Bighorn Sheep and Mountain Goat Herd Health Assessments

Federal Aid in Wildlife Restoration Grant W-166-SI

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Project Background:
Respiratory disease continues to have pronounced effects on bighorn sheep populations throughout the western US (Aune et al. 1998, Gross et al. 2000, Singer et al. 2000, Cassirer et al. 2007, Cassirer et al. 2013). In Montana, bighorn sheep populations have experienced approximately 25 known respiratory disease epizootic events since 1979 (Sells et al. 2015). During the single winter of 2009-10, 4 bighorn sheep populations covering a large portion of western Montana experienced simultaneous all-age die off events due to respiratory disease (Edwards et al. 2010).

Translocation is a commonly used tool for the management of bighorn sheep in Montana and has historically been used in mountain goat population management as well. The need for proactive health monitoring to guide translocation decisions is well understood in Montana (Carlsen & Erickson 2010). Research suggests that translocated bighorn sheep face higher mortality rates from pneumonia when compared to their resident counterparts (Plowright et al 2013). In addition, there are now several observed cases throughout the western US of pneumonia die-offs in recipient bighorn sheep herds following a translocation event, at least raising the possibility that new pathogens or strains were inadvertently introduced or that immunologically naïve transplants fueled local disease transmission (Sandoval et al. 1987). Respiratory disease, and its associated pathogens, serves as one important example of a larger range of infectious organisms that are capable of affecting translocation success in both bighorn sheep and mountain goats. Proactive monitoring for microbial pathogen communities of source or recipient herds prior to translocation could improve the success of these actions. Montana Fish, Wildlife, and Parks' (FWP) 2010 Bighorn Sheep Conservation strategy states that Montana will obtain and utilize health profiles for both donor and recipient herds to help guide bighorn sheep translocations (Carlsen & Erickson 2010).

Mountain goats and bighorn sheep are susceptible to many of the same parasites and pathogens and often overlap in distribution, raising the question of how these two species may affect each other's health, including cases in which one species is translocated into another species' range. An outbreak of respiratory disease among sympatric mountain goats and bighorn sheep in Nevada in 2013 underscores the potential for these two species to share parasites and pathogens (Blanchong et al. 2018). Mountain goats in the Greater Yellowstone Area carry the same respiratory pathogen community as bighorn sheep populations in the region, indicating the potential for cross-species transmission in Montana (Lowrey et al. 2018).

This report covers six years of effort to evaluate the pathogen communities and baseline health status of bighorn sheep and mountain goat herds across Montana. This information on bighorn sheep and mountain goat herds is needed to inform translocation efforts that are intended to help conserve these species, and to minimize the introduction and spread of novel pathogens within and between the two species. As part of FWP's Bighorn Sheep and Mountain Goat Health Program, we have developed a sampling and monitoring plan consistent with programs in other western states and which prioritizes pathogen sampling for herds that are likely to be involved in translocation events in the near future, either as donor or recipient herds.

Methods:

Study areas

Between 2016 and 2021, we sampled 516 animals across 14 bighorn sheep herds (N = 465) and 3 mountain goat herds (N = 51) that FWP regional wildlife program managers prioritized for sampling to inform current management and for near-future use as translocation source or recipient herds (Table 1; Figures 1 & 2). Some of these herds were sampled over multiple years to increase sample sizes (e.g. HDs 122, 250); others were sampled multiple times because they were used as source herds for translocations (e.g. HDs 199, 482, and 622) or within-range translocations (e.g. HDs 302).

Table 1. Bighorn sheep (BHS) and mountain goat (MG) herds receiving a health assessment between 2016-2021. Herd size, demographic performance, population objectives, target and actual sample sizes, capture dates, methods and rationale for sampling are noted. Numbers of captured yearlings and lambs, and adult (≥2 yrs) females and males are also noted.

					Information from handled animals						
HD & Herd Name	**Est. herd size**	**Recent (5 yr) demographic performance**	**Population objective**	**Target sample size**	**Dates of capture**	**Total animals caught**	**Adult Females (≥2 yrs)**	**Adult Males (≥2 yrs)**	**Lambs/ Kids & Yearlings**	**Capture Method(s)**	**Reason for health assessment**
BHS HD 101: Koocanusa	25	Declining	≥150	18	2/10/2017-3/14/2017	2	2	0	0	Ground darting	Candidate for augmentation
BHS HD 102: Galton	90	Stable	≥150	29	1/12/2017	32	13	11	8	Drop-net	Possible source herd
BHS HD 121: North Clark Fork	50	Decline	250	8	2/2-3/2016	3	3	0	0	Helicopter net-gunning	Candidate for augmentation
BHS HD 122: Clark Fork Cut-off	18	Declining	100-125	12	2/4/2016 & 2/14/2017	6	6	0	0	Helicopter net-gunning	Candidate for augmentation
BHS HD 122: Clark Fork Cut-off	30	Decline	115	8	2/2-3/2016	4	4	0	0	Helicopter net-gunning	Candidate for augmentation
BHS HD 199: Wildhorse Island BHS	140	Stable	120	28	2/3-4/2020	26	15	9	2	Helicopter net-gunning	Possible source herd
BHS HD 199: Wildhorse Island BHS	140	Declining	120	30	2/18/2021	26	17	4	5	Helicopter net-gunning	Translocation to Tendoy Mountains
BHS HD 250: Painted Rocks	65	Stable	120	30	12/13/2018; 1/7/2019 – 2/21/2019*	15	11	4	1	Helicopter net-gunning (2018) and ground darting (2019)	Evaluate health to update population objective
BHS HD 250: Painted Rocks	70	Declining	120	30	2/19/2021	11	7	3	1	Helicopter net-gunning	Evaluation of *Psoroptes ovis* infection and continued deployment of GPS collars.
BHS HD 301: Spanish Peaks	172	Stable	150	30	2/20/2018	15	13	2	0	Helicopter net-gunning	Evaluation of health of native herd
BHS HD 302: Taylor Hilgard	184	Stable	200-300	NA	2/20/2016	35	22	6	7	Drop-net	Within range translocation

HD & Herd Name	Est. herd size	Recent (5 yr) demographic performance	Population objective	Target sample size	Dates of capture	Total animals caught	Adult Females (≥2 yrs)	Adult Males (≥2 yrs)	Lambs/ Kids & Yearlings	Capture Method(s)	Reason for health assessment
BHS HD 302: Taylor Hilgard	184	Stable	200-300	NA	12/18/2016	30	13	6	11	Drop-net	Health survey; one of the statewide bighorn sheep study herds
BHS HD 302: Taylor Hilgard	186	Stable	200-300	NA	1/20/2018	32	16	5	11	Drop-net	Within range translocation
BHS HD 330: Greenhorn BHS	50	Stable	125 (+/- 20%)	23	2/24/2021	22	11	5	6	Helicopter net-gunning	Herd health to inform future management
BHS HD 340: Highlands	75	Stagnant	125	16	2/4/2016	16	13	0	3	Helicopter net-gunning	Evaluation of health
BHS HD 441: North Fork Birch Creek – Teton	90	Stable/ Increasing	200	24	2/13/2021	7	2	3	2	Helicopter net-gunning	Candidate for augmentation
BHS HD 482: Fergus	422	Declining	325	60	12/13/2016 & 2/21/2017	60	43	0	17	Helicopter net-gunning	Translocation to Beartooth Wildlife Management Area
BHS HD 482: Fergus	440	Stable	325	50	12/15-16/2020	50	39	4	7	Helicopter net-gunning	Translocation to Little Belt Mountains
BHS HD 622: Middle Missouri Breaks	236	Stable	175-200	20	2/10/2018	20	14	0	6	Helicopter net-gunning	Evaluation as source population
BHS HD 622: Middle Missouri Breaks	380	Growth	200	19	1/26/2016	20	10	2	8	Helicopter net-gunning	Translocation to HD 122
BHS HD 680: Missouri Breaks	458	Increasing	405-495	33	2/20/2017	33	26	0	7	Helicopter net-gunning	Evaluation of herd health
MG HD 313: Crazy Mountains	350	Stable/ Declining	NA	20	2/24/2016	20	15	*	4	Helicopter net-gunning	Evaluation as possible source population
MG HD 314: Gallatin Crest	268	Increasing	NA	30	2/12/2018	19	9	8	2	Helicopter net-gunning	Evaluation as possible source population
MG HD 393: Bridger Mountains	130	Stable	NA	30	12/13/2020	12	9	2	1	Helicopter net-gunning	Evaluation of herd health

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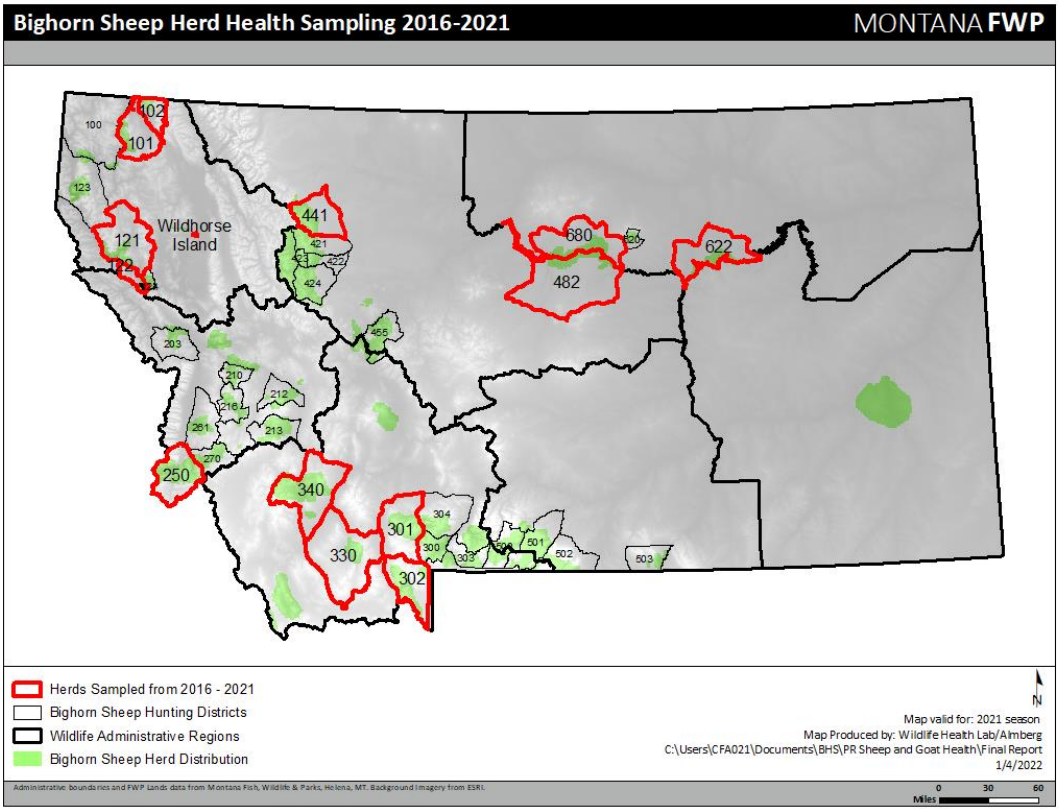

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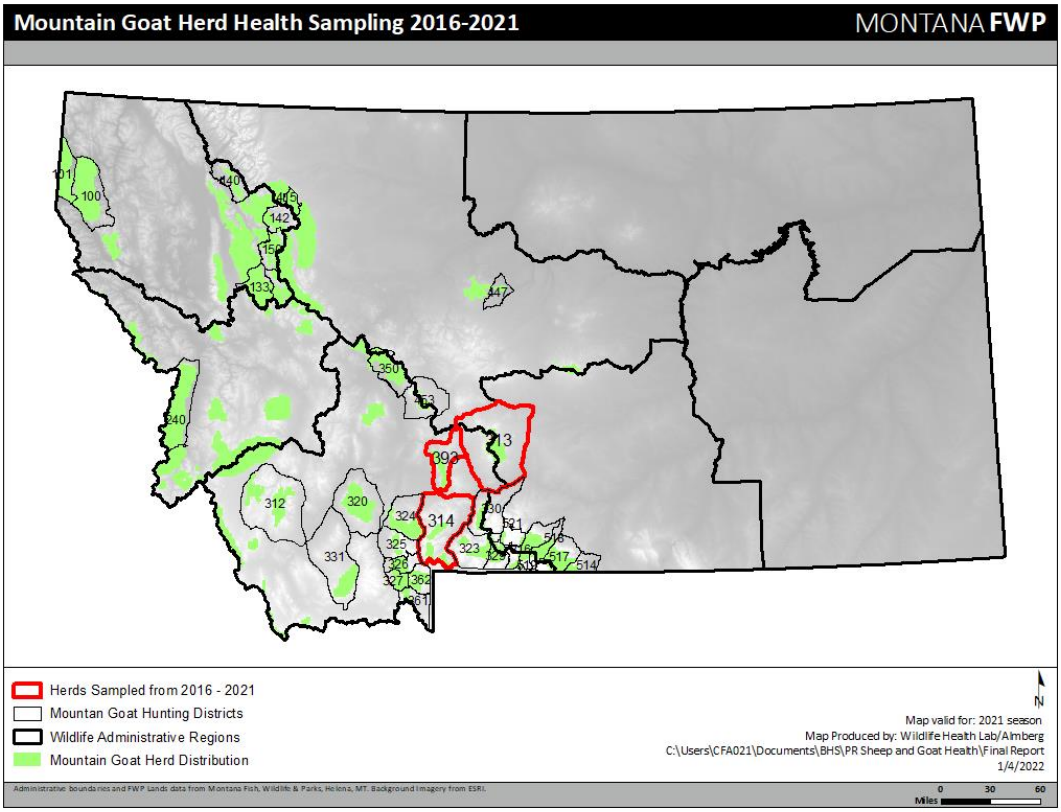

Figure 1. Map of Montana's (A) bighorn sheep and (B) mountain goat hunt districts (outlined

and numbered) and associated herd distributions (green polygons). Herds within hunt districts outlined in red were visited for health sampling between 2016-2021.

