RISK ASSESSMENT ON THE USE OF SOUTH AMERICAN CAMELIDS FOR BACK COUNTRY TREKKING IN BRITISH COLUMBIA

Final Report

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Division of Wildlife Conservation, Alaska Department of Fish and Game

Submitted by:

Centre for Coastal Health

900 Fifth St., Nanaimo, BC

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A. Executive summary

Risk, for the purpose of this report, is a composite measure that takes into account the probability or likelihood of an event occurring, the magnitude of impact of said event, and an interpretation of the uncertainty around the criteria used to estimate probabilities and impact. The Center for Coastal Health (CCH), on behalf of the British Columbia (BC) Ministry of Forests, Lands, Natural Resource Operations and Rural Development (FLNRORD) and the Division of Wildlife Conservation, Alaska Department of Fish and Game, set out to update a previous risk assessment by Stephen and Schwantje (2003) on the potential for South American Camelids (SACs) to transmit disease to wild ungulates in BC; to identify emerging diseases of SACs; to describe and evaluate recent findings regarding the epidemiology, diagnosis and control of pathogens that affect both SACs and other ungulates; and to document reports of pathogen transfer from SACs to wild or domestic ungulates. For this report, we focused mainly on pathogens that might impact the wild sheep and goat populations of BC, although other species such as Caribou (*Rangifer taraandus*), Elk (Roosevelt Elk, *Cervus canadensis rooseveiti* and Rocky Mountain Elk, *Cervus canadensis neisoni*), Deer (Mule and Black-tailed, *Odocoileus hemionus* and White-tailed deer, *Odocoileus virginianus*) and Moose (Northwestern Moose, *Acles andersoni;* Alaskan Moose*, Alces gigas;* and Shiras' Moose, *Alces shirasi*) were considered. As part of this risk assessment, the CCH conducted a number of research activities including; a rapid and targeted literature review of peer-reviewed and grey literature from 2007 to 2016; a review of government policies and documents from other jurisdictions regarding SAC use in backcountry areas; interviews of camelid infectious disease experts and wildlife managers; and an analysis of sample submissions from SACs to diagnostic animal health laboratories in two western Canadian provinces.

Our risk assessment activities identified seven SAC pathogens that were of greatest concern to wild ungulates in BC. These were *Mannheimia haemolytica* (*M. haemolytica*)*, Pasteurella* spp., contagious ecthyma (CE, parapoxvirus), bovine viral diarrhea virus (BVDV), *Mycobacterium avium paratuberculosis* (Johne's Disease)*,* Bluetongue virus (BTV) and *Mycobacterium bovis (M. bovis)*. Estimates of prevalence and disease transmission dynamics for these and other SAC pathogens in North America are very limited, due to gaps in surveillance, a lack of effective diagnostic tests, and the potential for an asymptomatic carrier state.

We found that there is high uncertainty about the probability of pathogen transmission from SACs to wild ungulates. We found no peer-reviewed publications documenting pathogen transmission from camelids to wild ungulates or to domestic sheep and goats for the identified pathogens. However, because there was almost no research examining the shedding and transmission dynamics for pathogens in camelid herds, or between camelids and other ruminants, a lack of peer-reviewed evidence should not be considered proof that transmission has not, or could not, occur. We did find anecdotal evidence that the introduction of trekking llamas near Atlin, Terrace and the Babine Mountains of BC (Skeena region) coincided with the first reports of CE in Mountain Goats (*Oreamnos americanus*) in these regions.

Overall, we assessed the composite disease risk posed to wild ungulates by SACs accessing backcountry areas as medium-high with medium associated uncertainty. This assessment was driven primarily by the

high impact and the medium-high risk posed by the respiratory pathogens *M. haemolytica* and *Pasteurella* spp., the medium-high risk posed by CE, and the medium risk posed by Johne's Disease. Mitigation could be undertaken to partially reduce risk posed by respiratory pathogens, although mitigation for CE and Johne's Disease is much more challenging.

It is important to note that over time, new pathogens might emerge in SACs that create significant new risk not discussed in this report. In particular, risk would increase significantly if SACs are documented to be susceptible to infection with *Mycoplasma ovipneumoniae (M. ovipneumoniae)* or *Mycoplasma conjuntivae (M. conjuntivae)*.

Uncertainty surrounding the probability of disease transmission from SACs to wild ungulates as a result of camelid trekking activities in BCs backcountry could be reduced with more research into prevalence and transmission dynamics for identified pathogens in llamas and alpacas; and into SAC health status and movements, with particular focus on SAC herds used for trekking in BC.

Until more information is available, banning camelids from key wild ungulate habitat is the most effective risk reduction strategy. However, where access is permitted, careful diagnostic screening for pathogens of concern and mitigation activities might be beneficial in partially reducing risk.

B. Background

A risk assessment is conducted when a decision about a certain action is unclear, such as when the facts about the issue of concern are unknown or equivocal, or when the threshold for making a decision is not apparent. Risk assessments aid in systematically identifying and considering evidence on the determinants of risk in a given situation. Strictly defined**,** risk is the probability of the occurrence of an outcome combined with the magnitude of impact from that outcome, although it may be affected by the level of uncertainty in a situation. Because risk perception can vary between different stakeholders for a variety of social, political, and economic reasons, cost-benefit analysis and surveys on social values may also be conducted to aid in decision making.

South American camelids (SACs)[1] are popular pack animals for back-country trekking and hiking excursions in many regions across North America, due in large part to their hardy nature and versatility. In 2003, Stephen and Schwantje predicted that demands to allow SACs into wilderness areas in BC would increase, and set out to evaluate the risk of pathogen transmission from SACs to wild ungulates in the province. Although Stephen and Schwantje (2003) defined criteria for high risk pathogens, they did not find documented evidence for the transmission of any pathogen from SACs to wildlife; citing the precautionary principle, they recommended that local, risk-based policies and practices be developed to manage disease risks to wildlife from SACs. A second risk assessment, following the guidelines set forth by the Canadian Wildlife Health Centre (CWHC) for "Health Risk Analysis in Wild Animal Translocations[2]", was released in 2009 (Garde et al., 2009). It identifies a number of pathogens that can infect domestic SACs, sheep and goats and that also have the potential to negatively impact Dall's Sheep and Mountain Goats. Again, the authors found no documented cases of pathogen transmission from SACs to wildlife. In 2015, Alaska National Park Service did not implement a proposal to ban llama and alpaca use in Alaska's backcountry in part to a lack of evidence for pathogen transmission from SACs to wild ruminants. The need for an updated risk assessment has become even more apparent in recent years, with public pushback causing the BC government to replace a proposed province-wide ban on SACs in backcountry areas with a reduced ban restricted to thinhorn sheep and Mountain Goat ranges in the northern half of the province.

For this report, the Center for Coastal Health (CCH), on behalf of the BC Ministry of Forests, Lands, Natural Resource Operations and Rural Development (FLNRORD) and The Wildlife Health Program of the fish and Wildlife Branch of the Division of Wildlife Conservation, Alaska Department of Fish and Game, set out to; 1) identify emerging diseases of SACs, 2) describe and evaluate recent findings regarding the epidemiology, diagnosis and control of pathogens that affect both SACs and other ungulates, and 3) collect evidence about the risk of pathogen transmission from SACs to domestic or wild ungulates. The CCH conducted a rapid and targeted literature review of peer-reviewed and grey literature, and supplemented this with interviews of camelid infectious disease experts and wildlife managers, a review of government policies and documents from other jurisdictions regarding SAC use in backcountry areas,

[1] Llama, alpaca, vicuna and guanaco are the four species of South American Camelids (SACs). They belong to the Order Artiodactyla. All SACs are non-native to North America, but llamas and alpacas are kept as domestic animals.
[2] The guidelines can be found online at http://www.cwhc-rcsf.ca/wildlife_health_topics/risk_analysis/

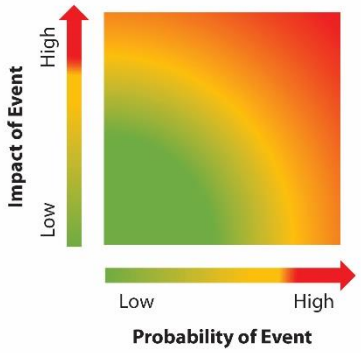
and an analysis of SAC sample submissions to the provincial diagnostic animal health laboratories in BC [Animal Health Centre (AHC)] and Saskatchewan (SK) [Prairie Diagnostic Services (PDS)]. Findings from these activities were used to estimate the risk (probability and impact) of disease transmission from SACs traveling in the backcountry of BC to local wild sheep and goats specifically, and to wild ungulates[3] more generally, and to describe the uncertainty associated with that risk. In addition, we developed a list of potential risk mitigation strategies and assessed their possible feasibility and effectiveness. The CCH did not undertake a cost-benefit analysis, nor did we set out to survey social values associated with camelid trekking in the backcountry.

C. Methods

C.1. Overview

For the purposes of this report, we define risk as a composite measure that takes into account the probability of the event occurring, the magnitude of impact of the event, and an interpretation of the uncertainty surrounding the criteria used to estimate probabilities and impact. A visual representation of this is provided in Figure 1. We highlight that decisions based on the content of this report may need to be periodically re-assessed in light of any future updates to our collective understanding of SAC pathogens and transmission dynamics to wild and domestic ungulates.

Figure 1: Visual representation of a risk assessment.



Probability

For this report, the *probability* is the probability that a wild ungulate will contract a pathogen from one or more SACs entering the ungulate range during trekking activities. Qualitative evaluation of this probability requires information about disease transmission that include:

1. The prevalence of the pathogen in SACs, particularly in the SAC population used for backcountry trekking in BC.
2. The likelihood and duration of asymptomatic or preclinical infection in SACs.
3. The amount of pathogen shed by infected SACs.
4. The role, if any, that co-housing SACs with ruminant livestock (sheep, goat and cattle primarily) has on the transmission of pathogens to SACs.
5. The probability that a pathogen will transmit from infected SACs to wild ungulates. This is dependent upon;
    a. Temporal overlap in range use by SACs and wild ungulates.
    b. Frequency and duration of SAC visits to wild ungulate habitat.
    c. Method of pathogen spread.
    d. Environmental survival of the pathogen.

[3] For this report, wild ungulates are the thinhorn and bighorn sheep, mountain goats, caribou, elk, moose and deer species that live in BC, although our specific focus is the thinhorn sheep and mountain goat populations.

6. The probability that a wild ungulate population will be infected by the pathogen. This is dependent upon;
    a. Ungulate species or population innate or genetic susceptibility/resistance to the pathogen.
    b. Presence of other diseases or stressors in either SAC or wild ungulate populations (e.g. parturition, low food availability).
    c. Health and environment

For this report, probability was assessed in two components. The first, which we termed the probability of SAC infection, was the probability that an infected SAC might enter backcountry areas during trekking activities. This probability was dependent upon the prevalence of the pathogen in SACs used for trekking in BC and the likelihood and duration of asymptomatic shedding. Pathogens with asymptomatic infection or long pre-clinical phases would be much more likely to be inadvertently carried into backcountry areas by SACs than those that resulted in obvious clinical signs or debilitation. The second, which we termed the probability of transmission, was dependent upon the amount of pathogen shed by SACs, the method of pathogen spread, the environmental resilience of the pathogen and the susceptibility of individual wild ungulates to the pathogen.

Impact

For this report, the *impact* is the anticipated impact of any identified pathogen on wild ungulates in BC from a transmission event. Pathogens are expected to impact different ungulate species, and even different populations of the same species, differently due to variation in population size and structure, innate susceptibility to the pathogen (i.e. naïve animals are generally considered more susceptible), and the presence or absence of other environmental and health stressors that may influence the effectiveness of an immune response by the animal. We focused primarily on impact on wild sheep and goat populations in BC, as these vulnerable populations are considered to be naïve to many domestic livestock pathogens, and utilize habitat that may be attractive to llama trekkers.

Information gathering activities

This review set out to develop a list of pathogens that might create risk of disease transmission from SACs to wild ungulates, and to gather information about the probability and impact of those pathogens. To do this, we undertook a review of scientific and grey literature, a review of camelid case submissions to two provincial veterinary diagnostic laboratories, and an interview tool to collect expert knowledge and opinion about the topic.

C.2. Review of scientific and grey literature, and government policies

Two previously completed risk assessments (Garde et al., 2009; Stephen & Schwantje, 2003) that examined the risk of disease transmission from SACs to wild ungulates were reviewed for relevant information and references. Information from the two reports were used to inform the formulation of search terms for the subsequent literature review.

The rapid, targeted literature review was conducted using PubMed, Web of Science, Google Scholar and CAB Abstracts, to search for peer-reviewed literature. The common search phrase combined “llama” or

"alpaca" or "camelid", with "bighorn" or "caribou" or "reindeer" or "elk" or "Mountain Goat" or "mt. goat" or "mt goat" or "thinhorn sheep" or "Dall's sheep" or "Stone's Sheep" or "cattle" or "bovine" or "ovine" or "caprine" or "goat" or "sheep" or "livestock"; and "transmission" (a full list of keywords are provided in Appendix 1. Literature search keywords). Papers were included if they had been published after 2007, from any English-speaking country but with a preference for North America, and mentioned pathogen transmission between camelids and domestic or wild ungulates. Papers that described case reports or research on emerging pathogens in camelids, especially of pathogens known to also effect sheep, goats and cattle, were included for further review.

