jace Taylor², Annette Roug², Mike Cox³: A preliminary look at what drives individual and herd response to *Mycoplasma ovipneumoniae*: Integrating information from focal herds and wider-scale monitoring

ABSTRACT:

The mechanisms that generate variation in severity of *Mycoplasma ovipneumoniae*-associated pneumonia in bighorn sheep remain poorly understood. Here, we present preliminary evidence associated with several plausible factors, including age, strain type, and herd substructuring, that might help determine outbreak severity. We combine data from a captive disease event, intermediate-term monitoring of more- and less-severe events, and wider-scale statewide monitoring efforts. Our findings suggest roles for age and condition in shaping immunological dynamics, and a key role for strain type in shaping longer-term outbreak severity. Additionally, this preliminary assessment underscores some important data requirements for understanding drivers of variation in outbreak severity more fully going forward.

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PETRA L. MCDUGALL¹, Kathreen E. Ruckstuhl²: Nonconscious behavioural mimicry is a cornerstone of effective group functioning in social animals.

Nonconscious behavioural mimicry is a cornerstone of effective group functioning in social animals. These constant behavioural adjustments to social stimuli allow a group to remain cohesive – if individuals act completely independent of one-another, a social group will eventually dissolve. Nevertheless, behavioural mimicry remains difficult to predict. Why does it occur in some situations and not others? We investigated the spread of vigilance behaviour in free-ranging bighorn sheep to evaluate whether several different variables affected the likelihood of vigilance behaviour being mimicked. These variables of interest relate to the relationship between the individuals in

proximity and the qualities of the vigilance behaviour. The results of two separate observational studies indicated that vigilance behaviour was more likely to spread 1) when the individual performing the behaviour was socially relevant (e.g. familiar, in close proximity, and similarly ranking), and 2) when a particular attribute of the behaviour was suggestive of important environmental stimuli. In the latter case only a single behavioural attribute (the absence of chewing during vigilance) predicted whether the behaviour would be mimicked. Chewing cessation was also strongly expressed during induced vigilance bouts (i.e. those stimulated by external events), prompting the question of whether these mimicry responses may be affected by experience. Future research would benefit from determining whether age (and therefore, learning) plays a role in the development of these trends. These results have implications for social structure (e.g. which individuals are likely to remain together when groups fission) and may help wildlife managers predict, and possibly mitigate, the effects of removing key individuals from a social web (e.g. in the case of relocations, predation events, or hunting/poaching events).

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CHARLES R. MENZIES¹: Mountain Goats and People: cultural resurgence as Indigenous methodology

Abstract: *Mati* -Mountain goats in Gitxaala's indigenous language- are iconic beings that play an important role in Indigenous histories and culture. This is an Indigenous led project involving social and ecological components of *Mati*/Gitxaala relations. It has been generations since we have hunted *Mati* in the old way by hand in intimate contact with *Mati*. Oral histories recount the close relations between our ancestors and *Mati*. Engaging in cultural resurgence acts of walking with *Mati* through our shared *laxyuup* (territory) in *K'tai* (a space within Pitt Island) builds our understanding of what it was like and how it can become. This paper describes the methods and results that have come from walking along side of, and learning from, *Mati* as a proxy for humans in the context of cultural resurgence –relearning and re-establishing our relations with *Mati* within our shared *laxyuup*.

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Peter Neuhaus¹, Susanne Schindler², Kathreen E. Ruckstuhl¹: Fast phenotypic change in a sexually selected trait: a new mechanism