Herd Summaries

BHS HD 101: Koocanusa

The Koocanusa herd, also known as the Ural-Tweed herd, is located approximately 20 miles southwest of Eureka, in northwest Montana. Historically, this herd occupied both open bottom-land and the steep, rocky terrain along the Koocanusa River. However, with the creation of the Libby Dam and Lake Koocanusa in the 1970s, this herd's range was restricted to the steep, rocky, and forested eastern shore of Lake Koocanusa. Both the Koocanusa and Galton herds were historically considered native herds of Trench sheep, a genetically distinct group of sheep whose larger range extends northward through British Columbia. The Koocanusa herd has received two small augmentations: 5 rams from the National Bison Range were released within the Koocanusa herd in 1963, as well as 2 sheep from the Galton herd in 2006. It also may have some genetic connectivity to the Kootenai Falls herd (HD 100), which was founded by introductions of Sun River sheep. The Koocanusa herd contained 150-200 sheep in the 1960s, fell to 20-25 animals in the 1970s, and rebounded to 150-200 sheep in the 1990s before declining and remaining low ever since. The herd currently contains approximately 25 animals. Habitat loss, predation, and inbreeding depression are all potential contributors to the low population size. There has been discussion of potentially augmenting this population with a small number of sheep from the Galton herd.

BHS HD 102: Galton

The Galton herd is located north of Eureka, in northwest Montana. The herd occupies a mix of private and public land, including the Woods Ranch Wildlife Management Area, and their range spans the US-Canadian border. Both the Koocanusa and Galton herds are believed to be native herds of Trench sheep, a genetically distinct group of sheep whose larger range extends northward through British Columbia. Much of this herd's home range is forested, so population counts are difficult. Historic estimates of population size are low (ranging from <10 to >60) and highly variable. Currently, 90 animals are estimated to live within this herd. The Galton herd has been of potential interest as a source population to augment the Koocanusa herd or the Wildhorse Island herd.

BHS HD 121: North Clark Fork

The North Clark Fork bighorn sheep herd is generally located along the Clark Fork River Valley between Thompson Falls and Plains, MT (Figure 1). This herd was founded in 1959 by the reintroduction of 19 sheep from the Gibson Lake North (HD 423) and Wildhorse Island herds. The population reached a high of over 400 sheep in the 1980s, fluctuated around 200 sheep from 1990-2009, and more recently has declined to 50-70 individuals (Figure 2). Mortality due to vehicle collisions is significant within this herd. The current population is comprised of two subgroups. This herd has been suggested as a possible candidate for future herd augmentation.

BHS HD 122: Clark Fork Cut-off

The Clark Fork Cut-off bighorn sheep herd is situated between Sesame Creek, Kennedy Creek, and the Clark Fork River in northwest Montana (Figure 1). This herd was founded in 1979 with a transplant of 41 sheep, and augmented with 5 more sheep in 1981, in both cases using sheep from Wildhorse Island. The population has generally ranged from 60-140 animals, but following a dramatic decline in 2013, counts have been as low as 18 animals (Figure 2). This herd is currently comprised of just one group of animals. Data within this report combines information from 2017 (when 2 animals were captured) and 2016 (when 4 bighorn sheep were sampled) capture efforts. This herd was augmented with 20 sheep from HD 622 in the winter of 2017/18.

BHS HD 199: Wildhorse Island

Bighorn sheep were successfully introduced to Wildhorse Island, in Flathead Lake, Montana, via the translocation of a ram and ewe from the Mission Mountains in 1939, and 6 additional sheep from Sun River in 1947. By 1953, the island was home to an estimated 100 bighorn sheep, 200 mule deer, and 100 horses. The population was augmented with 2 bighorn sheep from the Ural-Tweed herd in 1987. The population goal for the island has been between 100-120 sheep. There is no hunting allowed on the island. Instead, FWP has periodically captured and translocated sheep off the island for reintroduction or augmentation of other populations around the state. Between 1955 – 2021, over 500 sheep have been removed from the island and translocated elsewhere. Transplants have been conducted in cooperation with the Confederated Salish & Kootenai Tribal Wildlife Program. Domestic sheep and goats are not allowed on the island. Mountain lions occasionally inhabit the island and in recent years, 2-3 lions are believed to have significantly contributed to predation mortality. The population currently consists of ~75 sheep.

BHS HD 250: Painted Rocks

As with many native sheep herds in Montana, the Painted Rocks herd was likely driven to local extinction in the age of market hunting, and the herd was re-stocked with 36 sheep from the Sun River Range in 1990 (Picton and Lonner 2008). However, a remnant population of native sheep persisted across the Idaho border in the Selway drainage, which regularly crossed into Montana during summers and for which Montana hunting permits were issued. Within the last 5 years, hunters and biologists have observed sheep throughout the year around the Painted Rocks Reservoir, north to Nez Perce Pass and the Watchtower/Sheephead drainages (believed to be the remnant Idaho herd), east along Little Boulder and Slate Creeks, and southeast into the Warm Springs drainage. If and how these herds are connected is unknown, although a 1991 Survey & Inventory Report indicated one of the sheep transplanted from Sun River moved to the Warm Springs drainage the first September after the transplant.

The Painted Rocks herd is generally surveyed by helicopter every spring before lambing season, but counts have been inconsistent in recent years due to lack of familiarity with high-use sheep areas, tendency for this herd to scatter into small groups, and sightability issues in the heavily-timbered foothills of their range. These surveys focus mainly on the Painted Rocks area, with short and inconsistent forays into neighboring drainages not always including the Nez Perce. The population objective has been 120 sheep, but this number has only been reached once since 2006, with the counts in the years since averaging 65. Lamb: ewe ratios range from a high

of 75 lambs:100 ewes in 1999 to a minimum of just 8 in 2002, averaging 42 lambs:100 ewes between 1995-2016. The size of the remnant Idaho/Montana herd is currently unknown, if it still exists; FWP reports prior to the 1990 re-stocking indicated it averaged 100-120 individuals. One motivation for this health assessment was to gather information to evaluate whether the population objective of 120 sheep remains reasonable.

To date, Montana FWP has not documented any pneumonia outbreaks in this herd. Given this herd's remote location and difficulty of assessing population dynamics, outbreaks could have occurred without FWP's knowledge. The sheep observed in the Warm Springs drainage are of particular interest, given their location between the Painted Rocks herd and the East Fork of the Bitterroot herd, the latter having experienced two well-documented pneumonia outbreaks, including an all-age die-off, in 2011 and 2015.

BHS HD 301: Spanish Peaks

This population is a native sheep herd that has been augmented with 10 rams spread across 3 separate occasions, in 1944, 1947, and 1963. The population was generally stable since this time, with 75-150 bighorn counted for many years. This herd has not experienced an all-age die-off, but it has experienced successive years of poor lamb recruitment. A recent period of poor lamb recruitment in the early 2000's resulted in as few as 50 bighorn sheep detected during aerial surveys and a temporary closure of the area to hunting. During this time, a special mountain lion management area was implemented on top of the bighorn winter range to discourage mountain lion predation on the struggling herd. By 2010, more than 200 bighorn sheep were observed on the winter range, a record high count. Unfortunately, this high count was followed by a severe winter and the starvation loss of many sheep. As the population rebounded, the first ever ewe hunt was implemented to maintain sheep counts below 200 to prevent further starvation loss incidents. Concurrently with the highest counts ever observed on the main winter range, we have noted new dispersal events. Up to 20 bighorn sheep have been seen in Jack Creek in winter, approximately 20 miles from their traditional winter range. The sporadic observations of bighorn sheep in Beartrap Canyon have continued in summer through winter, and are becoming more predictable, with up to 12 bighorn sheep observed there, approximately 30 miles from traditional winter range.

In 2018, MFWP documented the first known interchange between the Spanish Peaks herd and the Taylor-Hilgard (HD 302) herd to the south. The Taylor-Hilgard herd core winter range is approximately 35 airline miles away from the Spanish Peaks herd. An ear-tagged ewe transplanted to Wolf Creek as part of the within-mountain range augmentation effort there was observed along Highway 191 two years later. A second interchange between HD 302 and HD 301 was recently documented when a 2.5 year old ram that was translocated to Wolf Creek in 2015, was legally harvested in HD 301 in 2021. Interestingly, these sorts of movements have never been observed among the many collared, non-transplanted individuals in the Taylor-Hilgard population, suggesting that the act of translocation spurred exploration. Connection between these herds is expected to strengthen in future years.

BHS HD 302: Taylor-Hilgards

At the southern end of the Madison Mountain Range, the Taylor-Hilgard herd can be observed wintering predominantly near the Slide Inn, but also in Wolf Creek, in Moose Creek, on Monument Mountain at high elevation, and even in Sheep Creek of the Henry's Mountains. This native herd shows genetic similarity to the Spanish Peaks (HD 301) herd at the north end of the Madison Range. The population has struggled with several all-age die-offs and was augmented with 18 sheep from Lost Creek in 1989 and 26 bighorn sheep from Wild Horse Island in 1993 and 1994. Some Lost Creek and Wild Horse Island genetic signatures remain in the Taylor-Hilgard bighorn herd, but the native Madison Range genetics remain predominant. The most recent all-age die-off occurred during the winter of 1996-1997. By the early 2010s, the population had recovered to the highest numbers ever documented and continued to increase. During 2014, a record 266 bighorn sheep were counted. It was discovered the herd had received an unknown amount of medication, feed, and mineral supplementation from a local resident, potentially contributing to this increase. Feeding and supplementing wildlife is illegal in Montana, and the well-meaning local resident was warned and ceased the behavior.

This herd served as a source for a series of within-mountain range translocations to attempt to repopulate historic but unoccupied winter ranges between the Spanish Peaks and the Taylor-Hilgards. In sum, 97 bighorn sheep were moved to Wolf Creek, an intermediate drainage. Results from this transplant included a diversity of responses including mortalities (often predation), individuals which returned to the Taylor-Hilgards, individuals which dispersed completely (to the Gallatin Range and to Point of Rocks), individuals which joined the Spanish Peaks herd, and individuals which stayed in the Wolf Creek area. After the series of transplants and a few years of limited ewe hunting concluded, herd counts stabilized between about 150 and 190 bighorn sheep, an appropriate level for habitat of this winter range. During the period of supplementation, lamb:ewe ratios were as high as 65 and 78 lambs per 100 ewes. More recent springtime lamb:ewe ratios have varied from a low of 8 to a high of 36.