Articles were initially included or excluded from further review based on the relevance of the title. Where there were more than 100 returned articles, the titles of the first 100 articles were reviewed and any remaining articles were examined in groups of 30 until 150 articles were examined or no article was included in 30 consecutive articles. The abstract for all articles included based on title review were then reviewed for relevance, and the article rated using a three-star system with three stars indicating high importance (article/document significantly contributes to answering research questions), through to one star indicating low importance (article/document may assist with answering the research questions). A full-text copy of three-star publications were retrieved and reviewed, and their 'literature cited' section was further reviewed for potentially relevant articles. These articles were also subjected to a forward search using "web of science" to examine and include any articles that had cited it.

A Google search was performed to determine what regulations exist with regard to SAC use and/or restrictions in wilderness areas. Search phrases included 'llama' or 'camelid', and 'backcountry' or 'ban' or 'park'. Individual websites for the United States government[4], the United States National Park Service, Parks Canada[5], the Western Association of Fish and Wildlife Agencies[6], the Alberta (AB) provincial government, and the state government for nine western states (Arizona, California, Colorado, Idaho, Montana, Oregon, Utah, Washington, and Wyoming) were more specifically searched for documents on SAC restrictions in backcountry areas. Searches were also performed for hunting regulations for AB and the nine western states. The wildlife state departments for the nine western states were contacted by phone to enquire about regulations on SACs in backcountry areas that were not posted online.

Additional resources that were either suggested to the CCH by the FLNRORD, or that were found as part of the literature review and Google search, were reviewed for relevance to this assessment. This included the Journal of Small Ruminant Research[7], the Northern Wild Sheep and Goat Council proceedings[8], the Alpaca Research Foundation[9], the International Camelid Institute[10], the International

[4] https://www.usa.gov/
[5] http://www.pc.gc.ca/eng/index.aspx
[6] http://www.wafwa.org/
[7] http://www.sciencedirect.com/science/journal/09214488
[8] http://www.nwsgc.org/proceedings.html
[9] http://www.alpacaresearch.org/
[10] https://www.icinfo.org/content/infectious-diseases

Society of Camelid Research and Development[11], and the United States Animal Health Association page on diseases of cattle, bison and camelids[12].

C.3. Provincial diagnostic data for South American camelids

A request was submitted to the BC AHC and to SK PDS for access to diagnostic data associated with SAC submissions. PDS granted permission to access SK diagnostic data from the Canadian Animal Health Surveillance Network (CAHSN) database, which contains data from 2013 to present. AHC provided diagnostic data directly from their laboratory information management system (LIMS) from 2007 to present. Diagnostic data was analyzed using Microsoft Excel.

C.4. Interviews of camelid disease experts and wildlife managers

An interview tool was created to address information gaps identified during the literature review, with specific emphasis on the epidemiology of camelid diseases and the probability of, and potential impact from, pathogen spread to wild ungulates (Appendix 2. Interview questions). This tool was then emailed to 11 camelid disease experts (based on authorship of 2 or more of the 3-star publications) and 13 wildlife managers in BC, Yukon Territory (YT), Northwest Territories (NT), AB, Alaska and the northwestern states between May 8th and June 21st, 2017. Emails consisted of a project description, preliminary findings from the literature review, and a request to respond in writing or via telephone to interview questions. All contacts were given the opportunity to nominate a colleague for the interview, and up to two follow-up emails were sent to unresponsive contacts. Results of wildlife disease manager interviews were reviewed with wildlife veterinarians in BC and Alaska to gather further data for the risk assessment.

D. Results and discussions

As of March 15, 2017, the literature search had returned 1415 papers for initial screening based on title alone. A search of the 6 websites suggested by FLNRORD staff, or identified as part of the general Google Search, resulted in the addition of 38 papers for initial screening. One-hundred-twenty-eight (128) papers were subjected to secondary screening of the abstract, of which 53 were assigned three-star status; full-text publications were available for forty-four of the three-star papers, and were reviewed in full.

The Google search returned policies from Washington and Utah state governments, but not from any of the other northwestern States. The individuals responding to our phone calls to the nine state departments (Arizona, California, Colorado, Idaho, Montana, Oregon, Utah, Washington and Wyoming) were unable to provide policy statements on the use of llamas and alpacas in the back country.

[11] http://www.isocard.net/en/proceedings
[12] http://www.usaha.org/Committees/InfectiousDiseasesOfCattleBisonAndCamelids.aspx

Diagnostic data from alpacas and llamas submitted to the BC AHC and SK PDS was assessed. Because wildlife disease data from BC is incompletely entered into the CWHC database (Helen Schwantje, pers. comm., 2017), an assessment of CWHC data on pathogens in wild ungulates in BC was not conducted.

Nine of 24 individuals contacted by email responded to the interview questions, of which one requested a phone-based interview. Five respondents answered the small ruminant and camelid infectious disease questionnaire, and four responded to the wildlife disease questionnaire.

Table 1: Interview respondents by affiliation.

Last Name	*First Name*	*Affiliation*
Barrington	George, M.	Professor, Washington State University, Food Animal Med and Surgery
Besser	Tom	Professor, Washington State University, Rocky Crate D.V.M. and Wild Sheep Foundation Chair in Wild Sheep Disease Research
Evermann	James	Infectious Disease Professor, Washington State University, Washington Animal Disease Diagnostic Laboratory
Fenton	Heather	Wildlife Veterinarian, Government of North West Territories
Harms	Jane	Wildlife Veterinarian, Government of Yukon Territories
Pybus	Margo	Fish and Wildlife Division of Environment and Parks, Government of Alberta
Ridpath	Julia, F.	Former Lead Scientist, National Animal Disease Center, Agricultural Research Service, United States Department of Agriculture, Ruminant Diseases and Immunology Research Unit
Twomey	D. Fin	Animal and Plant Health Agency, Starcross Regional Laboratory, United Kingdom
Wernery	Habil Ulrich	Scientific Director, Central Veterinary Research Laboratory, Dubai, United Arab Emirates

D.1. What is at risk?

Wild ungulates in British Columbia

There are nine wild ungulate species in BC, with multiple recognized subspecies in different ecoregions (e.g. Roosevelt Elk on Vancouver Island, and Rocky Mountain Elk in the Rockies, see Box 1 on the following page). Abundance and distribution maps, with conservation list status, habitat preference, and migration patterns for the species and subspecies that live in BC, are located in Appendix 3. Wood Bison (*Bison bison athabascae*) and Plains Bison (*Bison bison bison*) are out of scope for this review and will not be discussed further. Red-listed ungulate populations (i.e. those that are extirpated, endangered or threatened) include Boreal caribou, Central Mountain caribou and Southern Mountain caribou. Ungulate populations of special concern, or blue-listed wildlife species, include all Bighorn Sheep (*Ovis Canadensis)* populations, Mountain Goat, Northern Mountain Caribou, Dall's Sheep (*Ovis dall*), Stone's Sheep (*Ovis dalli stonei)* and Roosevelt Elk. These ranking classifications are based on factors such as range extent, area of occupancy, population size, environmental specificity, observed population trends,

global significance, and threats. Threats may include human activities, environmental changes, and health status[13].

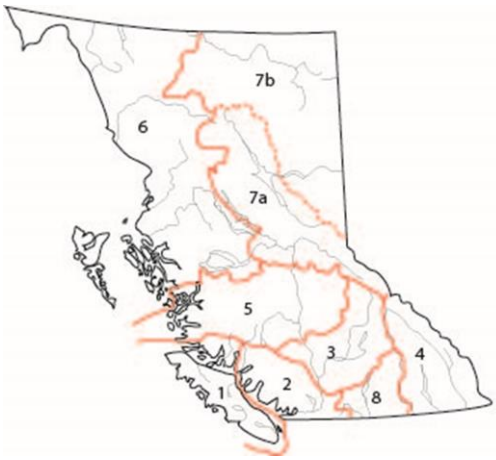
Individual animal and herd health is difficult to measure in wildlife populations in general, unfortunately, and information on pathogen and disease presence and prevalence in such populations usually comes from opportunistic live or dead animal sampling, specific targeted surveillance projects, or outbreak investigations on large mortality events. Within BC, the Canadian Food Inspection Agency (CFIA) in collaboration with BC agencies may assist with surveillance on Federally Reportable Diseases such as BTV and *M. bovis*, and this has provided opportunities for targeted surveillance for these pathogens by FLNRORD staff. Observational surveillance for CE, culture for *Mannheimia* and *Pasteurella*, larval identification for *Muellerius*, and serology for Johne's Disease, and serology and PCR for *M. ovipneumoniae* has been conducted on some wildlife populations in BC, although surveillance may be targeted or opportunistic, and no comprehensive reports have been generated for these pathogens in BC's wildlife. The presence, prevalence and significance of many of the pathogens listed in this review on individual wild animals and herd health status, therefore, is not completely understood (Helen Schwantje, pers. comm., 2017).

Box 1: Wild ungulates of BC, by list status and range.

	Fish & Wildlife Management Regions								
Species	**1**	**2**	**3**	**4**	**5**	**6**	**7a**	**7b**	**8**
Boreal Caribou							R		
Central Mt. Caribou							R	R	
Southern Mt. Caribou			R	R	R		R		
Northern Mt. Caribou					B	B	B	B	
Roosevelt Elk	B								
Mountain Goat		B	B	B	B	B	B	B	B
Bighorn Sheep			B	B					B
Dall's Sheep						B			
Stone's Sheep						B	B	B	
Mule Deer	Y	Y	Y	Y	Y	Y	Y	Y	Y
White-tailed Deer				Y				Y	Y
Rocky Mt. Elk			Y	Y				Y	Y
Moose			Y	Y	Y	Y	Y	Y	Y

Status
R = Red
B = Blue
Y = Yellow

Fish & Wildlife Management Regions
1 Vancouver Island
2 Lower Mainland
3 Thompson-Nicola
4 Kootenay
5 Caribou
6 Skeena
7a Omenica
7b Peace
8 Okanagan



Publicly available BC population range data (summarized in Box 1) suggests that red-listed wild ungulates (of which all are caribou and Wood Bison) are present in 5 of the 8 Fish and Wildlife Management Regions designated by the province (9 regions if counting Omineca and Peace separately). Blue-listed wild ungulates are present in all regions. Due to the potential for respiratory disease epizootics in Mountain Goats and wild sheep, particularly thinhorn

[13] NatureServe Conservation Status Assessments: Factors for Evaluating Species and Ecosystem Risk, April 2012

sheep (Dall's and Stone's), a regulation is in place to restrict the use of SACs for hunting purposes in northern BC (Helen Schwantje, pers. comm., 2017).

South American camelid industry in British Columbia

The BC Llama and Alpaca Association[14] lists 18 registered members and four honorary members in 2016; at the time of writing, eight members were listed with Llama Canada[15] and 7 with Alpaca Canada[16], of which 2 and 6 members, respectively, were also registered with the BC Llama and Alpaca Association. In total, 25 farms in BC were members of one or more associations. Five of the registered farms were located on Vancouver Island or in the Lower Mainland, three were near Fort St. John, and the rest were in the Okanagan Valley between Oliver and Sicamous. Stephen and Schwantje (2003) identified 165 farms in BC through links to alpaca or llama associations, but commented at that time that they felt this was a significant underestimate. Not every individual who owns llamas and alpacas will be registered with the associations, especially if these individuals own only one or two such animals as backyard pets. Interestingly, the number of submissions from SACs to the BC AHC dropped off significantly after 2010 (see Pathogens detected in SAC submissions to BC AHC), which may suggest a decrease in the size of the llama and alpaca industry in BC. There was no attempt for this report to contact or assess the number of non-members of SAC associations.

The SAC association websites provided very little by way of content on the specific use of these animals other than for breeding and fibre production, and it was outside the scope of this assessment to survey the association membership. In a previous survey sent to 165 alpaca and llama farms, three quarters of the 90 respondents used their animals for fibre, about the same amount kept these animals as pets, and 26 described using their animals for trekking (Stephen & Schwantje, 2003). A Google search for llama trekking in BC found a single website[17] listing 7 companies offering llama hiking in BC, only one of which was found to have a current, active company website.

The BC Government has requested economic impact information from the camelid industry in BC, but as of the writing of this report, such information has not been provided. From the publicly available information, SAC farming and guided hiking and trekking appears to be a small industry in BC. A ban on the use of SACs as pack animals for hunting in the Skeena, Omenica and Peace Regions (Management Regions 6 and 7; see also Wildlife Act's Hunting Regulations (BC Reg. 190/84) article 18.1) is, therefore, unlikely to impact BC's overall agricultural and tourism economy.