Intra- and intersexual selection on male secondary sexual traits generally confer increased reproductive success in bearers with the most prominent traits. Strong selective harvest pressure of such trophy males can lead to a negative selection for trait size, and, over time, favour males with slow horn growth (genetics). However, this view ignores the role of plasticity in phenotypes and behaviour, and its impact on accelerating or decelerating the expression of sexually selected traits. We argue that changes in selection pressures (e.g. predation, selective harvest) may cause a cascade of behavioural responses, and a rapid change in trait size. We propose that selective removal of individuals with the most prominent traits induces behavioural changes in the surviving males, and thus in trait size (phenotypic

expression). To test this idea, we used an individual-based simulation, parametrized with empirical data of male bighorn sheep, *Ovis canadensis*. Our model shows that the expression (phenotype, not genotype) of the trait under selection (horn size) can be negatively impacted, if the biggest, most dominant males in the population are removed. The selective removal of prime males opens up breeding opportunities for younger, smaller males, which we predict would come at the expense of growth and maintenance. Indeed, we observed a rapid decline in average male horn length in our model. This result is further supported by empirical evidence in Alpine ibex, *Capra ibex*, which we will discuss. We argue that this nongenetic mechanism is important because it describes how heritable traits can rapidly change because of behavioural plasticity, before any genetic changes might be detectable.

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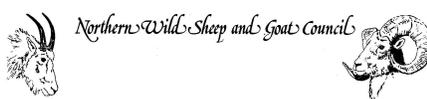
LAUREN RICCI¹, Mike Cox², Kezia Manlove¹: Identifying Environmental and Demographic Drivers of Foray Behavior in Bighorn Sheep

ABSTRACT: Transmission of *Mycoplasma ovipneumoniae*, the causative agent of pneumonia outbreaks in bighorn sheep (*Ovis canadensis*), is contingent on direct contact between naïve and infected hosts. Bighorns increase their chances of encountering infected bighorn or domestic (*Ovis aries*) sheep when moving outside their home range, especially in large exploratory movements termed forays. Therefore, understanding what drives bighorn sheep to leave their home range is an important step towards mitigating spillover risk. We examined the environmental and demographic factors associated with the initiation of foray events using GPS data from 48 herds across Nevada. We used a Hidden Markov Model to decompose animal movement trajectories into sets of home-ranging and foraging behavioral states based on the characteristics of the movement trajectories. We then investigated the drivers of foray behaviors by linking habitat and herd demographic variables to the time steps at which individuals transition from home-ranging to foraging behaviors. We identified four behavioral states, three consistent with the shorter, more circuitous movements associated with home-ranging behavior, and one characterized by the longer, more directed movements that define forays. We found that rams are more likely to foray than ewes and their forays last longer and cover greater distances. For both rams and ewes, foray events are more frequent during rut. The initiation of foray events is associated with the number of ewes in a herd, the ratio of rams to ewes within the herd, and the extent of an individual's viewshed.

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HELEN SCHWANTJE¹: A Walk on the Wild Side: BC Wild and Domestic Sheep Update

ABSTRACT: A summary of BC wild and domestic sheep Initiatives



AARON B.A. SHAFER¹, Sarah E. Haworth¹, Daria Martchenko¹, Jesse F. Wolf¹, KIANA B. YOUNG¹: From pellets to genomes: new tools provide novel insights into mountain goat ecology and evolution

ABSTRACT: Advancements in DNA sequencing technology combined with increased use of non-invasive sampling provide a unique lens to understand demographic and behavioural patterns in natural populations. We have several ongoing projects that use these novel tools with the goal of informing mountain goat management and conservation planning. Of note, we recently characterized the fecal microbiome of mountain goats and showed it changes within a population over time and could be used to distinguish populations. We have extended the microbiome assay by integrating it with GPS radio-collar data from 24 individuals where we have detected a link to movement and space-use patterns. We have also assembled the first mountain goat genome that will be used as a backbone for understanding population and adaptive processes in this species. Our genome-wide demographic analysis has shown a dramatic decline (i.e. reduced effective population size) of the species during the last ice age with no evidence of a range-wide recovery. Spatially genetic patterns assessed in 265 individuals from across the range appear to be driven almost exclusively by distance, with genetic variation strongly correlated to latitude ($r^2 = 0.83$). These new tools and analyses should be of interest to the wild sheep and goat research and management community.