MG HD 313: Crazy Mountains

The Crazy Mountain goat herd is located at the headwaters of Big Timber, Sweet Grass, Porcupine, and Cottonwood Creeks (Figure 1). This herd was founded in 1941 and augmented in 1943 with mountain goats caught in the Deep Creek area west of Choteau (HD 442). The population expanded to over 300 goats by the late 1950s before experiencing an unexplained population crash, after which goat numbers remained low (<100) until the early 1990s (Figure 2). Since the 1990s, the mountain goat population has steadily increased to over 300 goats as of 2013 (Figure 2). This population has as many as eight subgroups, but they tend to congregate and mix on winter range. Thus, for the purposes of sampling, we treated mountain goats on the winter range as a single, mixed population. Despite a slight decline in recent years, this herd has historically exhibited long-term population growth, and it has been identified as a potential source herd for future mountain goat translocations.

MG HD 314: Gallatin Crest

Mountain goats were first detected on the Gallatin Crest during a bighorn sheep survey in 1992 and were thought to have naturally colonized from non-native populations in either the

Absaroka Range or the Spanish Peaks. The first dedicated mountain goat survey was conducted in 1997 and detected a total of 38 goats in the southern portion of the range. Goats gradually expanded their range into the north end of the district and currently inhabit all suitable habitat along the Gallatin Crest. The most recent count in August 2017 detected 238 goats, which is the highest number ever observed. A hunting season was opened for goats in 1996 with a quota of 2 licenses. As the population has expanded hunting opportunity has been increased with the license quota currently set at 30. Mountain goats share the Gallatin Crest with several herds of bighorn sheep which summer in the Hyalite area, the Ramshorn area and along the Yellowstone Park boundary. There have been two disease outbreaks documented among bighorn sheep on the Gallatin Crest, including a pneumonia event among sheep that summer in the Hyalite area in 2013, and a second pneumonia event among sheep that summer in the Ramshorn and Park boundary areas in 2015. In the fall of 2016, a hunter observed a dying mountain goat in the Hyalite area. FWP staff were able to locate and collect samples from the dead goat and confirmed respiratory disease. During the August 2017 survey, observed kid ratios were at or above average in the middle and southern portions of the district, and below average in the Hyalite area. Despite this, it does not appear that disease is having population level impacts as the population has continued to increase. Likewise, the sympatric bighorn sheep population has been increasing in recent years with no indications of active disease.

BHS HD 330: Greenhorn Mountains

Prior to the establishment of the Greenhorn bighorn sheep herd, Montana Fish, Wildlife, and Parks entered into a management Memorandum of Understanding (MOU) with the U. S. Forest Service, U. S. Bureau of Land Management and two area domestic sheep producers. The purpose of the MOU was to address possible negative implications to domestic sheep producers as a result of bighorn sheep re-establishment. Following the guidelines of the MOU, bighorn sheep were established through releases of 30 sheep from the Missouri River Breaks in 2003 and 39 sheep from Sun River in 2004. All sheep were released in proximity to Greenhorn and Willow creeks along the west slope of the Greenhorn Mountains. A portion of the sheep quickly dispersed across the west Greenhorn, north Snowcrest, and east Ruby Mountains. From the time of establishment through 2009, the population was monitored through aerial surveys completed during the summer and aided by radio-collar tracking. During that period, the population increased to a minimum of 80 individuals and then declined to a minimum of 30 individuals by 2009. Several management removals and relocations occurred during this period in accordance with the management MOU. No such management actions have occurred since 2009. No population monitoring occurred from 2010 through 2014. Beginning in 2015, population trend and vital rates have been monitored through ground surveys during late winter and early spring. Since that time, the minimum counts ranged from 41 to 59.

No disease events have been documented within the Greenhorn Herd. During January 2021, 21 bighorn sheep were captured via helicopter net gun as part of a herd health assessment. Three rams and seven ewes were radio collared to update herd distribution understanding. Forest management practices aimed at maintaining or restoring shrub grassland slopes across the western slope of the Greenhorn range are in progress on U. S. Bureau of Land Management,

Montana Department of Natural Resources and Conservation, and private lands. These treatments are expected to benefit the Greenhorn bighorn herd through increased foraging habitat. Similar treatments are being evaluated by the U. S. Forest Service.

BHS HD 340: Highlands

The Highland bighorn sheep herd is located amidst the Highland and East Pioneer Mountains (Figure 1). This herd was founded in 1967 with 22 sheep from the Gibson Lake North (HD 423) herd and augmented seven more times in the following years from six source herds (Castle Reef (HD 422), Bonner (HD 283), East Fork Bitterroot (HD 270), Greenhorn (HD 399G), Ford Creek (HD 424), and Gibson Lake North (HD 423)). The population grew steadily to over 300 sheep until it experienced an all-age die-off in 1995 (Figure 2). The population has failed to recover since, ranging between 25-75 animals, with consistently low recruitment rates. The Highlands herd has four subgroups with differing apparent health and recruitment rates. This herd had been suggested as a possible candidate for future herd augmentation and will be the focus of a test-and-remove and mineral supplementation program to determine the population-level effects of these actions.

HD 393 Bridger Goats:

Mountain goats were introduced to the Bridger Mountains of southwest Montana in 1969 when Montana Fish, Wildlife and Parks (MFWP) moved 13 goats from the Gates of the Mountains to Fairy Lake. The introduction was a great success with a record 127 goats counted in 2019 in the Bridgers. Mountain goats in this herd have trophy-quality horn development, and the unit ranks among the most popular goat hunting districts in the state: 2,209 hunters applied for the opportunity in 2020. MFWP's goals are to ensure the long-term viability of the mountain goat population while continuing to provide a quality hunting experience. The herd is surveyed every 2 years using ground-based counts coordinated between the Rocky Mountain Goat Alliance and Montana Fish, Wildlife and Parks. The herd appears healthy, with no known die-off or disease events in its short history. The major management concerns into the future will be 1) continuing to obtain good-quality count data and commensurate number of hunting licenses and 2) understanding the roles of mountain goat habituation or avoidance related to the high human recreational uses in the Bridger Mountains.

BHS HD 441: North Fork Birch Creek – Teton

Bighorn sheep in this area exist in several small herd segments and frequently move to and from neighboring use areas. Sheep occupy steep, rocky ridges, avalanche chutes and cliff faces. The area includes the northeastern portion of the Bob Marshall Wilderness and Lewis and Clark national Forest east of the Continental Divide.

Historically, there have been approximately 150 bighorn sheep scattered from the North Fork of the Teton River to the North Fork of Birch Creek in several small herd segments: Jones Creek, Dupuyer Creek Walling Reef and upper Birch Creek. Bighorn sheep can occasionally be found on private lands in the Walling Reef – Swift Dam area and in the Forks of Dupuyer Creek.

Disease related die-offs have been documented twice, in 1984 and 2010 and the herd is still recovering from the most recent die-off. The herd has been augmented 3 times in 1976, 1991, and 1993, with a total of 86 sheep introduced from various source populations. This area has a full complement of predators, including grizzly bears, black bears, mountain lions, wolverines, lynx, coyotes and wolves.

This native bighorn population is a relatively old population and is characterized as having moderate lamb production and recruitment rates and is below population objective with stable to increasing numbers. Bighorn sheep observations have ranged from a high of 141 in 1997 to a low of 35 in 2015. The population objective for this hunting district is 200 with a diverse age structure of rams. Recent surveys have shown an increasing population trend with relatively good production and recruitment. The current population is estimated to be between 90 -100 bighorn sheep.

BHS HD 482: Fergus & BHS HD 680: Missouri Breaks

The Missouri Breaks, which encompass the rugged landscape surrounding the Missouri River in central Montana, are home to a metapopulation of bighorn sheep that span HDs 482 (Fergus), 680 (Missouri Breaks), 620 (Little Rockies), and 622 (Middle-Missouri Breaks). This metapopulation was founded through a series of introductions between the 1940s and 1980s. Sheep in HDs 482 and 680, which are across the river from one another, were founded in 1958-1961, with 45 animals from a combination of sheep from Sun River and the National Bison Range. In 1980, an additional 28 sheep from Sun River were released in this area. Sheep moved across the river, and both the Fergus and Missouri Breaks sub-populations steadily increased.

Bighorn sheep population objectives for HD 482 (300-350 sheep observed during aerial surveys) are designed to keep bighorn sheep habitat in healthy condition and sheep numbers well below carrying capacity to minimize the spread of diseases and to prevent or minimize the occurrence of catastrophic die-offs. Despite a relatively low objective in relation to habitat, bighorn sheep in HD 482 have thrived, reaching a peak of 498 observed animals during the annual aerial survey in 2010. Supplemental forage in the form of agricultural fields juxtaposed with escape terrain help provide excellent habitat conditions for producing and growing sheep. Five bighorn sheep transplants have occurred from HD 482 since 2010, with 191 animals relocated to other areas of the state, primarily the Beartooth WMA and the Little Belt Mountains. The area biologist observed 440 sheep during the last aerial survey, conducted in 2020.

In HD 680, the average population count was 413 sheep between 2012-2021, with the highest count of 532 sheep in 2006. In 2016, biologists counted 499 animals. Assuming observed sheep represent 60% of the total population, the actual population size may be over 700 animals. This population is fairly dispersed across its range with two connected sub-populations in the east and west half of the hunt district. There have been no documented cases of pneumonia from this herd.

BHS HD 622: Middle Missouri Breaks

The Middle Missouri Breaks bighorn sheep herd is located north of Fort Peck Reservoir (Figure 1). This herd was founded in 1980 through a reintroduction effort using 28 bighorn sheep from the Gibson Lake North (HD 423) herd. The overall population has steadily increased from the original 28 reintroduced animals to over 300 bighorn sheep (Figure 2). This population was historically comprised of two subgroups, the smallest one located in the Mickey and Brandon Buttes area and the larger subpopulation in the Iron Stake/Larb Hills area, and has recently expanded east of Timber Creek to the Bone Trail area. The smaller of the two subpopulations averaged 50 bighorn sheep between 1986 and 2010, peaked at 80 bighorn sheep in the mid-1990s, and has decreased annually over the last 10 years until only six sheep were observed during 2016 surveys. None have been seen in that area since. The larger of the two subpopulations has increased from 160 sheep in 2010 to a high of 318 bighorn sheep in 2016. This herd had been suggested as a candidate source herd, and following the health assessment, was used as a source herd for a translocation of 20 bighorn sheep to the Cut-off herd in HD 122 in 2018.