D.2. Is there any evidence that South American camelids can be a source of disease to wild ungulates in British Columbia?

Previously reported pathogens of SACs

This risk assessment did not set out to recreate the SACs pathogen tables that can be found elsewhere, such as in Stephen and Schwantje (2003), Garde et al. (2009) and Wernery, Kinne, and Schuster (2014).

[14] British Columbia Llama and Alpaca Association membership page
[15] Llama Canada page "find a farm"
[16] Alpaca Canada's 2017 Membership List
[17] British Columbia Llama Treks, on WorldWeb.com, http://www.bc.worldweb.com/ToursActivities/LlamaTreks/

A table of pathogens known to affect llamas has been adapted from Garde et al. (2009) and is located in Appendix 4 for quick reference only.

Previously identified pathogens of SACs that are of concern for wild ruminants

In 2009, Garde et al. stratified infectious diseases of sheep, goats and llamas into high, low and unknown risk to Dall's Sheep and Mountain Goats based on the probability of transmission to, and impact on, the health of these wildlife species, and categorized the following nine infectious agents as high risk: Johne's Disease, *M. conjuntivae* and *M. ovipneumoniae, Pasteurella* spp., *M. haemolytica*, CE (parapoxvirus), Parainfluenza-3 virus (PI-3), *Muellerius capillaris* (lung nematode), and *Oestrus ovis* (nasal bot fly). In 2003, *Pasteurella* was the only pathogen specifically identified as high-risk by Stephen and Schwantje (2003) on the basis of the then knowledge of the impact of this bacteria on wild sheep health. Rather than name other specific pathogens, Stephen and Schwantje (2003) identified criteria for high risk pathogens as those that 1) are shed in feces and can persist in the environment for extended periods of time, or 2) persist in the environment after being excreted via respiratory secretions, urine or saliva, or 3) may be perpetuated or magnified outside of camelids through a secondary host.

More recent evidence suggests that *M. ovipneumoniae* plays a significant role in the initiation of respiratory epizootics in wild sheep and goats with *Pasteurella* playing more of a secondary role. In addition, *M. ovipneumoniae* may be actively shed by survivors of epizootics with subsequent juvenile mortality for many years (Besser et al., 2014; Handeland et al., 2014); however, *M. ovipneumoniae*, *M. conjuntivae* and *Muellerius capillaris* have not been reported from SACs. They were included by Garde et al. (2009) because the report also reviewed pathogens that might be transmitted from domestic sheep and goats. Table 2 summarizes the pertinent findings from Garde et al. (2009) for the nine previously identified high risk pathogens.

Table 2: Summary of findings from Garde et al. (2009) for pathogens in domestic ruminants (sheep, goat and/or llama) that were identified as high risk to Dall's Sheep and possibly Mountain Goat. LL – Llama; DS – Dall's Sheep; MG – Mountain Goat

Pathogen	*Transmission Risk (LL to DS or MG)*	*Health Impact (on DS or MG)*	*Present in LL*	*Mode of Transmission*	*Environmental Survival*
Mycobacterium avium paratuberculosis (Johne's Disease)	Low	Moderate	Yes	In utero Ingest contaminated feed at young age	Up to 385 days in ideal situations
Mycoplasma conjuntivae	Not stated	High	No*	Insect vector Direct contact	Low outside of suitable host
Mycoplasma ovipneumoniae	Not stated	High	No*	Aerosol Direct contact	Low outside of suitable host
Pasteurella spp	Unknown	High	Yes	Aerosol Direct contact	Low outside of suitable host
Mannheimia haemolytica	Unknown	High	Yes	Aerosol	Low outside of suitable host

Pathogen	*Transmission Risk (LL to DS or MG)*	*Health Impact (on DS or MG)*	*Present in LL*	*Mode of Transmission*	*Environmental Survival*
				Direct contact	
Contagious Ecthyma	Not stated, possibly high	Moderate to severe	Yes	Direct contact Fomites	Long term in scab material
Parainfluenza-3	Unknown	Predispose to pneumonia	Yes**	Direct contact	Low outside of suitable host
Muellerius capillaris	Not stated	Predispose to pneumonia	No†	Intermediate host	Long term
Oestrus ovis	Not stated	Moderate to severe	Yes¥	Insect	Flies develop in ~ 6 wks, adults survive < 3 wks

* *Mycoplasma conjunctivitis and M. ovipneumoniae* have not been reported in SACs
** Antibodies to Parainfluenza-3 have been documented in clinically healthy llamas, and PI-3 was recently detected in neonatal alpacas that died of acute pneumonia, but the significance of this virus in those mortalities is currently unknown
† *Muellerius capillaris* has not been reported in llamas, but is the most common lungworm known to infect domestic sheep and goats (Garde et al., 2009)
¥ It is not known if the larvae are able to molt into a sexually mature adult stage in llamas

Emerging pathogens of SACs of potential concern for wild ruminants

Clinical illness in SACs as a result of PI-3, *Corynebacterium pseudotuberculosis*, Alpaca Coronavirus and Bovine Leukemia Virus (BLV) was newly identified in our literature review. Given that SACs were first introduced to North America in the mid 1980's, and "health management and diagnostic medicine practices [in SACs in the North American context] are still relatively new (Crossley, Mock, Callison, & Hietala, 2012)", it is not unexpected to identify novel pathogens in SACs.

PI-3 is a highly contagious respiratory virus that is transmitted by close contact between animals. Garde et al. (2009) wrote that "virus has been isolated from both healthy and pneumonic bighorn sheep and has clearly been associated with fatalities in bighorn sheep". Although seropositivity may be common in wild ruminants, the significance of this pathogen is still largely unknown. Antibodies to PI-3 in the absence of clinical illness in camelids was reported by Garde et al. (2009). Since 2009, a single publication examining causes of fatal acute pneumonia in 24 alpaca neonates from two experimental research stations and one farm in southern Peru detected PI-3 by direct fluorescent antibody test in nine animals (Rosadio, Cirilo, Manchego, & Rivera, 2011). Because PI-3 was identified as the sole pathogen in three animals, but was present in association with *Pasturella multocida*, *Mannheimia heamolytica* or Bovine Respiratory Syncytial Virus (BRSV) in the other six animals, Rosadio et al. (2011) were unable to confirm PI-3 as the causative agent of the pneumonia and therefore could not conclusively assign causation between the virus and mortality.

The gram-positive bacteria responsible for caseous lymphadenitis (CLA), *Corynebacterium pseudotuberculosis*, causes abscesses in lymph nodes of domestic sheep and goats, and is transmitted

between animals via ingestion, inhalation or inoculation into wounds. *C. pseudotuberculosis* can persist in the environment for up to 5 months, and is commonly found in domestic sheep and goats in Canada. Garde et al. (2009) write that *C. pseudotuberculosis* has been reported in white-tailed deer, mule deer and alpacas, but not in llamas or bighorn sheep, although CLA was recently cultured from a bighorn sheep in BC (Helen Schwantje, pers. comm., 2017). CLA may be present but under-reported in wild ungulates given that diagnosis requires the submission of a sample to a diagnostic lab. Wernery (2012) describes CLA as the most important skin disease in camelids – although this statement may be skewed towards Old World camelids, CLA has been reported in alpacas from a number of locations globally, with sometimes severe clinical outcomes including fever, mastitis and death (Wernery et al., 2014). The isolation of *C. pseudotuberculosis* Strain Cp267 from a submandibular abscess in an 11 year old llama from California (Lopes et al., 2012) constitutes the only published report of CLA in a llama that we were able to find, although *C. pseudotuberculosis* was recently cultured from an abscess in a llama in BC (AHC data, see Pathogens detected in SAC submissions to BC AHC).

In 2007, Alpaca Respiratory Coronavirus was identified as a novel Alphacoronavirus in alpacas that developed acute respiratory disease, fever, abortions and occasional sudden death after co-mingling at a national exposition and sale in California (Crossley et al., 2010). A follow-up paper suggested a common genetic link between Alpaca Respiratory Coronavirus and Human Coronavirus 229E (Crossley et al., 2012), and speculated on a zoonotic or anthroponotic transmission event between humans and alpacas. While coronaviruses are known to be important respiratory and enteric pathogens of avian and mammalian species, and recent years has seen the identification of many new coronaviruses, transmission tends to be species-specific (Crossley et al., 2012). At this time, Alpaca Coronavirus is likely of limited concern for wild ungulate management.

Lymphoma is a commonly reported neoplasia in SACs. Lee, Scarratt, Buehring, and Saunders (2012) published a case study of lymphoma in a 13-month-old male alpaca in Virginia, USA, with evidence of BLV, an oncogenic virus associated with lymphoma in cattle. This was the first such report of BLV in a SAC, and the first time that lymphoma and BLV were identified in the same alpaca. Unfortunately, the authors were not able to confirm the source of infection, nor were they able to determine the causal role of BLV in the pathogenesis of lymphoma in this animal.

Our literature review identified BVDV, BTV and *M. bovis* as pathogens that are known to affect wild ruminants and that appear to be emerging in significance among SACs since the assessments by Stephen and Schwantje (2003) and Garde et al. (2009).

BVDV was identified by Garde et al. (2009) as a pathogen of unknown consequence to wild ruminants despite its propensity to cause severe disease in domesticated ungulates; these same authors stated in their assessment that BVDV was “uncommon in camelids but it has been detected on necropsy”. More recently, BVDV has been identified as an important and emerging infectious disease of SACs (Byers et al., 2009; van Amstel & Kennedy, 2010). BVDV in SACs is thought to have originated from co-mingling with infected cattle (Wernery et al., 2014). Byers et al. (2009) hypothesize that the increase in BVDV cases, particularly in North American alpacas, may be the result of the “emergence of a novel strain, differences in animal management practices, or increased awareness of BVDV by alpaca owners.”

BVDV has been reported at herd seroprevalences of 1 to 20% for SAC herds in the United States (van Amstel & Kennedy, 2010). As with cattle, clinical signs of BVDV in SACs are variable and range from transiently infected animals with minor (e.g. partial anorexia and mild lethargy) or no clinical symptoms, through to more severe acute and chronic symptoms (e.g. chronic lethargy, nasal discharge, diarrhea, abortion, premature birth) and death (van Amstel & Kennedy, 2010). Infection during early gestation may result in a persistently infected (PI) cria[18] (van Amstel & Kennedy, 2010). The immune system of PI animals does not recognize BVDV and these individuals shed very large amounts of virus. Although PI animals tend to be unthrifty and usually die or are culled within their first 6 months (Bedenice, 2014), there is one report of a PI alpaca that survived for 30 months (Wernery et al., 2014). Naïve camelids can become viremic within three to five days of indirect or direct exposure to PI crias (Byers et al., 2011). Persistently infected animals are known to be the main sources of virus for disease transmission, and natural or experimental PI infections have been reported in bighorn sheep, mountain goats, domestic sheep, swine, mule deer and white-tailed deer (Nelson, Duprau, Wolff, & Evermann, 2016; Passler & Walz, 2010; Wolff et al., 2016). Evidence exists for the transmission of BVDV from camelid to camelid, and from cattle to wild ungulates (Passler & Walz, 2010). There are no documented cases of transmission of BVD from camelids to any non-camelid wild or domestic species; however, investigations have not been reported in the literature.

BTV and epizootic hemorrhagic disease (EHD), a genetically distinct orbivirus with similar clinical signs, are commonly found in the United States. Occurrences in Canada are rare for both viruses, but in BC they have been reported from the Okanagan Valley[19]. These vector-borne viruses (transmitted via *Culicoides* biting midges) typically cause subclinical disease in cattle, but can result in high morbidity and mortality in sheep and some wild ruminants (Allen et al., 2015), including white-tailed deer and bighorn sheep[20]. Prior to the death of an alpaca in Germany in 2007, and an outbreak in two llama herds in France in 2008, BTV was not thought to affect SACs. In August 2013, BTV was detected in a deceased 9-year old llama in Washington State and was the suspected cause of respiratory disease in 4 llamas from the same property that eventually recovered (Allen et al., 2015). A month later, BTV was diagnosed in a deceased alpaca located 150 miles north of the index property, and in mid-October of the same year two sentinel cattle herds near Penticton and Oliver, BC, tested positive for BTV despite the absence of clinical signs (Allen et al., 2015). We found no reference of EHD in SACs. However, reported changes in the global distribution and nature of BTV infection (Maclachlan & Mayo, 2013), in addition to the recent case reports of BTV in llamas and an alpaca in Washington State, serve as a reminder that pathogen-host dynamics can change unpredictably over time.