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KYLIE SINCLAIR¹, Mike Cox², Peregrine Wolff³, Kezia Manlove⁴: Identifying drivers of bighorn sheep population recovery in the wake of pneumonia die-off events

ABSTRACT: Bighorn sheep populations across the Intermountain West are subject to disease pressure from the respiratory pathogen *Mycoplasma ovipneumoniae*. Although the effects of *M. ovipneumoniae*-associated disease die-offs are well documented, less is known about the factors driving long-term variation in post-die-off demographic responses. While many herds experience years to decades in which recruitment is less than 20 lambs per 100 ewes, some herds' lamb survival rates are able to rebound rapidly following die-off events. The reason why these herds recover quickly while others do not is currently unknown. Here, we assess the roles environmental, demographic, and pathogen-associated factors could play in shaping bighorn sheep herd recovery. Our analysis relies on more than 30 years of data from over 40 bighorn sheep herds across the state of Nevada. Our results suggest that herd demographic responses to *M. ovipneumoniae* vary dramatically across subspecies, and that environmental factors may be more important in shaping those demographic responses in desert bighorn than in Rocky Mountain or California bighorn herds. Our results could have important implications on prioritization of bighorn sheep recovery efforts throughout the Intermountain West.

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ROBERT SPAAN¹: Impact of *Mycoplasma ovipneumoniae* on juvenile bighorn sheep (*Ovis canadensis*) survival in southeastern Oregon and northern Nevada

Abstract: Determining the demographic impacts of wildlife disease is complex because extrinsic and intrinsic drivers of survival, reproduction, body condition, and other factors that may interact with disease vary widely. *Mycoplasma ovipneumoniae* infection has been linked to persistent mortality in juvenile bighorn sheep (*Ovis canadensis*), although mortality appears to vary widely across subspecies, populations, and outbreaks. Hypotheses for that variation range from interactions with nutrition, population density, genetic variation in the pathogen, genetic variation in the host, and other factors. We investigated factors related to survival of juvenile bighorn sheep reestablished populations in the northern Basin and Range ecosystem, managed as “California” lineage populations. We investigated whether survival probability of 4-month juveniles would vary by (1) presence of *M. ovipneumoniae*-infected or exposed individuals in populations, (2) population genetic diversity, and (3) an index of forage suitability. We monitored 121 juveniles across a 3-year period in thirteen populations in southeastern Oregon and northern Nevada. We established 4-month capture histories from semi-monthly observations of each juvenile and GPS-collared mother. All collared adult females were PCR-tested at least once for *M. ovipneumoniae* infection. The presence of *M. ovipneumoniae*-infected juveniles was determined by observing juvenile behavior and PCR-testing dead juveniles. We used a known-fate model with different time effects to determine if the probability of survival to 4-months varied temporally or was influenced by disease or other factors. We detected *M. ovipneumoniae*-infected juvenile mortalities in only two populations. Derived four-month juvenile survival probability in those populations was 22 times higher when the infection was not present. Detection of infected adults or adults with antibody levels suggesting prior exposure was less predictive of juvenile survival. Survival varied temporally but was not strongly influenced by population genetic diversity or nutrition, although genetic diversity within most study area populations was very low. We conclude that the persistence of *M. ovipneumoniae* can cause extremely low juvenile survival probability in translocated “California” bighorn populations, but found little influence that genetic diversity or nutrition affect juvenile survival. Yet, after the PCR+ adult female in one population died, subsequent observations found 11 of 14 (~79%) collared adult females had surviving juveniles at 4-months, suggesting that targeted removals of infected adults should be evaluated as a management strategy.

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CAELEY THACKER¹, Helen Schwantje², Thomas Iohuis³, Kathreen Ruckstuhl¹, Douglas Whiteside¹:
Respiratory Disease Pathogens in Thinhorn Sheep – Preliminary Findings and Review of Methods