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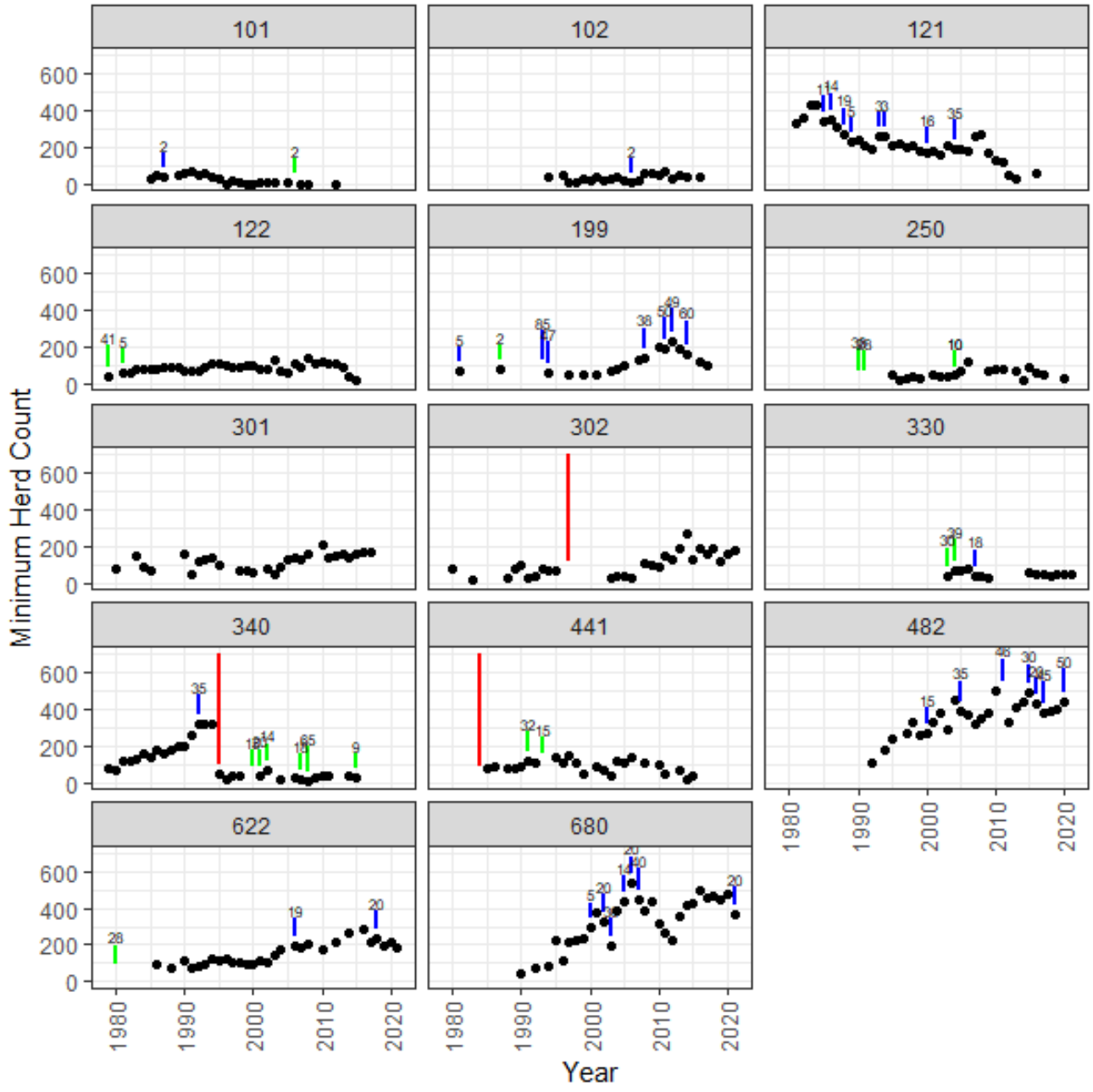

101
102
121
122
199
250
301
302
330
340
441
482
622
680
Minimum Herd Count
Year
0
200
400
600
1980
1990
2000
2010
2020

B

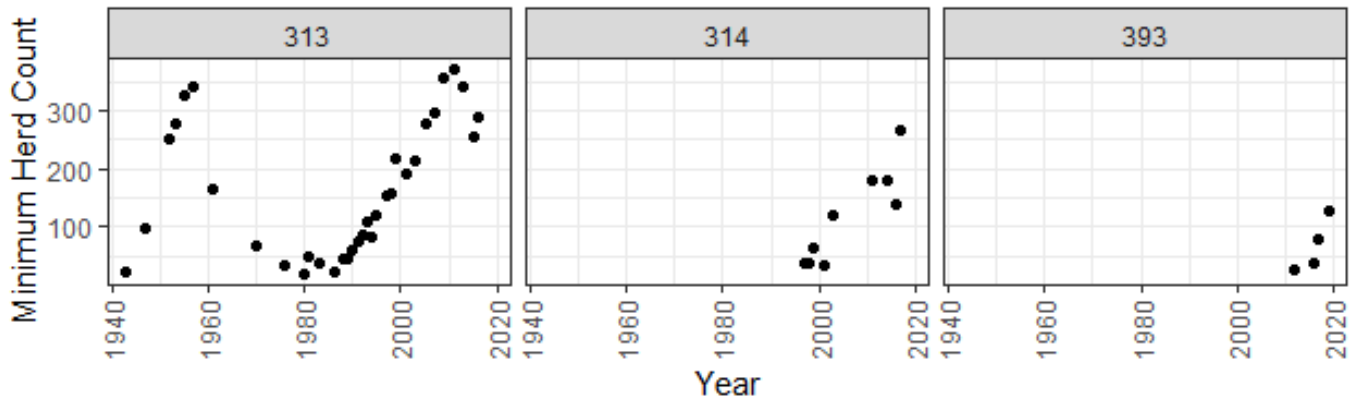
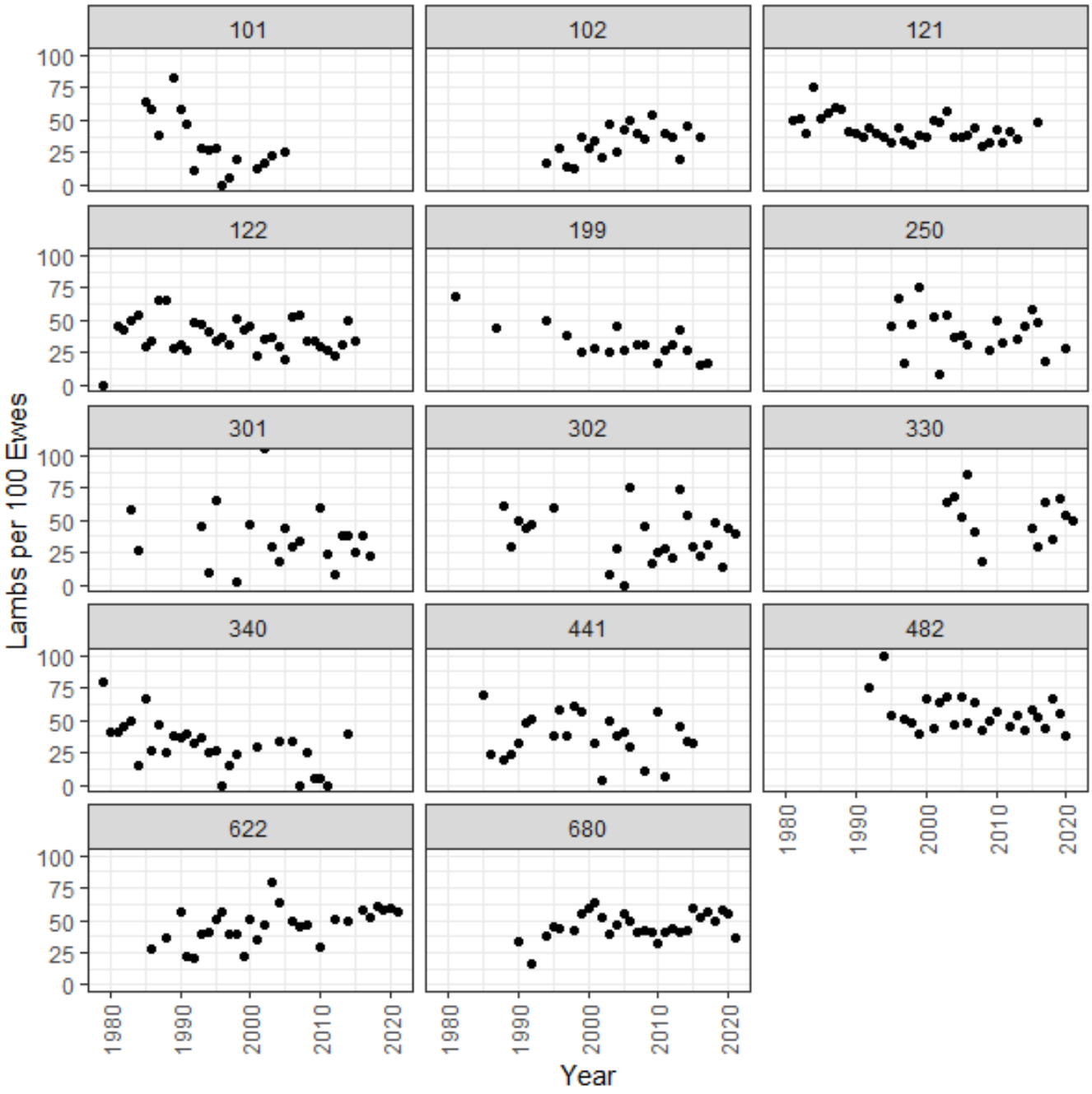


Figure 2. Minimum herd counts over time for sampled (A) bighorn sheep and (B) mountain goat herds, denoted by hunting district number. Bighorn sheep district 199 is Wildhorse Island. All-age pneumonia die-offs are denoted by vertical red lines. Translocations into (green) and out of (blue) the herds, along with total number of animals moved, are noted by the green and blue vertical lines. Surveys of the herds were conducted by helicopter or fixed-wing aircraft by FWP staff.

A


101
102
121
122
199
250
301
302
330
340
441
482
622
680
Lambs per 100 Ewes
Year
0
25
50
75
100
1980
1990
2000
2010
2020

B

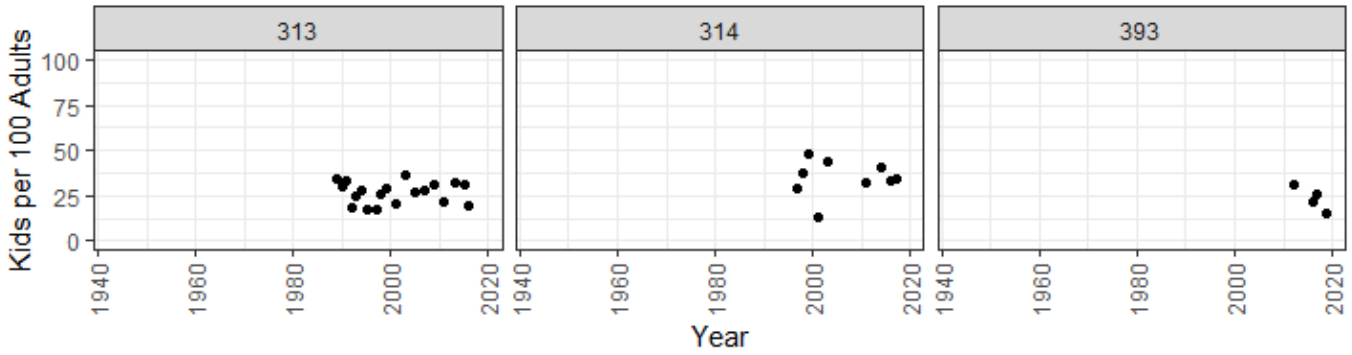


Figure 3. (A) Minimum bighorn sheep lambs per 100 ewes or (B) mountain goat kids per 100 adults observed over time by hunting district number for sampled herds. Surveys of the herds were conducted by helicopter or fixed-wing aircraft by FWP staff. Surveys were not always conducted at the same time of year, making between-year and herd comparisons difficult.

Data collection

Sample sizes, animal capture and handling

All capture and handling procedures for bighorn sheep were conducted according to the Montana Fish, Wildlife, and Parks Bighorn Sheep Biomedical Protocol (Montana Fish, Wildlife and Parks IACUC #FWP03-2018). Montana Fish Wildlife and Parks' staff and Quicksilver Air captured most bighorn sheep and mountain goats via helicopter net gunning; Montana Fish, Wildlife and Parks' staff ground darted sheep in HD 101 and 250 and conducted a drop-net capture of bighorn sheep in HD 102 and 302 (Table 1). Target sample sizes for the population were defined to detect pathogens with 95% confidence, assuming perfect test sensitivity and that pathogen prevalence was 10% at the population level. Work by Butler et al. (2017) showed that detection probabilities based on culture for many respiratory pathogens of interest were lower than previously thought. To account for imperfect pathogen detection, we collected and tested duplicate tonsil swabs to increase our confidence in pathogen detection, and we calculated actual power for pathogen detection based on final sample sizes.

Efforts were made to broadly sample individuals across the herd. Captured animals were hobbled and blindfolded by the capture crew and either processed on site or transported to a central processing base. Upon restraint, we monitored vital signs while processing each animal. Captured animals were fitted with red plastic ear-tags prior to release. In addition, GPS-collars were deployed on 14 bighorn sheep (9 ewes, 5 rams) in HD 250, 10 (7 ewes, 3 rams) bighorn sheep in HD 330, and 5 (2 ewes, 3 rams) bighorn sheep in HD 441 to obtain basic home range and movement information. GPS collars were also deployed on 12 mountain goats (8 nannies, 2 billies) in the Bridger Mountains to obtain home range and movement information and as part of a research project on goat habitat use and human recreation. To improve our estimates of neck sizes for future collar sizing and fitting, we measured neck sizes in centimeters and report these data in Appendix II.