Garde et al. (2009) reported that *M. bovis*, the cause of bovine tuberculosis (TB), is not present in Canada except in wood bison in Wood Buffalo National Park (NWT), and in elk and white-tailed deer in Riding Mountain National Park (MB), and that it "is not considered a risk associated with the species [goat, sheep and llama] of interest". However, since that report, *M. bovis* appears to be an emerging

[18] A neonatel SAC is commonly referred to as a 'cria'.
[19] CFIA Fact Sheet – Bluetongue. Available at http://inspection.gc.ca/animals/terrestrial-animals/diseases/reportable/bluetongue/eng/1306107020373/1306117227621
[20] Epizootic hemorrhagic disease in British Columbia Wildlife Health Fact Sheet

disease of SACs in some parts of the world (Broughan et al., 2013; Twomey et al., 2007; Twomey et al., 2009; Wernery & Kinne, 2012). In Great Britain, where TB is endemic in cattle and badgers, the Animal Health and Veterinary Laboratories Agency has seen an increase in *M. bovis*-positive submissions in SACs since 2007 (Broughan et al., 2013; Wernery, 2012), and tuberculosis has been identified in alpacas in Ireland (Ryan et al., 2008), Spain and, when housed in close proximity to cattle and humans, in South America (Broughan et al., 2013). It is thought that TB in SACs is a result of spillover infection from local animal reservoirs such as cattle and wildlife, but alpaca-to-alpaca transmission has been documented in at least one instance (Twomey et al., 2009). *M. bovis* infections in alpacas and llamas can be persistent and prolonged (Broughan et al., 2013), with diagnosis in SACs complicated by high false-negative findings with the intradermal tuberculin herd tests (Twomey et al., 2007). Tuberculosis was identified in a single beef animal in 2007[21], but in 7 beef cattle on a ranch in southern BC in 2011[22], resulting in strict quarantine, trace-back investigations and humane destruction of all infected and susceptible exposed animals[23]. As follow-up, increased outreach and enhanced surveillance of harvested cervids for TB in a single Wildlife Management Unit has been in place since 2013 with no positive cases identified. TB is a serious and challenging pathogen to eradicate once it becomes established in wild populations.

Pathogens detected in SAC submissions to BC AHC

One-hundred-forty-six (146) alpaca and 69 llama submissions have been received by the BC AHC between 2007 and 2017, with over half of these submissions occurring between 2007 and 2010 (115/146, 79% for alpaca; 43/69, 62% for llama). Although a number of bacteria (Table 3) and parasites (Table 4) were identified, no viruses were detected in any of the submissions (Table 5). Analysis of PDS data showed similar results. Many of the pathogens found in SACs in BC are common to wild and domestic ruminants, and no reportable or foreign animal pathogens were described, a finding consistent with Stephen and Schwantje (2003). Of interest, however, is the culture of *Corynebacterium pseudotuberculosis* from an abscess in a three-year-old llama and the detection of *M. haemolytica* in a 26-day-old llama with fibrinous pneumonia.

Table 3: Bacterial species isolated from tissues of alpacas and llamas submitted to the British Columbia Animal Health Centre for postmortem examination (Jan. 1, 2007-Jan. 31, 2017).

Bacteria	***Alpaca***	***Llama***
Acinetobacter sp.		1
Actinobacillus capsulatus		1
Actinomyces sp.		1
Aeromonas hydrophila		1
Aspergillus fumigatus		2
Bacillus sp.	1	1
Bacteroides sp.		1
Clostridium perfringens	4	5
Clostridium septicum		1

[21] "Bovine TB forces cattle cull in BC, Alberta". CBC, Nov 11, 2007.
[22] CFIA information page, "Herds infected with bovine tuberculosis in Canada" in 2011 and in 2016
[23] CFIA information page, "What to expect if your animals are infected with bovine tuberculosis"

Bacteria	Alpaca	Llama
Clostridium sp.		1
Corynebacterium pseudotuberculosis [1]		1
Corynebacterium sp.		1
E.coli (non-haemolytic)	9	7
Mannheimia haemolytica [2]		1
Myroides sp.	1	1
Penicillium sp.	1	
Peptostreptococcus sp.		1
Pseudomonas aeruginosa	1	1
Pseudomonas fluorescens	1	
Salmonella serogroup C1/C4	1	
Staphylococcus aureus	1	
Staphylococcus sp.	2	1
Streptococcus sp (non-haemolytic)	1	
Streptococcus sp. (alpha)	6	6
Trueperella pyogenes [3]	1	1
Yersinia enterocolitica [4]	1	
Negative	**63**	**44**
Total	**94**	**80**

[1] Culture of an abscess from a 3 year old llama
[2] Culture of lung tissue from a 26 day old llama diagnosed on postmortem with fibrinous pneumonia. No BVDV results available
[3] Culture from a 15 year old llama with peritonitis
[4] Isolated from the colon of an adult alpaca with severe weight loss at postmortem exam

Table 4: Parasites detected in alpaca and llama fecal specimens submitted to the British Columbia Animal Health Centre (Jan. 1, 2007-Jan. 31, 2017).

Parasites	Alpaca	Llama
Ascarids	1	
Capillaria	1	
Coccidia	8	9
Nematode	3	4
Strongyles	5	11
Trichuris		1
Negative	**14**	**4**
Total	**32**	**29**

Table 5: Other pathogen testing and results from tissues of alpacas and llamas submitted to the British Columbia Animal Health Centre for postmortem examination (Jan. 1, 2007-Jan. 31, 2017).

Pathogens	Number of tests	Number of positive tests
Alpaca	**99**	**0**
Bovine Parainfluenza 3 vi	1	0

	Pathogens	Number of tests	Number of positive tests
	Bovine Viral Diarrhea PCR	79	0
	Infectious Bovine Rhinotracheitis Virus	1	0
	Malignant Catarrhal Fever virus - Sheep	1	0
	Bovine Adenovirus Type 3	2	0
	Bovine Coronavirus	1	0
	Bovine Respiratory Syncytial Virus	1	0
	Mycobacterium paratuberculosis	5	0
	Serum Neutralizing antibodies- BVD	8	0
Llama		**14**	**0**
	Apicomplexa	1	0
	Bovine Coronavirus PCR	2	0
	Bovine Viral Diarrhea PCR	8	0
	Cryptococcus neoformans	1	0
	Johne's PCR	2	0

Epidemiology and diagnosis of SAC pathogens

For each of the nine previously identified high risk (Garde et al., 2009) pathogens (Johne's Disease, *M. conjuntivae, M. ovipneumoniae, Pasteurella* spp., *M. haemolytica*, CE, PI-3, *Muellerius capillaris*, and *Oestrus ovis*) and those six newly identified in this review (BVDV, BTV, *M. bovis*, *Corynebacterium pseudotuberculosis*, Alpaca Coronavirus and BLV), a summary of known epidemiology, routes of transmission and diagnostic tests is presented in Table 6. This summary is based on information gleaned from the literature cited in this review and answers provided by interviewees.

In brief, PI-3, *M. haemolytica* and *Pasteurella* spp. have all been detected in young SACs with acute fatal pneumonia. There are no studies that investigate prevalence or shedding of these organisms in healthy SACs, although presumably the young crias with pneumonia were infected during interaction with herd mates, suggesting that some proportion of clinically normal animals may be infected. Antibodies to PI-3 that have been detected in other studies indicate the virus can probably circulate in SACs.

BVDV has been reported at herd seroprevalences of 1 to 20% for SAC herds in the United States (van Amstel & Kennedy, 2010). BVDV transmission between SACs in the same herd has been documented, indicating that SACs shed infectious viral particles in an amount sufficient to infect other animals.

Johne's Disease is generally considered to occur at lower prevalence in SACs than in cattle; however, infection of multiple animals within herds has been reported. It is generally presumed that transmission is similar to cattle, with oral-fecal transmission from infected individuals to younger animals. There has been one serological study in BC that detected antibodies in ten percent of SACs surveyed, however specificity of serologic testing in llamas is lower than in cattle (Miller et al., 2000).

BTV has been detected in Washington State in SACs with subclinical or mild infection as well as in SACs with fatal illness. There is very limited evidence about BTV viremia in SACs and about whether they can

be a source of disease to other animals. It appears, however, that they most likely act as dead-end hosts (Schulz et al., 2012).

Corynebacterium pseudotuberculosis has been cultured from abscesses in SACs, providing some indication that llamas with active draining wounds could spread infectious organisms.

CE has been associated with oral lesions in SACs similar to what has been reported in other ruminants, but reportedly of longer duration. Shedding might therefore be presumed to be similar to that reported in small ruminants. Documented spread between SACs within herds indicates that they actively shed the pathogen.

M. bovis has been detected in SACs, but only in regions where the disease is endemic in cattle and wildlife. The role of SACs in perpetuating disease is unknown, but hypothesized to be small.

Oestris ovis has been reported sporadically in SACs, but they are likely unimportant and possibly dead-end hosts.

BLV has been reported in one llama with lymphoma, but no information on epidemiology was available.

M. ovipneumonia, M. conjuntivae and *Muellerius capillaris* have not been documented in camelids, but are important pathogens of small ruminants, domestic and wild.

Alpaca coronoavirus has been detected in clinically ill alpacas during an outbreak associated with an alpaca show, and was suspected to spread via respiratory droplets. Cases in other species have not been reported.

Unfortunately, many of the molecular-based diagnostic tests for the organisms listed above have not been validated for use in camelids. Therefore, the rate of false positive and false negative results is unknown, but presumed to be equal or higher than the reported rates for the tests in the species that they have been validated in. Diagnosis or exclusion of diagnosis of these pathogens in camelids likely requires a multi-step approach including careful history taking and clinical evaluation, culture and microscopy of samples from live animals and gross mortem lesions, and supportive molecular test results.

Table 6: Epidemiology of previously identified high-risk and newly emerging camelid pathogens; interviewee ranking of probability of SAC infection; probability of transmission and impact to wild ungulates; and qualitative risk (assigned by authors based on information in previous columns).

Pathogen	***Epidemiology in Camelids***	***Transmission***	***Available diagnostic test(s)***	***Probability of SAC infection***	***Probability of transmission***	***Impact***	***Risk***
Mannheimia haemolytica [B ¥]	Common Severity may be increased by presence of other respiratory pathogens	Direct contact Aerosol Contaminated feed	Culture[†]	M	2,3 M	1,4, H 4,4	M-H

Pathogen	*Epidemiology in Camelids*	*Transmission*	*Available diagnostic test(s)*	*Probability of SAC infection*	*Probability of transmission*		*Impact*		*Risk*
Pasteurella spp. [B ¥]	Moderate infection rate Severity may be increased by presence of other respiratory pathogens Low severity on its own	Direct contact Aerosol Contaminated feed	Culture[†]	M	2,3	M	1,4, 4,4	H	M-H
Contagious ecthyma [V ¥]	Common Variable severity	Direct contact Secretions / scabs Biting insects	Electron microscopy[†] PCR Histology	M-H	2,3	M	1,2, 3,3, 4,4	M-H	M-H
Bovine viral diarrhea virus [V]	Prevalence unknown Limited surveillance Bovine to camelid and camelid to camelid cycling Persistent infection Variable severity	Vertical Direct contact Secretions Contaminated feed Fecal-oral Fomites	PCR ELISA Serum Neutralizing Antibody Virus isolation Immuno-histochemistry	M	*,4	H	**,0 ,1	L	M
Mycobacterium avium paratuberculosis (Johne's Disease) [B ¥]	Prevalence unknown Conact/shared pasture with domestic ruminants may increase risk. No treatment Mortalities reported	Fecal-oral Direct contact Diaplacental	PCR ELISA Culture Microscopy (ZN smear)	M-H	2,4	M	*,1, 3	L-M	M
Bluetongue virus [V]	Rare Limited information Subclinical infection Mortalities reported	Arthropod-borne	ELISA PCR Culture in embryonated eggs	L	0,2	L	*,4, 4,4	H	M
Mycobacterium bovis [B]	Rare except in UK No treatment Chronic debilitating disease with severe pathology	Aerosol Contaminated feed Fecal-oral	Intradermal skin testing Serum Tuberculin intradermal test Microscopy (ZN smear) Culture[†]	L	1,5	L/H	0,0, 4,5	L/H	M
Corynebacterium pseudotuberculosis [B]	Common Difficult to treat Highly contagious	Direct contact Secretions	Culture[†] ELISA Clinical Signs[†]	M	2,3	L-M	*,1, 2,3	L	L

Pathogen	*Epidemiology in Camelids*	*Transmission*	*Available diagnostic test(s)*	*Probability of SAC infection*	*Probability of transmission*		*Impact*		*Risk*
	Ovine-caprine strain isolated from camels Moderate mortality possible								
Bovine leukemia virus [V]	One reported case	Blood Biting insect	Serology PCR	L	*,3	U/M	***, 1	L	L
Parainfluenza-3 [V ¥]	Antibody detection in serology common Disease rare / insignificant	Aerosol	Virus Neutralizing Test Hemadsorption Immunosorbent Techniques	M	2,3	L-M	1,1, 1,2	L	L
Oestrus ovis [P ¥]	Rare Low morbidity	Insect	Clinical Signs†	L	1,2	L	*,0, 1,1	L	L
Alpaca coronavirus [V]	Rare Limited information Severe diarrhea and up to 80% mortality in outbreaks involving animals < 40 days old	Nasal secretion Direct contact	PCR Electron Microscopy (feces) RT-PCR Immuno-fluorescence ELMI from feces and nasal swab Capture ELSA	L	**	U	*** *	U	L
Mycoplasma ovipneumoniae [B ¥]	Infection in camelids has not been reported Pathogen of very high concern for wild sheep and goat	Aerosol Contaminated feed	Culture PCR	NR	*,4	H	0,5, 5,5	H	n/a
Mycoplasma conjunctivae [B ¥]	Infection in camelids has not been reported Limited information Unknown severity	Aerosol Insects Contaminated feed	Culture PCR	NR	2,4	M	0,0, 2,4	L-M	n/a
Muellerius capillaris [P ¥]	Infection in camelids has not been reported Potential pathogen of concern for wild sheep	Fecal-oral	Microscopy Post mortem	NR	2,3	M	1,1, 2,3	L-M	n/a

[B] Bacteria
[P] Parasite
[V] Virus
¥ Pathogens identified as high risk by Garde et al. (2009)
† Clinical signs, culture and electron microscopy may afford higher specificity and/or sensitivity than molecular diagnostics in camelids
* One or more wildlife managers indicated that the probability or impact of a pathogen incursion onto wild ungulates is 'unknown'

Evidence about the transmission of pathogens from SACs to wild and domestic ungulates

We found no peer-reviewed literature describing disease transmission from SACs to domestic or wild sheep and goats. However, we also found very scant information about the prevalence, and pathogen transmission dynamics for the identified SAC pathogens. Therefore, it is important to note that lack of documented transmission from camelids to wild ungulates cannot be considered evidence that transmission has not, or could not occur. Transmission of pathogens from other domestic livestock (cattle, sheep, goats) to wild ungulates under natural conditions has been well documented in the literature. Examples include respiratory disease and fatal pneumonia following contact between domestic and bighorn sheep (Schommer & Woolever, 2008), *M. bovis* from domestic cattle to elk in Riding Mountain National Park (Garde et al., 2009), and BVDV from cattle to deer (Passler & Walz, 2010).