ABSTRACT Thinhorn sheep (*Ovis dalli dalli* and *Ovis dalli stonei*) have significant economic, ecological, and cultural significance to northern communities, but little is known about their population and herd health status. Health is an important consideration for wildlife population resiliency and conservation. We are conducting a baseline herd health assessment of thinhorn sheep across jurisdictions by applying international sampling standards (WAFWA, 2009). We are evaluating comprehensive health measures including surveillance for exposure to infectious agents such as *Mycoplasma ovipneumoniae* and *Pasteurella* spp, nutritional status, fecal and hair cortisol levels, body condition, trace mineral and contaminant levels, and other biological indicators of health, incorporating genetic and genomic tools. We are using samples from live-captured and hunter-harvested thinhorn sheep. Remote locations and the time sensitivity of pathogens have previously prevented application of many tests that are now believed to be key to understanding the baseline health profiles of wild sheep. New sampling techniques, processing methods, and the development and application of standard operating procedures for bighorn sheep health testing are now available. We have detected *M. ovi* from live-captured Dall's sheep in Alaska, but not in Stone's sheep in British Columbia. Evidence of infection has been detected in Stone's rams harvested during the 2019 season, so further sampling efforts in key areas this winter is important to determine the infection status of these herds. We have isolated several commensal and potentially pathogenic respiratory bacterial species from tonsillar swab samples. Evidence of exposure to various other viral pathogens has been detected.

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KEVIN S. WHITE¹, David P. Gregovich¹, Taal Levi²: Climate and anthropogenic effects on mountain goat population dynamics in coastal Alaska

ABSTRACT:

Mountain goats (*Oreamnos americanus*) are an iconic, alpine adapted species that occur in remote mountain landscapes throughout northwestern North America. The species exhibits a slow life-history strategy in order to cope with the often strong negative effects of severe climate conditions on survival. Local populations are typically small, geographically isolated, genetically distinct and particularly sensitive to environmental and anthropogenic perturbations such as disturbance and harvest. To advance our understanding on mountain goat population dynamics and inform conservation decisions, we developed a climate-linked, sex- and age-structured population model based on demographic data collected from 447 mountain goats in 10 coastal Alaska populations over a 37 year time span. Specifically, we examined how projected changes in future climate (i.e. 10 different GCM-RCP scenarios) and anthropogenic harvest influence population viability. Our analyses indicate that projected future increases in summer temperature and declines in winter snowfall are likely to result in declining population trajectories for most scenarios. This occurs because the negative effect of increasing summer temperature on mountain goat survival is predicted to be stronger than positive effect of declining winter snowfall in our coastal Alaska study area; a situation that can only be temporarily ameliorated via distributional shifts to higher "thermoneutral" elevations (i.e. due to the

conical shape of mountains). We further determined that, given similar constraints, smaller populations were more sensitive to climatic and demographic stochasticity and, thus, more likely to decline than larger populations. Under contemporary climate conditions, anthropogenic harvest simulations indicated that populations <70 individuals should not be harvested to avoid >50% probability of decline; yet larger populations can sustain up to 2-4% harvest, depending on initial conditions. Overall, our analyses illustrate how climatic and anthropogenic factors can influence mountain goat population dynamics and provide a quantitative framework for promoting sustainable management and conservation of populations.

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STEVEN F. WILSON¹, Christina Small²: An Integrated Population Model for Rocky Mountain Bighorn Sheep in the Elk Valley, BC

ABSTRACT: The Elk Valley of southeast BC has a substantial population of Rocky Mountain Bighorn Sheep that are notable for their use of high-elevation winter ranges. The area is subject to extensive overlapping land uses including private land. Potential future threats may include the loss of high elevation winter range. Proactive mitigation and management is anticipated to contribute to the regional management objective of maintaining viable and ecologically sustainable populations across their native range. The objective of this project was to integrate the results of on-going research and inventory into a model that can be used to estimate the effect on the population of various stressors and mitigative management actions. The model is structured as a causal Bayesian Belief Network and includes 20 factors and associated relationships. The project involved drafting the structure and logic of the model collaboratively with a team of experts and then developing parameters for all of the factors based on available data and expert input. The completed model can function as a predictive tool to estimate the likelihood of a positive population trend, given the conditions of the different factors. Causal Bayesian Belief networks can blend empirical evidence with expert and traditional knowledge and can be used to characterize cause-and-effect pathways in ecological systems to support management planning and decision-making.

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PEREGRINE WOLFF¹: **ABSTRACT to come**

Funding Support