Sample Collection

Sheep captured as part of the Bighorn Sheep and Mountain Goat Herd Health Assessment Project received a full health inspection and evaluation including the collection of information on age, sex, a genetic sample, whole blood, blood serum, fecal samples, nasal and tonsil swabs (multiple tonsil swabs were collected and tested for all animals; swabs were placed in Tryptic soy broth medium and frozen at -80C until tested), and a sampling of any external parasites. Body condition scores were collected on a scale of 0.5-6 following a protocol developed by Stephenson et al. (2020), where possible. A variety of assays were employed to detect (1) a range of parasites and pathogens known to be relevant to bighorn sheep and mountain goat health and management (Appendix I, Table A1.1; Carlsen & Erikson 2010), (2) serum trace minerals, and (3) physiological condition, including pregnancy status, rump fat thickness as measured by ultrasound, and a body condition score for bighorn sheep. Samples were collected and data were analyzed according to standard protocols (Western Association of Fish and Wildlife Agencies 2015). Extra blood serum, swabs, and genetic samples (gene cards or biopsy punches) were collected and archived for future testing and analyses.

Animal and Field Site Monitoring

Aerial surveys, conducted by area wildlife biologists via helicopter and fixed-wing aircraft, were used to monitor population trend and recruitment ratios in herds across the state.

Lab analyses

All sheep and goat pathogen and parasite testing was carried out in accordance with standard protocols from the Western Association of Fish and Wildlife Agencies (Western Association of Fish and Wildlife Agencies 2015; Appendix I, Table AI). A serology panel was conducted at the Montana Veterinary Diagnostic Laboratory (MVDL) to evaluate exposure status for various pathogens. Aerobic culture on tonsil and nasal swabs and Mycoplasma ovipneumoniae PCR were conducted at the Washington Animal Disease Diagnostic Laboratory (WADDL). Leukotoxin A PCR testing was conducted from a swab of bacterial growth from the primary streak zone of the culture plate, also at WADDL. Serum trace mineral levels and fecal parasitology were performed at Michigan State University's Diagnostic Center for Population and Animal Health. Pregnancy-Specific Protein B assays were run at BioTracking Inc. (now Herd Health Diagnostics) to determine pregnancy status.

Data analyses

We estimated the proportion of the herd exposed (for serology tests) or infected (for PCR or other direct tests) with each pathogen, mean serum trace mineral levels, and mean body condition indices. Using estimated detection probabilities for respiratory pathogens from Butler et al. (2017), we corrected raw estimates of exposure and infection rates by dividing the raw estimates by estimated detection probabilities and calculated corrected confidence intervals using the delta method. When we failed to detect the presence of a respiratory pathogen, we calculated our statistical power to detect the pathogen if it were present, using the approach detailed in Butler (2017). Statistical power is defined here as the probability (ranging from 0-1) that we would have detected the pathogen if it was present in the herd at 10% prevalence,

given the herd size, our sample size, number of swabs collected per animal, and the estimated detection probability. Point estimates and confidence intervals for proportion and probability statistics were estimated with the binomial distribution. Point estimates and confidence intervals for continuous statistics were estimated with the normal distribution.

Results

Respiratory Pathogens

We detected serological exposure to *Mycoplasma ovipneumoniae* in bighorn sheep HDs 250, 301, 302, 330, 340, 441, 482, and 680 and in mountain goat HD 314; of these herds, we detected active infection with *Mycoplasma ovipneumoniae* by PCR on nasal swabs in HDs 250, 301, 302, 330, 340, and 680 (Figure 4). In HDs 314 and 441, where we detected serological exposure to *Mycoplasma ovipneumoniae* but did not detect the pathogen with PCR tests, low sample sizes and statistical power (<0.8; Figure 5) suggest we could have failed to detect the pathogen. In HD 482, we detected low seroprevalence to *Mycoplasma ovipneumoniae* in 2016, but by 2020, we found no evidence for infection or exposure, despite high detection power. We did not detect exposure or infection with *Mycoplasma ovipneumoniae* in bighorn sheep HDs 101, 102, 121, 122, 199, and 622, nor in mountain goat HD 393. We had sufficient power to detect *Mycoplasma ovipneumoniae* by PCR in HDs 102, 199, and 622, and in combination with serology, the evidence suggests these herds are free from *Mycoplasma ovipneumoniae* infection. We failed to meet our target power for detection in HDs 101, 121, 122, and 393, indicating we could have missed detecting *Mycoplasma ovipneumoniae* in those herds.

The Leukotoxin A gene associated with *Pasteurellaceae* growth was detected in all herds that were tested (Figure 4). By contrast, we detected hemolytic *Pasteurellaceae* in a much smaller subset of herds, consistent with a much lower detection probability on culture.

Due to the very low detection probability of *Pasteurellaceae* by culture and our inability to capture our target sample sizes, in many cases, we failed to meet detection probabilities of ≥ 0.8 (Figure 5), despite collecting and testing multiple tonsil swabs per animal. We detected hemolytic *Mannheimia haemolytica/glucosida* in bighorn sheep HDs 199, 250, 302, 330, 340, 482, 622, and 680; hemolytic *Mannheimia species/ruminalis* in bighorn sheep HDs 250, 302, 330, 482, 622, and 680; hemolytic *Bibersteinia trehalosi* in HDs 250 and 330; and *Pasteurella multocida* was detected in HD 199 and 302 on tonsil swabs but was also detected via nasal swabs in HDs 250, 302, 330, and 482 (Figure 4). Non-hemolytic *Bibersteinia trehalosi* was detected in all sampled herds, either from tonsil or nasal swabs, except in bighorn sheep HDs 101 and 122 and mountain goat HD 314 (Figure 4).

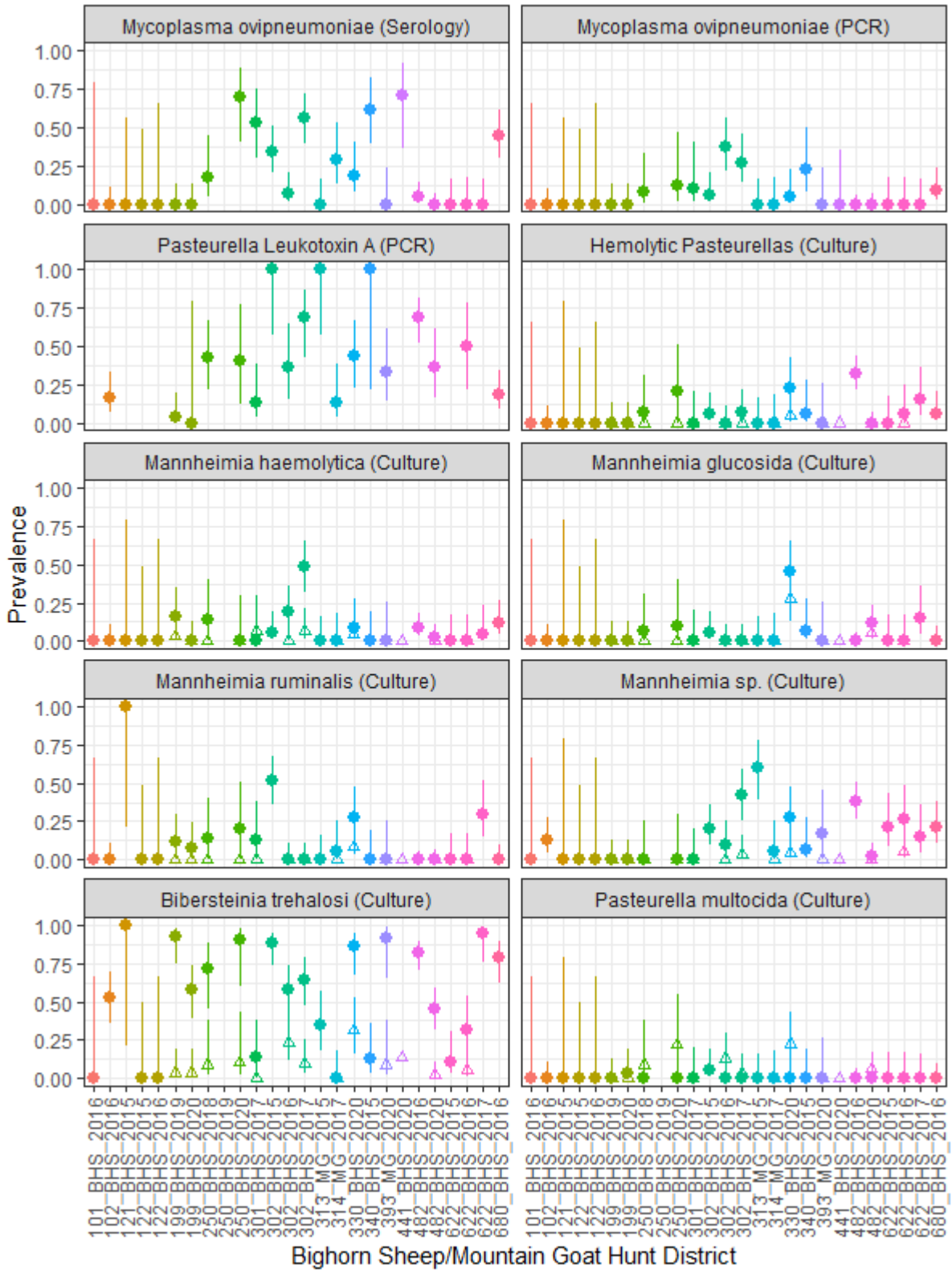


Figure 4. Summary of raw prevalence (proportion testing positive) and associated 95% binomial confidence intervals for respiratory pathogen exposures by herd and sample year.

Triangle symbols for cultured pathogens represent prevalence based on culture from nasal swabs. Data includes information from serology, PCR, and culture tests, as noted, for all pathogens we screened for. This figure does not account for imperfect pathogen detection, but we separately estimated detection-probability corrected prevalences for select pathogens for which we had estimated detection probabilities (see Figure 5).