During expert interviews, we collected an anecdotal case report that indicates the possibility of CE transmission from pack llamas to Mountain Goats near Atlin, Terrace and the Babine Mountains of BC. The Mountain Goat herds in those regions have been closely observed for decades through viewing and photography activities, and through hunter harvest sampling. Since their introduction to BC nearly 20 years ago, pack llamas have been used for assisted trekking in these regions because they damage the terrain less and manage the terrain better than horses. Lesions were first observed in these different mountain goat populations, coincident with the introduction and public use of pack llamas in those areas; no other domestic ruminants that can harbour contagious ecthyma are known to have travelled into those mountain goat ranges ahead of the observed infections (Bill Jex, pers. comm., 2017).

Other than the information regarding CE, the interview respondents did not add to the findings of the literature review with respect to pathogen transmission from SACs to wild ungulates.

Exposure risk factors for wild ungulates in British Columbia

Common routes of transmission for animal pathogens include direct contact between animals (e.g. nose-to-nose contact), indirect contact whereby pathogens are deposited onto a surface by one animal and acquired by another (e.g. saliva on feed material, presence in feces or fomites such as scabs), droplet and airborne transmission between animals, and vector-borne transmission where insects (midge, flea, tick, mosquito etc.) or intermediate hosts such as snails or slugs transfer pathogens from a diseased to naïve individual.

Transmission is dependent on geographic and temporal contact between animals, sufficient pathogen shedding by the infected animal and sufficient susceptibility of the exposed animal to the pathogen. Infection risk is also influenced by the specific characteristics of the pathogen that allow it to survive outside of a host, the suitability of environmental conditions for pathogen survival and in some cases, the presence of appropriate vectors or hosts.

Extrapolating this to the BC context, exposure risk factors include the following:

A. **Geographic and temporal contact between camelids and wild ungulates**. Many of the respiratory pathogens (e.g. *Pasteurella* spp., *M. haemolytica*) are spread by direct contact, but other pathogens such as CE, BVDV and *M. bovis* can also be spread indirectly via contaminated surfaces. In general, parasites and other viral/bacterial pathogens that use fecal-oral

transmission pathways are hardier in the environment than pathogens spread via aerosolized respiratory droplets. Given that direct contact with camelids used as pack animals under direct human supervision is less likely than indirect contact, the probability of disease transmission is lowest for pathogens that require direct contact than for those that can survive in the environment and spread by indirect contact. Another consideration is the length of contact: Johne's Disease, for example, typically requires prolonged contact over weeks to months, while much shorter timeframes will result in transmission of pathogens such as *M. haemolytica*. A final consideration is infective dose, with those pathogens with low infective doses being more likely to be transmitted.

B. **Ability of camelids to shed sufficient infectious material**. This is also largely unknown for the described pathogens, although transmission between camelids has been reported for BVDV, *Mycobacterium paratuberculosis*, *M. bovis*, CE and Alpaca Coronavirus. This implies sufficient shedding to infect another animal.
C. **Susceptibility of the wild ungulates to the listed pathogens**. It is generally accepted that naïve individuals and herds – those with no prior exposure – are more likely to be negatively affected by the introduction of novel pathogens. BTV, CE, *M. haemolytica*, *Muellerius capillaris*, Johne's Disease, *M. bovis*, *M. ovipneumonia* and *Pasteurella* spp. have all been reported to cause clinical disease in wild ungulates in North America, however, knowledge on the presence or absence of the pathogens identified in this report are variable across BC and among BC's wild ungulate populations.
D. **Presence of a vector.** Biting midges of the *Culicoides* genus are the primary mode of transmission for BTV, although other biting insects and mother-to-fetus transmission have been documented (Allen et al., 2015). BTV has been associated with large mortality events in free-ranging bighorn sheep, white-tailed deer and mule deer within the midge's natural range and biting season, or it unnatural range when blown North. Any environmental change that facilitates a northern expansion of the midge's natural range in conjunction with the introduction of infected livestock into the region could result in an outbreak of BTV.

D.3. Which of the described pathogens are of greatest concern for wildlife managers?

In addition to information on the epidemiology, mode of transmission and available diagnostic tests, Table 6 (above) also describes the opinion of the two interviewees who estimated the probability of transmission to wild ungulates for each of the 15 pathogens, and of the four wildlife managers who estimated the potential impact of these pathogens on wild ungulates.

Wildlife veterinarians in BC and Alaska agreed with the wildlife managers about the probability of transmission and the potential impact for 14 of 15 pathogens. For CE, wildlife veterinarians indicated that impact is high (rather than medium-low estimated by wildlife managers), particularly in Mountain Goats. Dr. Kimberlee Beckman (Division of Wildlife Conservation, Alaska Department of Fish and Game) found severe, proliferative and verrucose lesions in a survey of CE among Alaskan Mountain Goats, with death in two cases caused by exsanguination as a result of the location and size of the lesions (unpublished data). Dall's Sheep, muskoxen, caribou and Sitka black-tailed deer included in the same survey had lesser clinical signs and lesions. Dr. Helen Schwantje reported mortalities of Mountain Goats

with severe lesions as above in populations in contact with bighorn sheep herds with endemic CE, and a decrease in Mountain Goat numbers following observation of clinical signs (Helen Schwantje, pers. comm., 2017).

D.4. Qualitative risk posed by pathogens identified in SACs to wild ungulates

The final column in Table 6, 'Risk', is a qualitative assessment of the overall risk for 12 pathogens as assessed by the authors of this report based on an evaluation of all gathered information. We ranked three pathogens as medium-high risk for wild ungulates, and four pathogens as medium risk.

Overall, *M. haemolytica* and *Pasteurella* spp. and CE had the highest risk, followed by BVDV, Johne's Disease (Johne's Disease), BTV and *M. bovis*. *M. ovipneumonia* was of high concern to the interviewees based on impact in wild sheep and goats and probability of transmission, but because this pathogen has not been described in camelids, it was excluded from the risk assessment. *Mycoplasma conjunctivae* and *Muellerius capillaris* were likewise excluded from the risk assessment because they have not been reported in SACs.

D.5. Can the effects of or risk of South American Camelid diseases in wild ungulates be prevented, treated, or mitigated?

All three medium-high and four medium risk pathogens identified in our risk analysis can cause asymptomatic infection in camelids (i.e. camelids may be infected but not clinically diseased), making it impossible to determine whether a camelid is harboring the organism based on the presence or absence of clinical signs alone. In addition, there are no validated tests for these pathogens in SACs, creating uncertainty about the utility of diagnostic testing to confirm absence of disease in individual animals or herds.

Should a decision be made to permit SAC entry into some backcountry areas, it would be prudent to implement actions to reduce the probability of disease transmission to wild ungulates (Stephen & Schwantje, 2003). Table 7 contains a list of possible risk mitigation actions specific to each of the 12 pathogens identified in this report that have been detected in llamas and alpacas. Preventing direct contact includes keeping sufficient distance between camelids and wild ungulates to mitigate respiratory droplet spread, and preventing SACs from accessing habitat features such as salt licks and heavily-used watering points. Unfortunately, there is no evidence to suggest the optimal distance of separation required. Maintaining high herd health status could include measures such as closed herd status with animal identification and inventory, veterinary exams and health certificates issued shortly before planned trips, veterinarian administered parasiticides, and negative laboratory tests for specific pathogens. Although the actions suggested in Table 7 are based on available information about pathogen biology, there is currently no evidence about the effectiveness of these actions in a real-world setting. Furthermore, the effectiveness of these actions would depend on initial implementation and ongoing enforcement and compliance.

Mitigation at the policy level could conceivably consist of regional or seasonal closures to llama and alpaca trekking, based on the environmental needs, range, and health status of wild ungulate populations in the area. Such measures would aim to reduce direct and indirect contact between SACs

and wild ungulates, thereby reducing the probability of a transmission event. Such policies require solid information about wild ungulate populations and habitat use – where this information is lacking, additional study would be warranted. Regulations to ensure that llama trekkers maintain and demonstrate high herd health status in their herds before entering the backcountry could reduce the probability of a transmission event by ensuring that only animals that have high health status enter the backcountry. A permit is currently required for SACs to enter into many of BC's parks, with some parks prohibiting SAC entry all together, however, this can be difficult to enforce. Education about best practices to reduce the probability of contact between SACs and wild ungulates could be undertaken, although the commitment and capability of individual trekkers to engaging in best practices, and the occurrence of unforeseen events (e.g. camelid escapes) would be expected to impact the effectiveness of these practices.

Table 7: Mitigation strategies for preventing pathogen transmission from SACs to wild ungulates.

Pathogen	***Asymptomatic infection in camelids***	***Environmental persistence***	***Pre-trip mitigation***	***Probable effectiveness of pre-trip mitigation***	***During-trip mitigation***	***Probable effectiveness of during-trip mitigation***
Mannheimia haemolytica	Y	L	Normal clinical respiratory exam of herd	Low	Prevent direct contact	Moderate to high
Pasteurella spp	Y	L	Normal clinical respiratory exam of herd	Low	Prevent direct contact	Moderate to high
Contagious ecthyma	Y	Y	Normal dermatological exam of animals in herd No contact with domestic sheep or goats	Low to moderate	Flyspray, Prevent direct contact	Low
Bovine viral diarrhea virus	Y	N	Herd negative serological testing High herd health status Post mortem/BVD testing of any deaths in animals > 1 year of age	Moderate	Prevent direct contact	Moderate
*Mycobacterium avium paratuberculosis (*Johne's Disease*)*	Y	Y	Absence of clinical signs in herd High herd health status Negative fecal culture	Low to moderate	Prevent direct contact Pack out manure	Low
Bluetongue virus	Y	Y (in midges only)	Restrict/ quarantine	High	Flyspray	Low

Pathogen	*Asymptomatic infection in camelids*	*Environmental persistence*	*Pre-trip mitigation*	*Probable effectiveness of pre-trip mitigation*	*During-trip mitigation*	*Probable effectiveness of during-trip mitigation*
			movement of camelids out of Bluetongue endemic regions to other backcountry areas during midge season (July 15 to Oct 15)			
Mycobacterium bovis	Y	Y	High herd health status No import of camelids from TB positive regions	Moderate	Prevent direct contact	Moderate to high
Corynebacterium pseudotuberculosis	N	Y	Normal clinical exam of lymph nodes, and submandibular region of animals in herd	High	-	Absence of clinical signs
Bovine leukemia virus	U	U	Insufficient information to comment	-	-	-
Parainfluenza-3	Y	N	Normal clinical respiratory exam of herd	Low	Prevent direct contact	Moderate to high
Oestrus ovis	U	Y	Deworm with an avermectin or other appropriate anthelmintic	High	-	n/a
Alpaca coronavirus	U	U	Insufficient information to comment	-	-	-

E. Risk summary

SACs are susceptible to many of the pathogens also found in domestic livestock. Furthermore, some pathogens previously thought to be insignificant in SACs are emerging in significance, and a number of novel pathogens have been described from SACs in recent years. It is feasible that over time, new pathogens might emerge that create significant new risks.

Although camelid to camelid and ruminant to camelid transmission was suspected or reported for some pathogens, we found no peer-reviewed literature describing pathogen transmission from camelids to either wild or domestic sheep and goats. It is important to note that because there is almost no evidence about shedding and transmission dynamics for most pathogens in camelids, lack of documented transmission from camelids cannot be considered evidence that transmission has not, or

could not occur. For example, anecdotal evidence suggests a link between the introduction of pack llamas into northwest BC, and the emergence of CE in Mountain Goats.

For each of the 15 pathogens reviewed in this paper (nine previously identified high risk pathogens plus 6 newly emerging pathogens), we used available information about SAC medicine and pathogen biology, along with the opinion of SAC and wild ungulate health experts, to estimate the probability of disease transmission from SACs to wild ungulates; and gathered the opinion of wild ungulate experts to estimate the impact of infection in wild ungulate populations. Three of the 15 pathogens were found not to be reported in camelids, and were removed from the final risk assessment. We then used the probability and impact estimates to qualitatively rank the risk for each of the remaining 12 pathogens as high, medium-high, medium, medium-low or low.

No pathogens were ranked as high risk.

We ranked *M. haemolytica, Pasteurella* spp. and CE as medium-high risk.

M. haemolytica and *Pasteurella* spp. were assigned a medium probability of SAC infection. There is no specific information about prevalence of *M. haemolytica and Pasteurella* spp in SACs in western North America, however asymptomatic infections in SACs are probable, and both organisms are common in cattle and sheep in North America. Both were assigned a medium probability of transmission because both are transmitted by close and immediate contact with limited environmental survival. Both were assigned high impact based on documented serious negative impacts of these pathogens on wild sheep and goats. Because environmental survival is limited and close contact is needed for transmission, we estimate that risk could be reduced to medium by ensuring that pack camelids were prevented from any contact with wild ungulates and with heavily-used wild ungulate habitat niches.

CE has a medium-high probability of SAC infection, as infection can persist for weeks to months, and the disease is common among small ruminants in western Canada. Probability of transmission was assessed as medium because the causal agent can be asymptomatically carried and shed during stress and can survive in scab material in the environment for extended periods of time, even years. Impact was assessed as medium-high for wild ungulates in general. Impact in Mountain Goats particularly can be high, with observed mortality and population declines following clinical recognition of the disease. Mitigation for CE is difficult because infected animals can have asymptomatic infections or subtle clinical signs, and there is not a sensitive diagnostic test for this virus. Nonetheless, by ensuring that all animals in any herd that use SACs for backcountry trekking have a normal dermatological exam, we estimate that overall risk could be reduced to medium.

We ranked BVDV, *Johne's Disease*, BTV and *M. bovis* as medium risk overall, but recognize that this risk ranking may vary from one ungulate species to the next.

BVDV was assessed as high probability of SAC infection because serosurveillance in North America shows moderate exposure in SAC herds, and it is ubiquitous in cattle in western North America; infected camelids have been demonstrated to transmit virus to other animals; PI and acutely infected animals shed large amounts of virus; and there is environmental survival. It was ranked as low impact to wild ungulates by experts, giving an overall medium risk. Mitigation for BVDV could be somewhat onerous

for SAC owners, however we estimate that risk could be reduced to low-medium with implementation of all mitigation measures.

Johne's Disease was assessed as medium-high probability of SAC infection because the bacteria is known to affect SACs; it is ubiquitous in livestock in western North America; it can be shed by animals without overt signs of disease during a long pre-clinical infection; and it has long environmental persistence. However, this pathogen in general is not highly infectious, transmission requires prolonged or repeated contact with infected fecal material, and it is most likely to affect young or immunosuppressed individuals. The impact of Johne's Disease on wild ungulates was assessed by experts as medium-low. Mitigation for Johne's Disease is very difficult and we estimate it would only cause a slight decrease in risk.

BTV was assessed as medium probability for SAC infection and risk of transmission in the limited geographic range and season for the vector, and was assessed as high potential impact to wild ruminants. Risk of transmission may be lower if, as suggested by Schulz et al. (2012) camelids are dead-end hosts for this pathogen. Because of the epidemiology of BTV, we estimate that risk could be reduced to low by implementing the suggested mitigation strategies.

M. bovis was assessed as low probability of SAC infection because it is extremely rare in any animal species in Canada, and the disease is highly unlikely in a SAC born in Canada. There was divergent opinion from experts about the probability of transmission and impact. Given the recent findings of *M. bovis* in camelids in the UK, the federally reportable listing of this pathogen, the challenges in eradicating this pathogen once it becomes endemic in a wildlife population, and recent cases in cattle in AB and BC, we have kept the potential impact as high. We estimate that risk posed by *M. bovis* would be difficult to reduce with mitigation and we have therefore not changed the risk even with mitigation.

Corynebacterium pseudotuberculosis, BLV, PI3, *Oestris ovis* and Alpaca Coronavirus were all ranked as low risk because all were evaluated by wild ungulate experts as likely to have low impact on wild ungulate populations. In the case of Alpaca Coronavirus, there has only been one reported outbreak in camelids, and the disease has not been identified in BC.

Overall, our risk assessment determined that there is medium uncertainty about the probability of infection in SACs from the pathogens reported here, and about the probability for transmission of these pathogens from SACs to wild ungulates. This uncertainty is based on:

1. Lack of basic knowledge about prevalence and shedding of pathogens in SACs.
2. Lack of validated diagnostic tests and preventative products for pathogens in SACs.
3. Lack of knowledge about SAC -wild ungulate interaction or contact patterns in backcountry areas.
4. The relative recent introduction of SACs to North America, and the resulting moderate to high risk of newly emerging infections (with pathogens not identified in this report).

Activities that could be undertaken to reduce these uncertainties include enhanced passive or active surveillance for pathogens of interest in SACs, infection and transmission studies, and validation of diagnostic tests and preventatives (e.g. vaccines) in SACs. These activities would be helpful to confirm

whether SACs shed the pathogens of interest under natural conditions; to quantify the magnitude and duration of shedding; and to determine whether testing and preventative husbandry might reduce or eliminate shedding. Enhanced surveillance or transmission studies would help to determine whether pathogens circulate between SACs and sheep and goats during natural interactions. Domestic sheep and goats pastured with guard camelids may provide a good natural model for study.

Our risk assessment also determined that there is medium uncertainty about the impact that the pathogens identified in this review may have on wild ungulates. Medium uncertainty is caused by limited reporting specific to BC on the:

1. Prevalence of the pathogens in wild ungulate species of importance, history of prior exposure of wild ungulate populations to the pathogens, and basic knowledge about the immediate and long-term health effects some of the pathogens may have on some wild ungulate populations.
2. Presence of stressors or other cumulative effects on the ability of wildlife populations to withstand the emergence of new pathogens.

In summary, we assessed the composite disease risk posed to wild ungulates by SACs accessing backcountry areas as medium-high with medium associated uncertainty. This assessment was driven primarily by the high impact and the medium-high risk posed by the respiratory pathogens, the medium-high risk posed by CE, and the medium risk posed by Johne's Disease. Mitigation could be practically undertaken to reduce risk posed by respiratory pathogens, although mitigation for CE and Johne's Disease is much more challenging. It is important to note that over time new pathogens might emerge in SACs that create significant new risk not discussed in this report. In particular, if SACs are documented to be susceptible to infection with *M. ovipneumonia* or *M. conjuntivae*, this would increase risk.

F. References

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G. Glossary of abbreviations

AB	Alberta
AHC	Animal Health Centre
BC	British Columbia
BLV	Bovine Leukemia Virus
BTV	Bluetongue Virus
BVDV	Bovine Viral Diarrhea Virus
CAHSN	Canadian Animal Health Surveillance Network
CCH	Centre for Coastal Health
CE	Contagious Ecthyma
CFIA	Canadian Food Inspection Agency
CLA	Caseous lymphadenitis
CWHC	Canadian Wildlife Health Cooperative
EHD	Epizootic hemorrhagic disease
FLNRORD	Ministry of Forests, Lands, Natural Resource Operations and Rural Development
LIM	Laboratory Information System
MB	Manitoba
NT	Northwest Territories
PDS	Prairie Diagnostic Services
PI	Persistently Infected
PI-3	Parainfluenza Virus 3
SAC	South American Camelid
SK	Saskatchewan
TB	Tuberculosis
YT	Yukon

Appendix 1. Literature search keywords

Category	*Keywords*
Animal	Alpaca OR llama OR camelid OR bighorn OR caribou OR reindeer OR elk OR "mountain goat" OR "thinhorn sheep" OR "dall's sheep" OR "stone's sheep" OR cattle OR bovine OR ovine OR caprine OR sheep* OR goat* OR livestock OR "small ruminant" OR "south American camelid" OR SAC
Diseases	"Pasteurella multocida" OR "Pasteurella trehalosi" OR "Johne's disease" OR "Mycobacterium avium paratuberculosis" OR Orf OR "contagious ecthyma" OR "parainfluenza 3" OR "Nasal bot fly" OR "Oestrus ovis" OR Lungworm OR "Muellaris capillaris" OR Tuberculosis OR Brucellosis OR Keratoconjunctivitis OR KCS OR "Mycoplasma conjunctivae" OR "Mycoplasma ovipneumoniae" OR "Mannheimia haemolytica" OR BVD OR "bovine viral diarrhea"
Disease Alternate	(Bacteria* OR parasite OR parasitic OR virus OR viral OR "reportable disease")
Transmission	(Disease OR "fecal-oral" OR respiratory OR aerosol OR secretion OR excretion OR transmission OR exposure OR contamination OR vector)
Risk	(Risk OR probability OR impact)
Modified Animal	(Alpaca OR llama OR camelid) **AND** (bighorn OR caribou OR reindeer OR elk OR "mountain goat" OR "mt. goat" OR "mt goat OR "thinhorn sheep" OR "dall's sheep" OR "stone's sheep" OR cattle OR bovine OR ovine OR caprine OR sheep* OR goat* OR livestock)

Initial searches with detailed 'Animal' and 'Diseases' search phrases yielded too few results, leading to the use of 'Disease Alternate' and 'Modified Animal' search strings instead.

Appendix 2. Interview questions

< *Date* >

Dear < *Interviewee* >

The Center for Coastal Health (CCH, located in Nanaimo, BC, Canada), on behalf of the British Columbia Ministry of Forests, Lands, Natural Resource Operations and Rural Development (FLNRORD), was recently asked to undertake a risk assessment to help inform policy concerning llama and alpaca use in BC's backcountry regions with specific focus on the risk of disease transmission from South American Camelids (SACs) to wild sheep and goat populations, with particular concern in regards to thinhorn sheep in northwestern British Columbia. This will update previous risk assessments (see Stephen and Schwantje (2003)[24] and Garde et al (2009)[25]). Tasks include to identify new and emerging diseases of SACs, describe and evaluate recent findings regarding the epidemiology, diagnosis and control of pathogens that affect both SACs and other ungulates, and to document any reports of pathogen transfer from SACs to domestic or wild sheep and goats. We conducted a literature review (peer-reviewed and unpublished, including government polices from a number of States and Provinces in western North America), and summarized diagnostic results from submissions of SACs to provincial diagnostic laboratories.

We are now approaching individuals who have experience with llama and alpaca diseases, as well as those who can speak to the impacts of pathogens from domestic livestock on wild sheep and goats. Your name was identified as part of the literature review and with discussions with FLNRORD staff. Please let us know if you feel that you received this request in error, or if you know someone who you feel may be more qualified to speak on these issues. Otherwise, we greatly value your time and expertise in helping us fill in the gaps identified in our literature review. You are welcome to participate by responding in writing, or by providing a contact phone number and discussing these questions via a phone interview with one of the CCH staff. Please be advised that due to time constraints, we require all responses/interviews to be completed by **May 19, 2017**. Thank you in advance for your time.

We identified 15 pathogens that we classified as of most concern for reasons that include: 1) it was listed in previous risk assessments as of high risk for wild sheep and goat, 2) it is a novel pathogen, having been reported for the first time in SACs since 2009, or 3) it appears to have undergone a change in epidemiology and is now considered to be a more significant cause of disease of SACs.

Alpaca coronavirus	*Corynebacterium pseudotuberculosis*	*Mycoplasma conjunctivae*
Bluetongue virus	*Mannheimia haemolytica*	*Mycoplasma ovipneumoniae*
Bovine leukemia virus	*Muellerius capillaris*	*Oestrus ovis*

[24] Stephen, C., & Schwantje, H. (2003). *Communicable disease risks to wildlife from camelids in British Columbia*. Nanaimo, BC.

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Bovine viral diarrhea virus	*Mycobacterium avium paratuberculosis*	Parainfluenza-3
Contagious Ecthyma	*Mycobacterium bovis*	*Pasteurella* spp

Responses can be submitted by email to Stefan Iwasawa (Stefan.Iwasawa@viu.ca), or contact the CCH office at 250-753-3245, extension 2889.