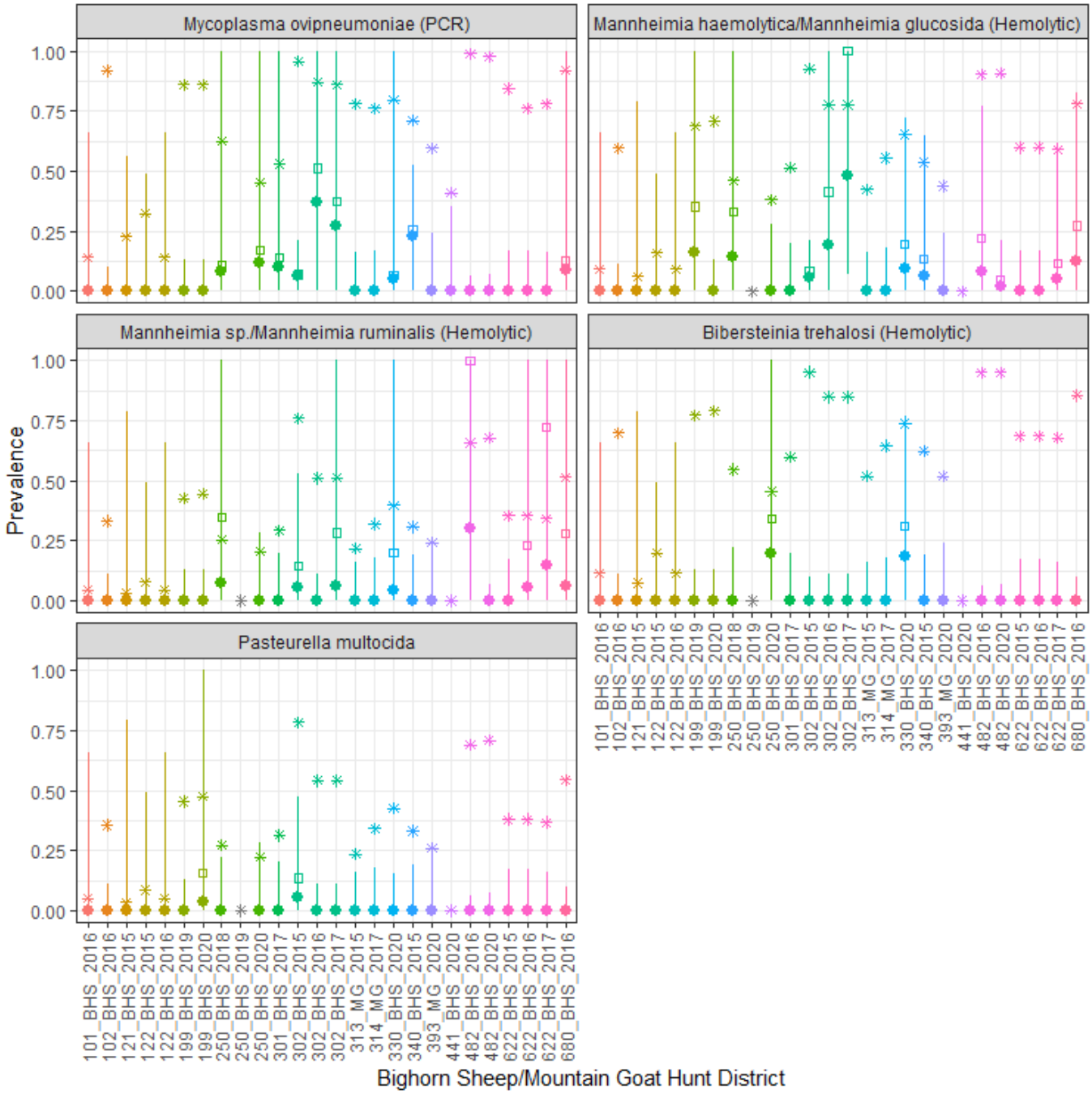


Figure 5. Summary of estimated raw (solid points) and adjusted (for imperfect detection; open squares) prevalences, and associated 95% confidence intervals, as well as estimated power (asterisk symbol) to detect select respiratory pathogens. Adjusted prevalences were calculated by dividing the raw estimates by estimated detection probabilities from Butler (2017), and corrected 95% confidence intervals were calculated using the delta method. We estimated the statistical power to detect the pathogen (denoted by the asterisk symbol) if it were present at 10% prevalence given the herd size, our sample size, number of swabs collected per animal, and the detection probability using the approach detailed in Butler (2017). Point estimates and 95% confidence intervals for raw prevalences were estimated using the binomial distribution. Cultured *Mannheimia haemolytica* was assumed to be beta-hemolytic.

Using data collected from this study, from the State-wide Bighorn Sheep Research Project, and from hunter-harvest and mortalities submitted to the Wildlife Health Lab between 1991-2021, we have updated a map, first created by Butler et al. (2018), of the respiratory pathogens detected in Montana's bighorn sheep herds across the state (Figure 6).

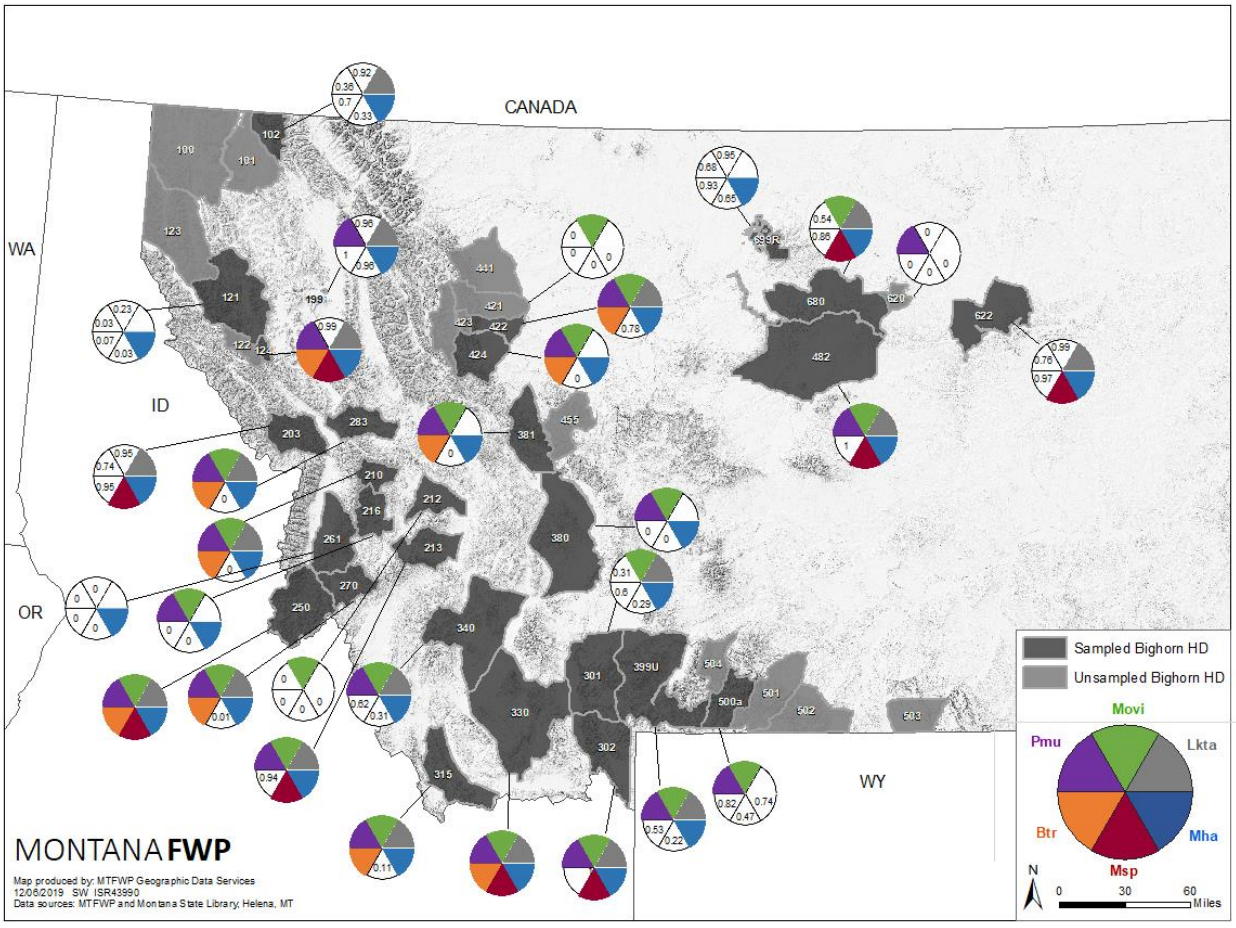


Figure 6. Map displaying bighorn sheep herds sampled for respiratory pathogens. Data comes from state-wide live-animal captures, hunter harvest, or mortalities submitted to the Wildlife Health Lab from 1991-2021. Pathogens are as follows: Movi = *Mycoplasma ovipneumoniae*, detected by PCR; Lkta = Pasteurella Leukotoxin A gene, detected by PCR; Mha = hemolytic

Mannheimia haemolytica or *Mannheimia glucosida*, detected by culture*;* Msp = hemolytic *Mannheimia species or Mannheimia ruminalis*, detected by culture; Btr = hemolytic *Bibersteinia trehalosi*, detected by culture; Pmu = *Pasteurella multocida*, detected by culture. Sampled herds are defined as those with ≥10 samples collected. Any detection from a bighorn sheep on nasal, tonsil or lung swabs from within the hunt district between 1991-2021 is reported. In cases where there have been no detections, the numbers displayed within empty pieces of the pie chart represent our power to detect the pathogen if it were present at 10% prevalence, given sample size, number of swabs collected per animal, and the detection probability using the approach detailed in Butler (2017). Power calculations only included data collected between 2011-2021 from live animal captures (nasal or tonsil swabs). There is no estimate for detection probability of the Leukotoxin A gene, so no power is reported. Note that while *Mycoplasma ovipneumoniae* has historically been detected within HD 482, recent testing suggest it has faded out from the population. Figure is based on version created by Butler et al. 2018.

Serological exposure to other pathogens

Across herds, we found ubiquitous serological exposure to Parainfluenza-3; frequent to intermediate rates of exposure to *Anaplasma*, contagious ecthyma, epizootic hemorrhagic disease virus, and *Leptospiria*; and infrequent or no exposure to blue tongue virus, bovine respiratory syncytial virus, bovine viral diarrhea I & II, *Brucella ovis*, infectious bovine rhinotracheitis, and ovine progressive pneumonia (Figure 7). Exposure across herds was most variable for *Anaplasma*, contagious ecthyma, and epizootic hemorrhagic, with some herds showing high seroprevalences suggestive of widespread and recent infection, and others showing low to no exposure. *Anaplasma* positive herds include HDs 102, 121, 122, 199, 250, 301, 302, 314, 340, 482, and 680. Contagious ecthyma positive herds include HDs 102, 199, 250, 301, 302, 314, 330, 340, 482, 622, and 680. Herds with evidence for exposure to epizootic hemorrhagic disease virus include HDs 301, 340, 482, 622, and 680. Evidence for exposure to bovine respiratory syncytial virus was limited to HDs 102, 482, 622, and 680. Low seroprevalence to bovine viral diarrhea I was limited to HDs 313 and 340, and bovine viral diarrhea II to HD 340 and 482. Serological evidence of exposure to *Brucella ovis* was limited to HDs 101, 313, and 393. Single animals seropositive to ovine progressive pneumonia were detected in HDs 102 and 680.

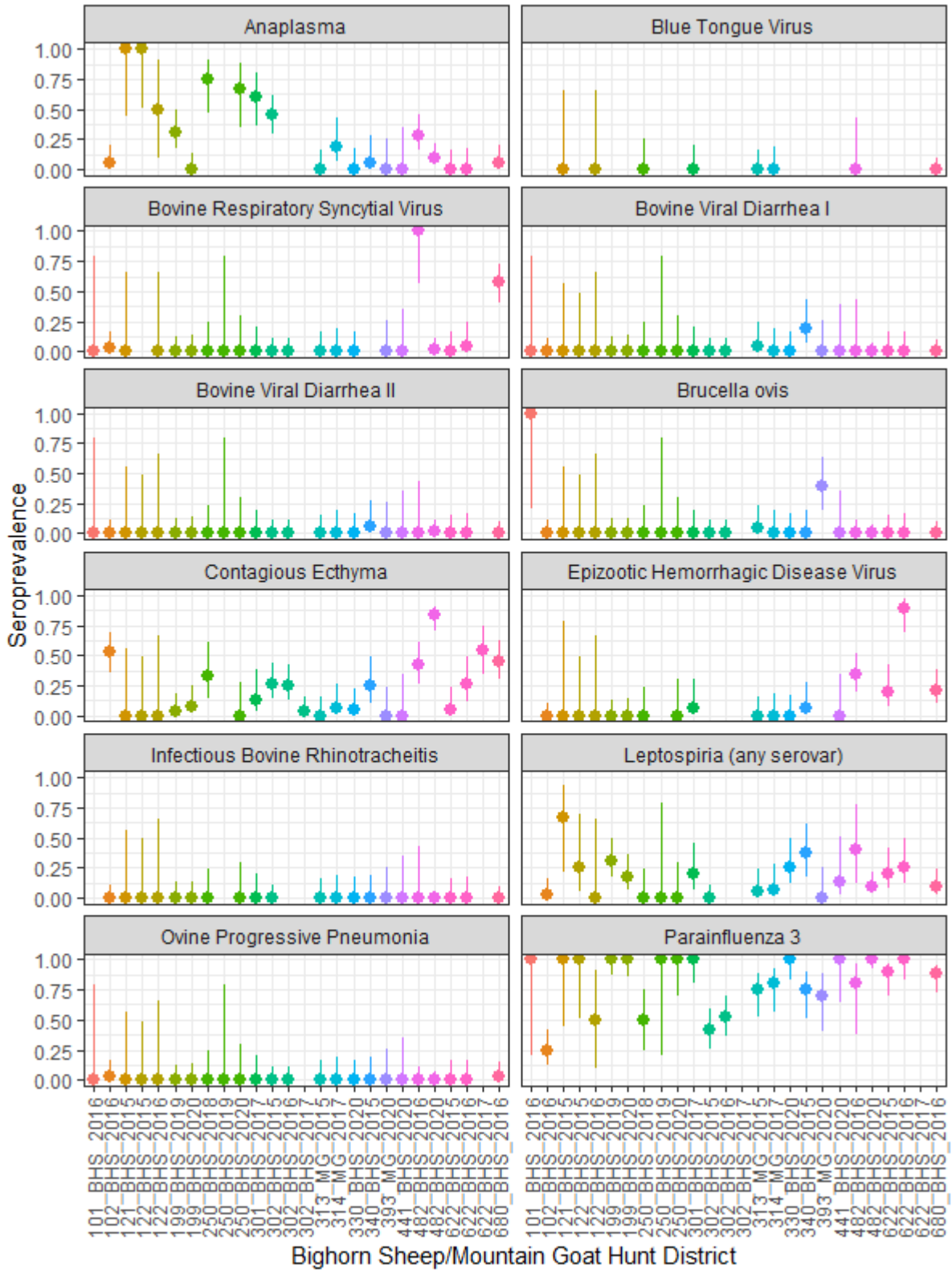


Figure 7. Summary of raw seroprevalence (proportion testing positive) and associated 95% binomial confidence intervals for pathogen exposures for moderate-risk pathogens, by herd and sample year.