We thank you in advance for your time,

Sincerely,

Tyler Stitt, DVM MPH&TM BSc
Centre for Coastal Health
900 Fifth St, Nanaimo, BC, V9R 5S5

and

Theresa Burns, DVM MSc PhD
Centre for Coastal Health
900 Fifth St, Nanaimo, BC, V9R 5S5

Questions for Camelid Disease Specialists

We would like to learn more about pathogens in SAC that might also cause disease in (wild) sheep and goats. Although we have identified 15 pathogens (listed below), we invite you to suggest other pathogens that you might recommend we investigate further. If you are completing this survey electronically, please type your responses directly into the tables below each question. The table cells will expand as needed to fit longer answers.

1. Please describe the following aspects of the epidemiology of the listed pathogens in South American camelids:

    a. Prevalence in domestic camelids in western and northern North America
    b. The route of infection and shedding
    c. The presence of infected sub-clinical carrier states / shedders
    d. Any evidence for transmission from, or to, other species, such as cattle, sheep and goat
    e. Survival of the pathogen in the environment

	EPIDEMIOLOGY
Alpaca coronavirus	
Bluetongue virus	
Bovine leukemia virus	
Bovine viral diarrhea virus	
Contagious ecthyma	
Corynebacterium pseudotuberculosis	
Mannheimia haemolytica	
Muellerius capillaris	
Mycobacterium avium paratuberculosis	
Mycobacterium bovis	
Mycoplasma conjunctivae	
Mycoplasma ovipneumoniae	
Oestrus ovis	
Parainfluenza-3	
Pasteurella spp	

EPIDEMIOLOGY	
OTHER	

2. Please describe current available methods for diagnosis and testing of these pathogens in South American camelids, including sensitivity and specificity of the tests in camelids where known.

	AVAILABLE DIAGNOSTICS / TESTS / SPECIMENS	**SENSITIVITY**	**SPECIFICITY**	**OTHER INFORMATION**
Alpaca coronavirus				
Bluetongue virus				
Bovine leukemia virus				
Bovine viral diarrhea virus				
Contagious ecthyma				
Corynebacterium pseudotuberculosis				
Mannheimia haemolytica				
Muellerius capillaris				
Mycobacterium avium paratuberculosis				
Mycobacterium bovis				
Mycoplasma conjunctivae				
Mycoplasma ovipneumoniae				
Oestrus ovis				
Parainfluenza-3				
Pasteurella spp				
OTHER				

3. Please describe current accepted methods for prevention, treatment and management of these pathogens in South American camelids, including efficacy of vaccines in camelids (and potential impacts on diagnostic tests) where known.

	PREVENTION AND VACCINES	**TREATMENT AND MANAGEMENT**
Alpaca coronavirus		
Bluetongue virus		
Bovine leukemia virus		
Bovine viral diarrhea virus		
Contagious ecthyma		
Corynebacterium pseudotuberculosis		
Mannheimia haemolytica		
Muellerius capillaris		
Mycobacterium avium paratuberculosis		
Mycobacterium bovis		
Mycoplasma conjunctivae		
Mycoplasma ovipneumoniae		
Oestrus ovis		
Parainfluenza-3		
Pasteurella spp		

Questions for Wild Sheep and Goat Disease Specialists

We would like to identify potential for opportunities for contact between camelids and wild sheep and goats (Q1), as well as anticipated outcomes if camelids should spread disease to wild sheep and goat (Q2). Although we have identified 15 pathogens (listed in Q2 below), we invite you to suggest other pathogens that you might recommend we investigate further. If you are completing this survey electronically, please type your responses directly into the tables below each question. The table cells will expand as needed to fit longer answers.

1. Given what you know about the behavior and habitat use of wild sheep and goat in Western Canada, please estimate the probability that a camelid used as a pack animal in backcountry areas would have contact with wild sheep and goat. Here, "contact" refers to the type of pathogen-specific contact required for transmission between two animals. Please rank the probability for contact and provide any comments or reasoning to support your ranking decision. We recognize many of the responses will be opinion/experience based, however given that scientific evidence is scarce, expert opinion can provide very helpful information.

    a. Use a scale of 0 to 5, where 0 = no chance, 1 = very low probability, 2 = low probability, 3 = moderate probability, 4 = high probability, 5 = almost for sure, U = unable to estimate.
    b. Please provide a reason for your ranking, for example, is there anecdotal or published evidence of disease transfer from camelids to sheep and goat (either domestic or wild)? If published, please provide a reference. If anecdotal, please describe it in detail.

	RISK	**REASON**
Direct contact between animals, for example, as nose-to-nose contact. e.g. CONTAGIOUS ECTHYMA		
Indirect contact between animals, where pathogens are deposited onto a surface by one animal and acquired by another (e.g. feces on pasture). This requires animals to be in the same location in a time period consistent with the environmental survivability of the pathogen, but for now assume within 4 weeks. e.g. BOVINE VIRAL DIARRHEA VIRUS		
Droplet or **airborne** transmission between animals in close proximity to one another. Animals need to be in the same general area at the same time, as respiratory pathogens tend to have short environmental survivability. e.g. *MYCOPLASMA OVIPNEUMONIAE*		
Vector-borne pathogens require a midge, mosquito, black fly etc to spread pathogens from an infected to non-infected animal. Animals need to be in the same general location within an active insect season. e.g. BLUETONGUE VIRUS		

2. Please rank the anticipated <u>impact</u> that the pathogens might have on wild sheep and goat populations in Western Canada, assuming these pathogens became established in these populations.

    a. Use a scale of 0 to 5, where 0 = no impact, 1 = minimal impact, 2 = minor impact, 3 = moderate impact, 4 = high impact, 5 = severe impact, U = unable to estimate.
    b. Please provide a reason for your ranking, for example, can the pathogen be maintained in the wild populations of sheep and goat? Or have the wild sheep and goat populations already been exposed to the pathogen? Is there anecdotal or published evidence of the disease in wild sheep and goat? If published, please provide a reference. If anecdotal, please describe it in detail.

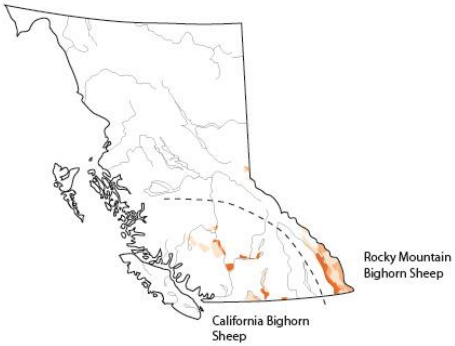
	IMPACT	**REASON**
Alpaca coronavirus		
Bluetongue virus		
Bovine leukemia virus		
Bovine viral diarrhea virus		
Contagious ecthyma		
Corynebacterium pseudotuberculosis		
Mannheimia haemolytica		
Muellerius capillaris		
Mycobacterium avium paratuberculosis		
Mycobacterium bovis		
Mycoplasma conjunctivae		
Mycoplasma ovipneumoniae		
Oestrus ovis		
Parainfluenza-3		
Pasteurella spp		
OTHER		

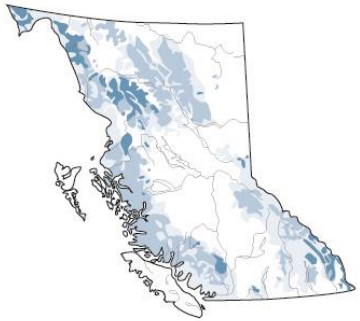
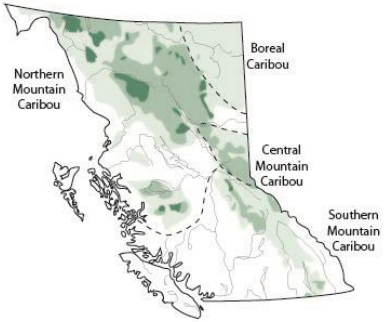
Appendix 3. Abundance and distribution of wild ungulates in British Columbia

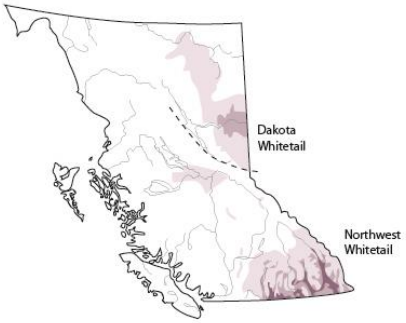
The figures in the following table have been adapted from Ecology, Conservation and Management reports available with the BC Ministry of Environment, Lands and Parks for clarity of printing. The distribution data on which these figures are based was last updated in 2000.

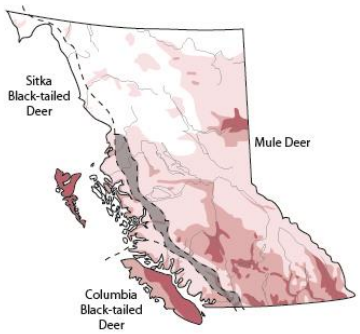
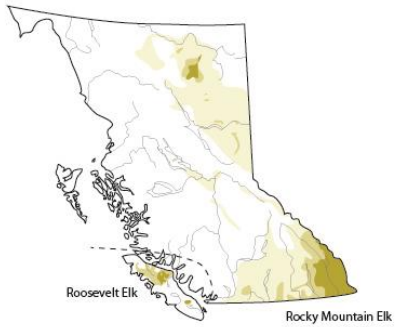
Legend: Dark colors/tints – Plentiful; Medium colors/tints – Moderate; Light colors/tint – Few; White – Absent

List Status: Red – extirpated, endangered or threatened; Blue – of special concern; Yellow – at least risk of being lost

Species	*Distribution*	***Subspecies***	***List Status***	***Summer/Fall habitat***	***Winter/Spring habitat***	***Recorded Interactions***	***Migration patterns***
Bighorn Sheep (REF)			Blue (2015)	Alpine May/Jun to Late Sep/Oct	Low-elevation grasslands in the Bunchgrass, Ponderosa Pine and Interior Douglas-fir Late Sep/Oct to May/Jun 300-1825 m, steep, south-to southwest-facing, and dominated by bluebunch wheatgrass Alpine ridges	Elk Cattle To a lesser degree, with mountain goat and deer	Local shifts in elevation Migrate through forested terrain to distant alpine ranges

Species	*Distribution*	***Subspecies***	***List Status***	***Summer/Fall habitat***	***Winter/Spring habitat***	***Recorded Interactions***	***Migration patterns***
Mountain Goat (REF)			Blue (2015)	Steep terrain At or above timberline	Steep terrain South to west exposure	Elk, deer, caribou and Mountain Sheep sometimes graze with goats on alpine-subalpine meadows near cliffs	Local shifts in elevation Short distance travel to winter-spring and summer ranges Lower elevation mineral licks
Caribou		Boreal (REF) (REF2)	Red	Boreal forests	Boreal forests Flat terrain Open forests and muskeg	Moose	Limited information available
		Northern Mountain	Blue	High elevations in spring / summer Low elevations in fall	Windswept alpine slopes Muskegs and low elevation forests		Up to 140 km reported
		Central Mountain	Red	Subalpine forest Alpine habitat	Subalpine forest and alpine habitat Windswept mountain ridges Low elevation pine forests		

Species	*Distribution*	***Subspecies***	***List Status***	***Summer/Fall habitat***	***Winter/Spring habitat***	***Recorded Interactions***	***Migration patterns***
		Southern Mountain	Red	Downslope to Engelmann Spruce-subalpine Fir or Interior cedar hemlock Alpine tundra	Rugged peaks & gentle highland terrain Alpine tundra	Deer Elk	
Thinhorn Sheep		Dall's Sheep (REF)	Blue (2010)	Precipitous terrain	Precipitous terrain and nearby treeless ranges Alpine zone from 1500 m to 2200 m in elevation		Lower elevation mineral licks
		Stone's Sheep (REF)	Blue (2010)	Precipitous terrain Alpine pastures at 1200 to 1500 m	Precipitous terrain and nearby treeless ranges Alpine zone from 1500 m to 2200 m in elevation		Lower elevation mineral licks
White-tailed Deer (REF)			Yellow (2015)	Low elevation Valley farmlands	Low elevation Valley farmlands South to southwest-facing slopes and terraces Aspen, cottonwood and willow groves along rivers and wetlands	Elk Mule Deer Cattle	Seasonal movements usually upstream or downstream along major valleys, or cross-valley from north slopes in summer to south-facing in winter

Species	*Distribution*	***Subspecies***	***List Status***	***Summer/Fall habitat***	***Winter/Spring habitat***	***Recorded Interactions***	***Migration patterns***
Mule Deer (REF)			Yellow (2015)	Low elevations primarily High elevations occasionally	Shrub lands in the dry forest zone and on steep south and west-facing sites with broken terrain Valley side ranges	Rocky Mountain Elk White-tailed Deer Cattle	Change in elevation dependant on time of year
Moose (REF)			Yellow (2015)	Valleys, lake shores, swamps and beaver ponds	River valleys	Caribou Elk Deer Mountain sheep	
Elk		Roosevelt (REF)	Blue (2010)	Mountainous areas Old growth forests Grassy interior valleys Subalpine meadows and avalanche tracks	Mountainous areas Old growth forests Grassy interior valleys River valley with low-elevation forest Riparian, floodplain, wetland and	Deer Less commonly with Moose, Bighorn Sheep, or Mountain Caribou	

Species	*Distribution*	***Subspecies***	***List Status***	***Summer/Fall habitat***	***Winter/Spring habitat***	***Recorded Interactions***	***Migration patterns***
					estuarine meadow habitats		
		Rocky Mountain (REF)	Yellow (2015)	Subalpine and alpine basins and avalanche tracks	Open forest Grassy benchlands Floodplain marshes Subalpine and alpine basins and avalanche tracks in May/June	Deer Less commonly with Moose, Bighorn Sheep, or Mountain Caribou	Distances vary

Appendix 4. Infectious agents of llamas, domestic sheep and goats, and wild sheep and goats

The following tables were adapted from Garde et al. (2009), and indicate documented natural and experimental infections where the organism, or antibodies to the organism, were detected from captive and free ranging animals. Please refer to _ENREF_9Garde et al. (2009) for the supporting references. These pathogen tables are provided here for quick reference only. It is not known if the authors reference llamas here as a unique species (*Lama glama*), or as category name for all 4 recognized SAC species.