Parasites

All herds, except for HD 680, exhibited infection with coccidia (Figure 8). Similarly, infection with *Protostrongylus* lungworms was detected in all herds, except mountain goat HD 393. Observed prevalence of both parasites tended to be high in most herds.

In addition, we detected *Psoroptes ovis* in bighorn sheep HD 250 in a lamb captured in 2018, an adult ram captured in 2019, and a hunter-harvested ram in 2020. Despite returning to this herd in 2020, we found no further evidence of infection among the captured animals.

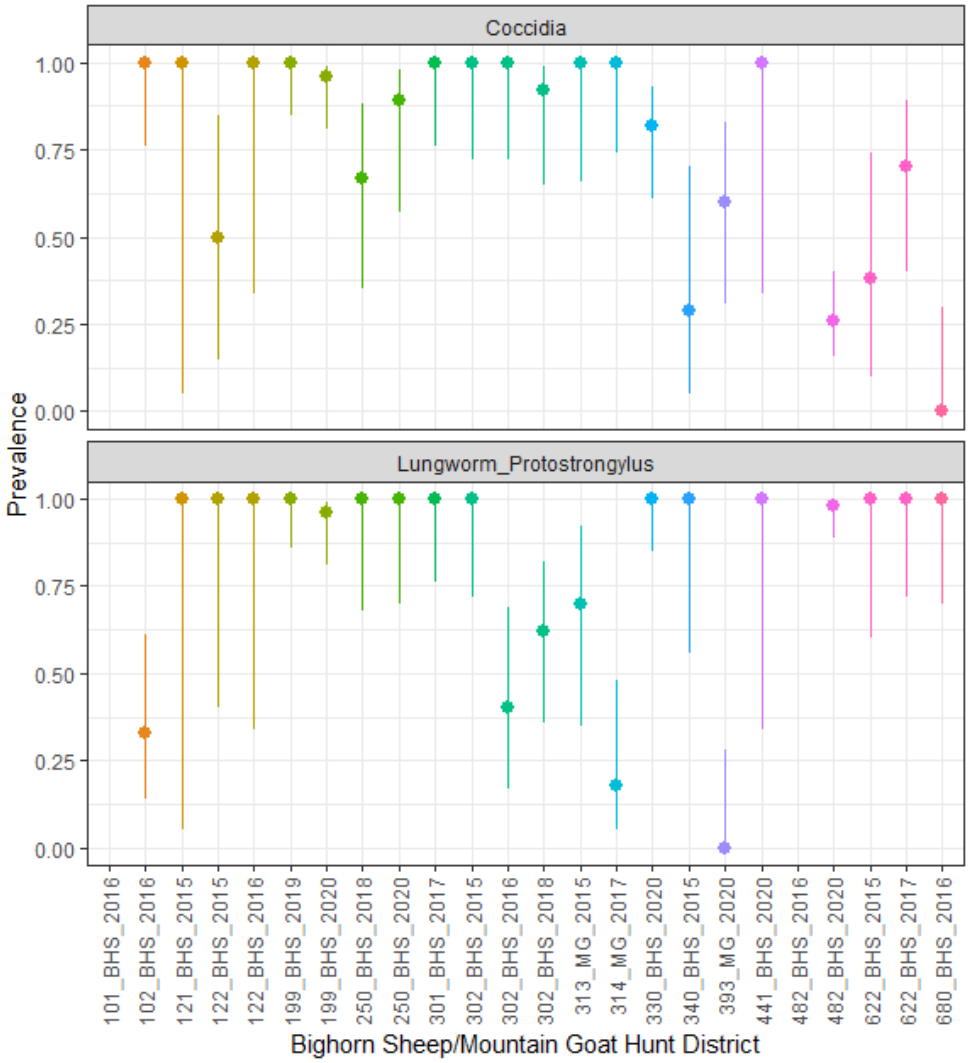


Figure 8. Summary of raw prevalence (proportion testing positive) and associated 95% binomial confidence intervals for Coccidia and *Protostrongylus* lungworm parasites, detected in feces, by herd and sample year.

Trace Minerals

Sampled bighorn sheep and goat herds exhibited serum-based trace mineral concentrations of cobalt, copper, manganese, and zinc within observed ranges for wild (Poppenga et al. 2012)

and/or domestic sheep (Herdt & Hoff 2011) (Figure 9). Mean trace mineral concentrations were below published ranges for iron in HDs 199, 250, 330, 393, 441, and 482 (in 2020); for molybdenum in HDs 314 and 393; and for selenium in HDs 102, 121, 122, 250, 301, and 314.

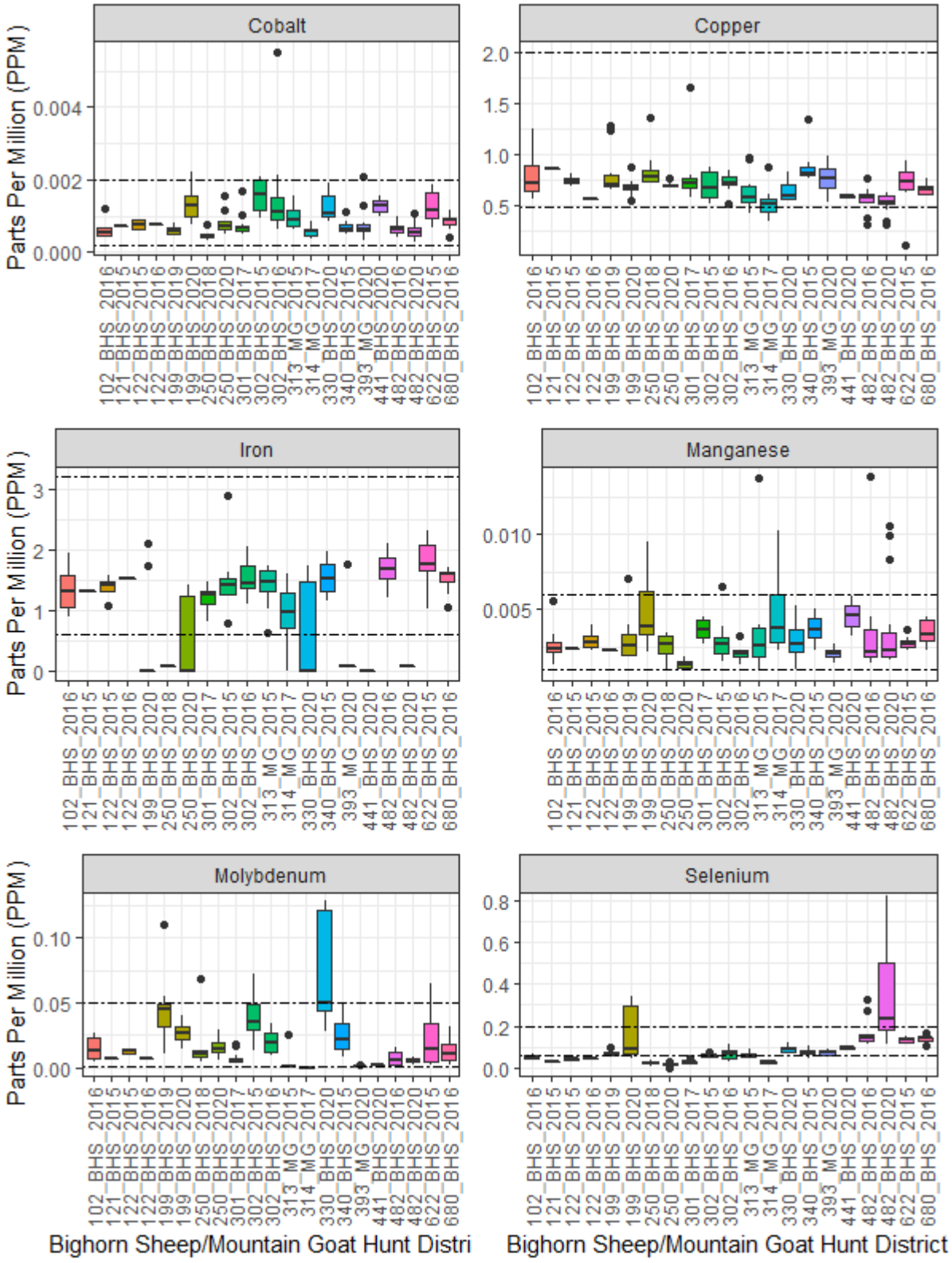


Figure 9. Boxplots of trace mineral concentrations in serum for cobalt, copper, iron, manganese, molybdenum, selenium, and zinc (displayed in parts per million, ppm) for each sampled bighorn sheep and mountain goat herd. Horizontal dashed lines represent the minimum and maximum range of values observed in wild (Poppenga et al. 2012) and/or domestic sheep (Herdt & Hoff 2011).

Adult female body condition, as measured by a body condition score index and a measurement of maximum rump fat thickness, indicated good to excellent body condition across sampled herds (Figure 10) and a reasonable correspondence between the two metrics (Figure 11). We were unable to measure maximum rump fat thickness for all herds, but body condition scores indicated that bighorn sheep in HDs 199 and 482 (especially in 2020) were among those in best condition.

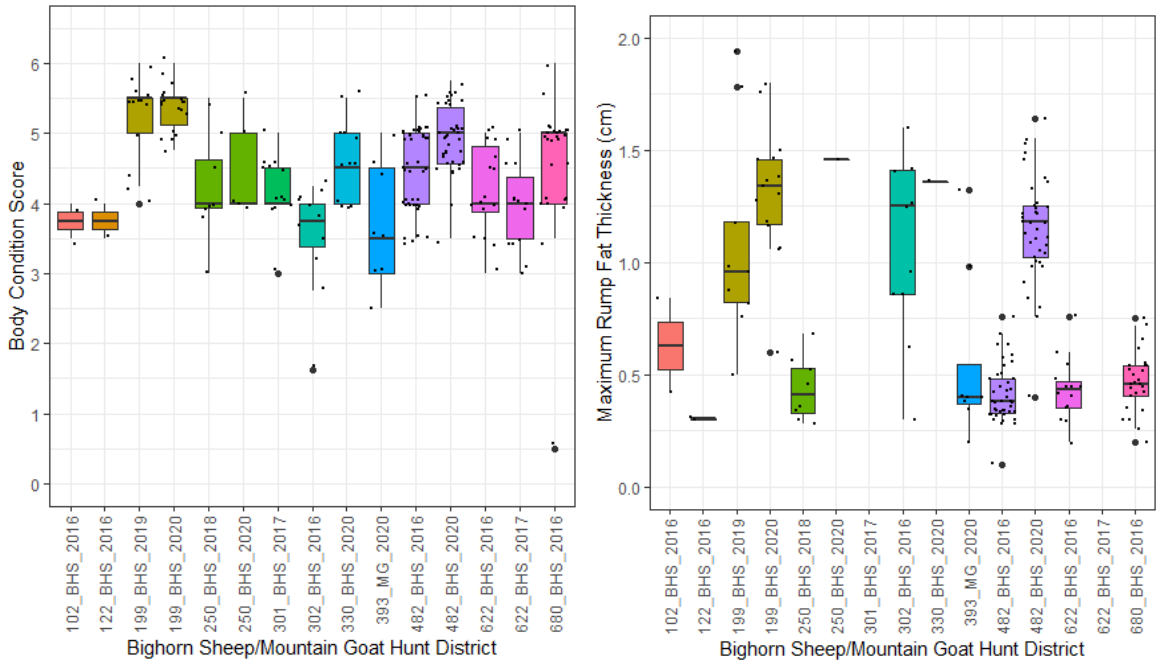


Figure 10. Boxplots of adult (≥2 yrs) ewe body condition scores (scale of 0.5-6, following a protocol developed by Stephenson et al. 2020) assessed by palpation and ultrasound-measured maximum rump fat thickness (cm) for each sheep herd. Raw data points are also displayed.