Legend: S – domestic sheep; G – domestic goat; L – llamas; D – Dall's sheep; BH – Bighorn sheep; SS – Stone's sheep; MG – Mountain goat; X – present; U – unknown

Bacteria

Bacteria	***S***	***G***	***L***	***D***	***BH***	***SS***	***MG***
Acholeplasma oculi	X	X					
Actinobacillus capsulates			X				
Actinobacillus lignieresii	X						
Actinomyces lamae			X				
Actinomyces bovis	X	X					
Actinomyces sp.	X	X	X	X	X	X	X
Anaplasma ovis	X	X					
Anaplasma sp.	X	X	X		X		
Arcanobacterium pyogenes	X	X	X	X	X	X	
Bacillus anthracis	X	X	X				
Bacillus sp	X	X	X		X		
Bacteroides fragilis			X				
Bordetella sp.					X		
Branhamella ovis	X	X					
Brucella abortus	X	X	X		X		
Brucella melitensis	X	X	X				
Brucella ovis	X	X			X		
Brucella spp.		X		X			
Burkholderia pseudomallei			X				
Campylobacter fetus	X	X					
Campylobacter jejuni	X	X					
Chlamydophila abortus	X	X					
Chlamydophila pecorum	X	X					
Chlamydophila psittaci	X	X			X		
Clostridium botulinum	X	X	X				
Clostridium chauvoei	X	X	X				
Clostridium haemolyticum	X	X					
Clostridium novyi	X	X	X				

Bacteria	S	G	L	D	BH	SS	MG
Clostridium perfringens	X	X	X		X		
Clostridium sordelli			X		X		
Clostridium septicum	X	X	X				
Clostridium tetani	X	X	X				
Corynebacterium pseudotuberculosis	X	X	X				
Corynebacterium renale	X	X					
Coxiella burnetii	X	X		X			
Dermatophilus congolensis	X	X	X				
Dichelobacter nodosus	X	X					
Enterococcus sp.			X				
Eperythrozoon ovis	X	X					
Erysipelothrix rhusiopathiae	X	X					
Escherichia coli	X	X	X	X	X		
Francisella tularensis	X						
Fusobacterium necrophorum	X	X	X	X	X	X	
Histophilus	X						
Hemophilus ovis	X				X		
Hemophilus somnus	X	X					
Hemophilus sp.			X				
Klebsiella pneumoniae	X	X	X		X		
Leptospira icterohemmorhagica			X				
Leptospira interrogans subsp Bratislava	X						
Leptospira interrogans subsp Grippotyphosa	X	X	X		X		
Leptospira interrogans subsp Hardjo	X	X			X		
Leptospira interrogans subsp Icterohaemorrhagica	X	X	X				
Leptospira interrogans subsp Pomona	X	X			X		
Listeria innocua			X				
Listeria monocytogenes	X	X	X				
Mannheimia haemolytica	X	X	X	X	X	X	X
Moraxella bovis	X	X					
Moraxella lacunata			X				
Moraxella liquefaciens			X				
Mycobacterium bovis	X	X	X				
Mycobacterium avium paratuberculosis	X	X	X	X	X		X
Mycobacterium tuberculosis			X				
Mycoplasma agalactiae	X	X					
Mycoplasma arginini	X	X			X		
Mycoplasma bovis	X	X					
Mycoplasma capricolum		X					
Mycoplasma conjunctivae	X	X					
Mycoplasma mycoides	X	X	X				

Bacteria	S	G	L	D	BH	SS	MG
Mycoplasma ovipneumoniae	X	X		X			
Mycoplasma sp.	X	X	X	X	X		
Neisseria sp.					X		
Nocardiosis sp.			X				
Pasteurella multocida	X	X	X	X	X		
Pasteurella trehalosi	X	X		X	X	X	
Rhodococcus equi	X		X		X		
Salmonella abortus ovis		X					
Salmonella cholerasuis			X				
Salmonella dublin		X					
Salmonella sp.			X				
Salmonella typhimurium	X	X					
Staphylococcus sp.	X	X	X		X		
Streptococcus sp.	X	X	X		X		
Streptococcus zooepidemicus			X		X		
Ureaplasma	X	X					
Yersinia enterocolitica		X					
Yersinia pseudotuberculosis		X	X				

Viruses

Virus	S	G	L	D	BH	SS	MG
Adenovirus	X	X	X				
Akabane virus disease	X	X					
Bluetongue	X	X	X		X		
Border disease virus	X	X	X				
Bovine adenovirus			X				
Bovine coronavirus			X			X	
Bovine enterovirus			X				
Bovine herpes virus 1		X	X				
Bovine viral diarrhea virus			X	X	X		X
Camel pox			X				
Caprine arthritis-encephalitis virus		X					
Caprine herpes virus	X	X					
Cache Valley virus	X						
Contagious ecthyma	X	X	X	X	X		X
Coronavirus	X	X	X				
Epizootic hemorrhagic disease	X	X		X	X	X	X
Equine herpes virus type 1			X				
Infectious bovine rhinotracheitis	X	X	X		X		
Influenza A virus			X				
Influenza B virus			X				

Louping ill encephalomyelitis		X					
Malignant catarrhal fever	X	X		X		X	
Ovine herpes virus 1	X						
Ovine lentivirus (ovine progressive pneumonia virus)	X	X					
Papilloma virus	X	X					
Parainfluenza Type 3	X	X	X	X	X		
Rabies virus	X	X	X	X	X		
Respiratory syncytial virus	X	X	X	X	X		
Rift valley fever			X				
Rotavirus	X	X	X				
Vesicular stomatitis		X	X				

Fungus

Fungus	***S***	***G***	***L***	***D***	***BH***	***SS***	***MG***
Absidia corynebifora			X				
Aspergillus sp.			X				
Blastocysistis sp.			X				
Microsporum canis	X	X					
Trichophyton canis	X						
Trichophyton gypseum	X						
Trichophyton mentagrophytes	X	X	X				
Trichophyton verrucosum	X	X	X				

Protozoa

Protozoa	***S***	***G***	***L***	***D***	***BH***	***SS***	***MG***
Cryptosporidium parvum	X	X	X				
Eimeria spp.	X	X	X	X	X	X	X
Eperythrozoon ovis	X	X	U				
Eperythrozoon-like			X				
Giardia	X	X	X				
Neospora caninum	X	X					
Pneumocystis carinii		X					
Sarcocystis ferovis					X		
Sarcocystis sp.	X	X	X	X	X		
Sarcocystis tenella					X		
Toxoplasma gondii	X	X	X	X	X		
Trichomonas sp.			X				
Trypanosoma sp.			X	X			

Helminths

Helminths	***S***	***G***	***L***	***D***	***BH***	***SS***	***MG***
Bunostomum sp.	X	X	X				
Camelostrongylus mentulatus			X				
Capillaria sp.			X		X		
Chabertia ovina	X	X	X		X		
Coenurus cerebralis (Taenia multiceps)		X					
Cooperia oncophera					X		
Cooperia spp.	X	X	X		X		
Cooperia surnabada					X		
Dicrocoelium dendriticum			X				X
Dictyocaulus filaria	X	X	X				
Dictyocaulus viviparous			X		X		
Echinococcus granulosus (hydatid cysts)		X	X				X
Elaeophorosis schneideri	X	X					
Fasciola gigantica			X				
Fasciola hepatica	X	X	X				X
Fasciola magna	X	X	X		X		
Graphinema aucheniae			X				
Haemonchus contortus	X	X	X		X		
Haemonchus placei					X		
Haemonchus sp.			X		X		
Marshallagia marshalli				X	X		X
Marshallagia sp.	X	X		X	X	X	X
Moniezia benedeni					X		X
Moniezia expansa					X		X
Moniezia sp.	X	X	X	X	X	X	X
Muellerius capillaris	X	X	X		X		
Muellerius minutissimus							X
Nematodirella antilocaprae							X
Nematodirus abnormalis					X		
Nematodirus archari				X	X		
Nematodirus battus	X	X	X				
Nematodirus becklundi							X
Nematodirus davtiani				X	X		X
Nematodirus filicollis				X	X		X
Nematodirus helvetianus					X		X
Nematodirus lamae			X				
Nematodirus lanceolatus					X		
Nematodirus maculosus				X	X		X
Nematodirus odocoilei					X		
Nematodirus oiratianus				X	X		X
Nematodirus sp.				X	X	X	X

Helminths	*S*	*G*	*L*	*D*	*BH*	*SS*	*MG*
Nematodirus spathiger				X	X		
Oesophagostomum spp.	X	X	X		X		X
Oesophagostomum venulosum					X		X
Onchocerca sp.	X	X					
Ostertagia gruehneri				X			
Ostertagia lyrata					X		
Ostertagia ostertagi	X	X	X	X	X		X
Ostertagia sp.	X	X	X		X		X
Parelaphostrongylus odocoilei				X		X	X
Parelaphostrongylus tenuis	X	X	X		X		
Pelodera strongyloides	X	X					
Protostrongylus rufescens	X	X					
Protostrongylus frosti					X		
Protostrongylus rushi				X	X		X
Protostrongylus spp.				X		X	X
Protostrongylus stilesi				X	X		X
Pseudostertagia bullosa					X		
Setaria cervi					X		
Skrjabinema oreamni							X
Skrjabinema ovis				X	X		X
Skrjabinema sp.					X	X	
Strongyloides papillosus	X	X					
Strongyloides sp.			X				X
Taenia hydatigena	X	X		X	X		X
Taenia krabbei					X		
Teladorsagia boreoarcticus				X	X		X
Teladorsagia circumcincta	X	X	X	X	X		X
Teladorsagia davtiani							X
Teladorsagia trifucata	X	X					X
Teladorsagia sp.			X				
Thelazia californiensis			X				
Thelazia rhodesii	X	X					
Thelazia sp.			X				
Thysaniezia giardi			X				X
Thysanosoma actinioides					X		X
Trichostrongylus axei			X		X		X
Trichostrongylus colubriformis					X		X
Trichostrongylus rugatus					X		
Trichostrongylus spp	X	X	X		X	X	X
Trichuris oreamnos							X
Trichuris ovis	X	X			X		X
Trichuris schumakovitschi				X	X		X

Helminths	S	G	L	D	BH	SS	MG
Trichuris sp.			X	X	X	X	X
Trichuris tenuis			X				
Wyominia tetoni				X	X		

Ectoparasites

Ectoparasites	S	G	L	D	BH	SS	MG
Bovicola jellisoni					X		
Bovicola ovis					X		
Cephenemyia sp.			X				
Chorioptes caprae		X					
Chorioptes bovis			X				
Chorioptes ovis	X						
Chorioptes sp.			X				
Damalinia breviceps			X				
Damalinia caprae		X					
Damalinia oreamnidis							X
Damalinia ovis	X						
Demodex caprae		X					
Demodex ovis	X						
Dermacentor albipictus					X	X	X
Dermacentor andersoni	X	X			X		X
Dermacentor hunteri					X		
Dermacentor variabilis	X	X					
Lignonathus ovillus	X						
Lignonathus pedalis	X						X
Lignonathus stenopis		X					
Melophagus ovinus	X						
Microthoracius cameli			X				
Microthoracius mazzai			X				
Microthoracius praelongiceps			X				
Oestrus ovis	X	X	X		X		
Otobius megnini			X		X		X
Psoroptes cuniculi		X					
Psoroptes equi var cervinus					X		
Psoroptes ovis	X		X				
Ectoparasites:	S	G	L	D	BH	SS	MG
Psoroptes sp.			X		X	X	
Pthiraptera spp.			X				
Sarcoptes scabei	X	X	X				
Vermipsylla sp.			X				

* Scrapie has been described in domestic sheep and goats, but not in llamas, alpacas or wild sheep and goat