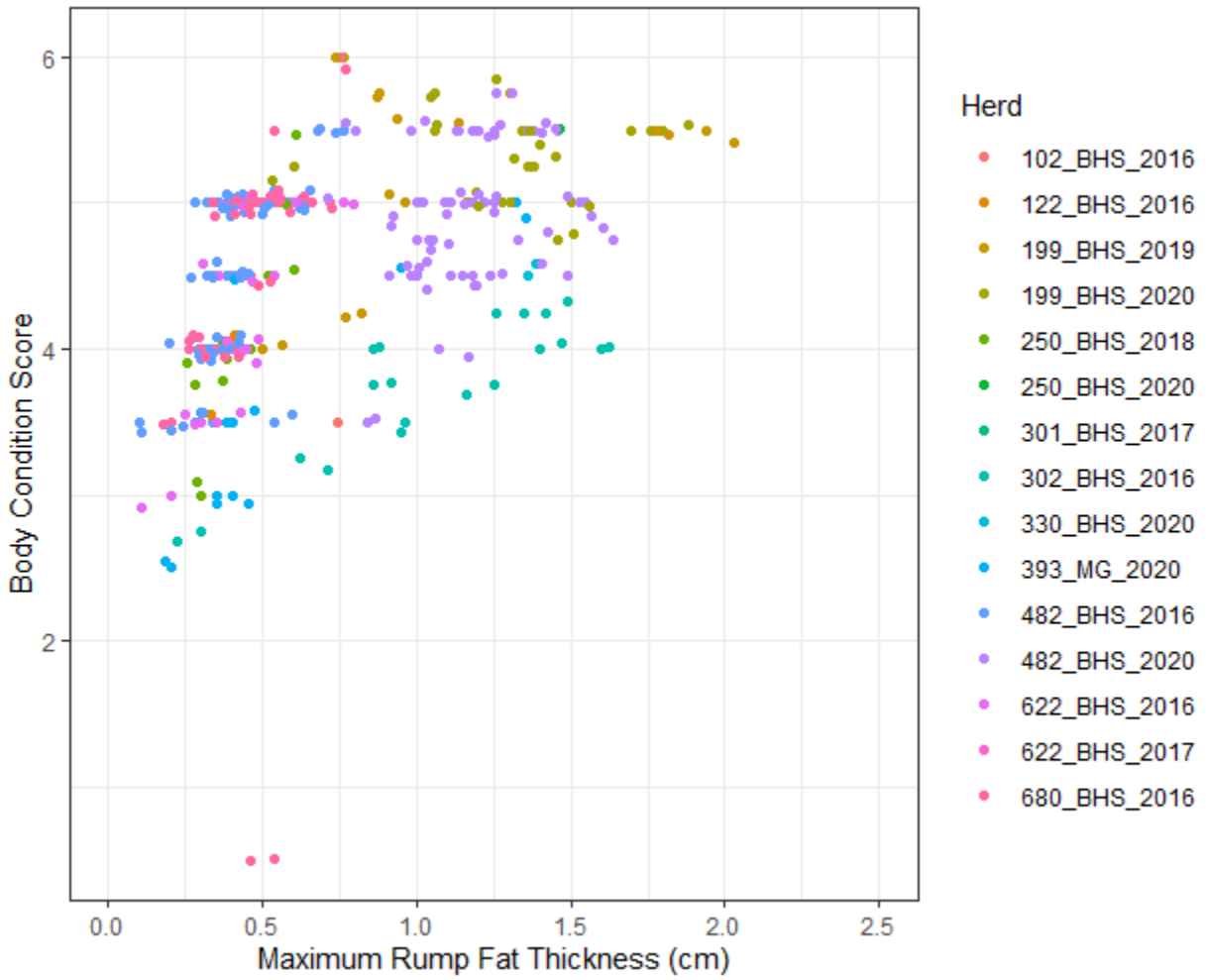


Figure 11. Jittered plot of maximum rump fat thickness (cm) against body condition score for individuals within sampled herds.

We detected high pregnancy rates among bighorn sheep and mountain goat herds sampled in February (Figure 12). Populations sampled in December (HD 250 in 2018 and HD 393 in 2020) exhibited very low pregnancy rates and were likely sampled too early to reliably detect pregnancy using Pregnancy-Specific Protein B in serum.

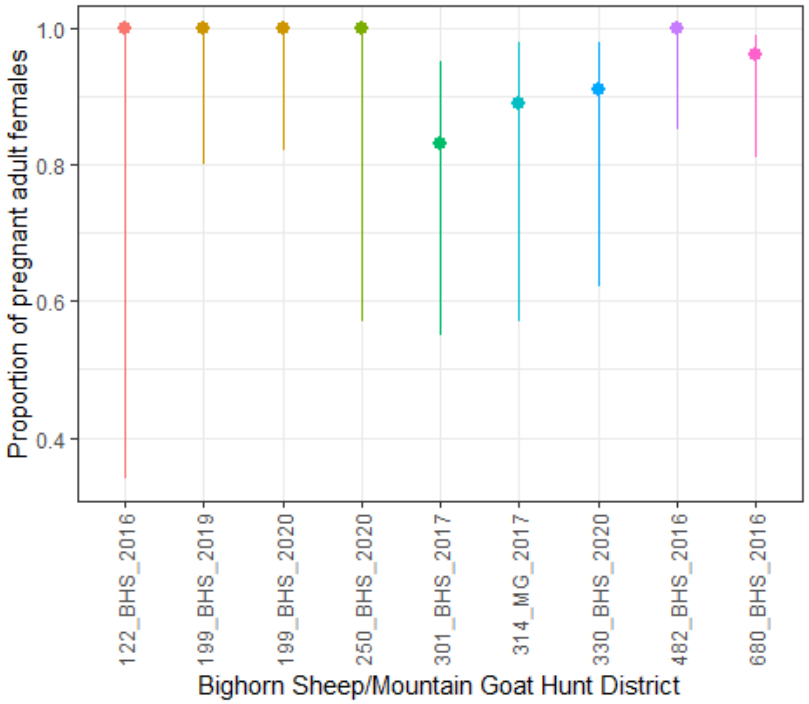


Figure 12. Proportion of pregnant adult (≥2 years old) females among bighorn sheep and mountain goat herds sampled in February, when we can reliably detect pregnancy using Pregnancy-Specific Protein B in serum.

Movement

HD 250 BHS: Painted Rocks

Two rams and six ewes were GPS-collared in winter 2018-2019 (Figure 13). Three collars included fabric rot-off spacers; unfortunately, one ewe collar fell off after just one week, but was redeployed on another ewe and is still active. Three ewe collars were retrieved when the sheep were killed by mountain lions (n=2) and an unknown predator (n=1) in March 2019, January 2020, and November 2020. The two ram collars rotted off after 4 and 6 months.

An additional three rams and three ewes were GPS-collared in February 2021. Two of each sex were recaptures. One ewe collar was retrieved in May 2021 after the sheep was found dead on a trail (no obvious signs of predation). Two ram collars were retrieved in May 2021 (mortality) and June 2021 (dropped collar). As of January 2022, five sheep remain collared (4 ewes and 1 ram).

All rams exhibited unexpected long-distance movements into the Frank Church River of No Return Wilderness in Idaho to the west, and the Bitterroot Mountains to the north. The first two collars ultimately dropped near the capture site at Painted Rocks Reservoir, while the third dropped far up the Soda Springs drainage in the Bitterroot Mountains. All surviving ewes also moved into high elevation alpine habitats during the summer, including Trapper Peak to the north and Piquette Mountain to the east.

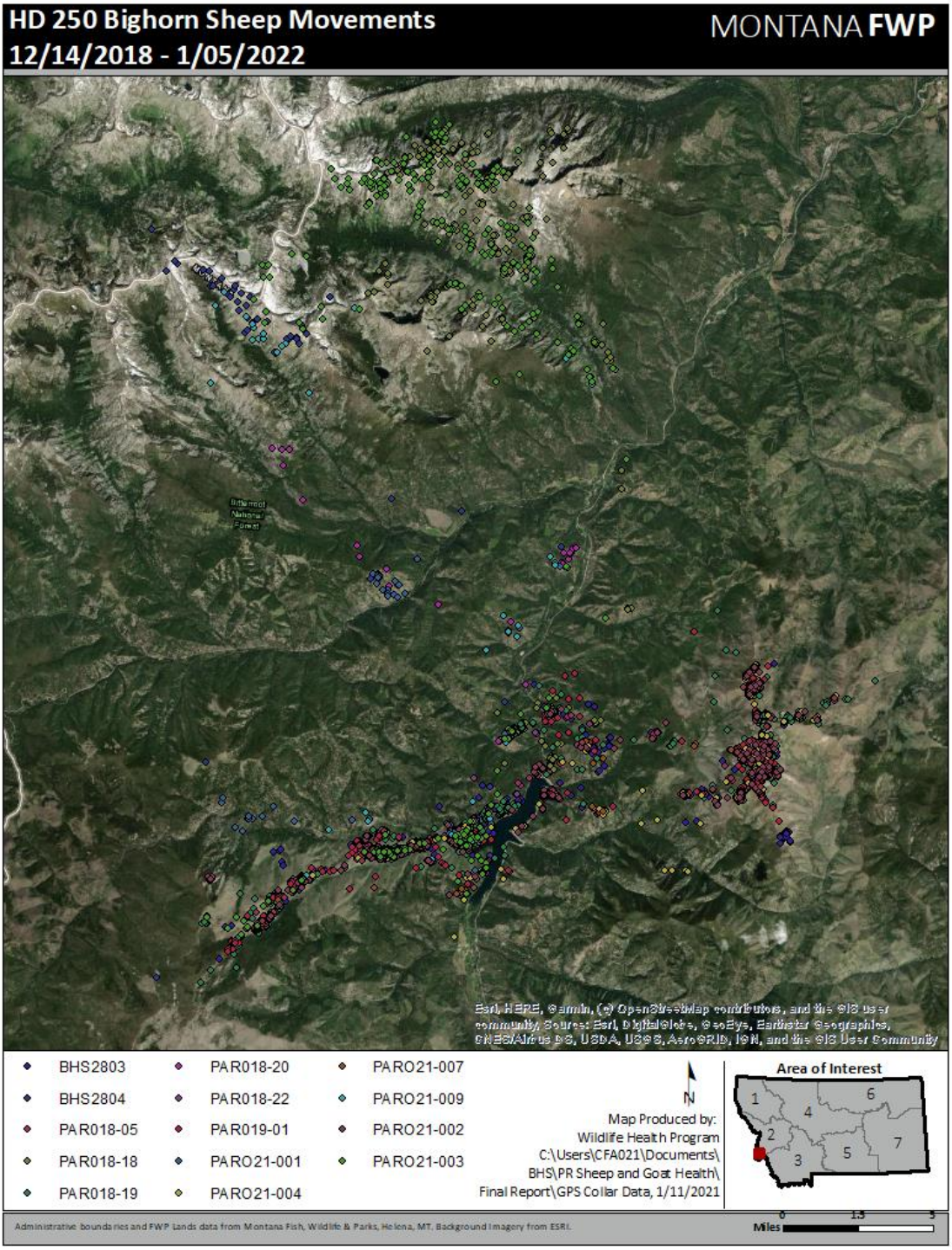


Figure 13. Map of HD 250 Painted Rocks bighorn sheep GPS collar locations, December 2018-January 2022, color coded by animal.

HD 330 BHS: Greenhorns

In 2021, 10 collars were deployed on 7 ewes and 3 rams in the Greenhorn Mountain bighorn sheep herd (Figure 14). Collars will continue to collect data for the next 2-3 years, improving our understanding of the of this herd's movements. Collars were deployed to better

understand the home range of this herd as well as to better understand bighorn sheep movement with respect to domestic sheep allotments in the area.

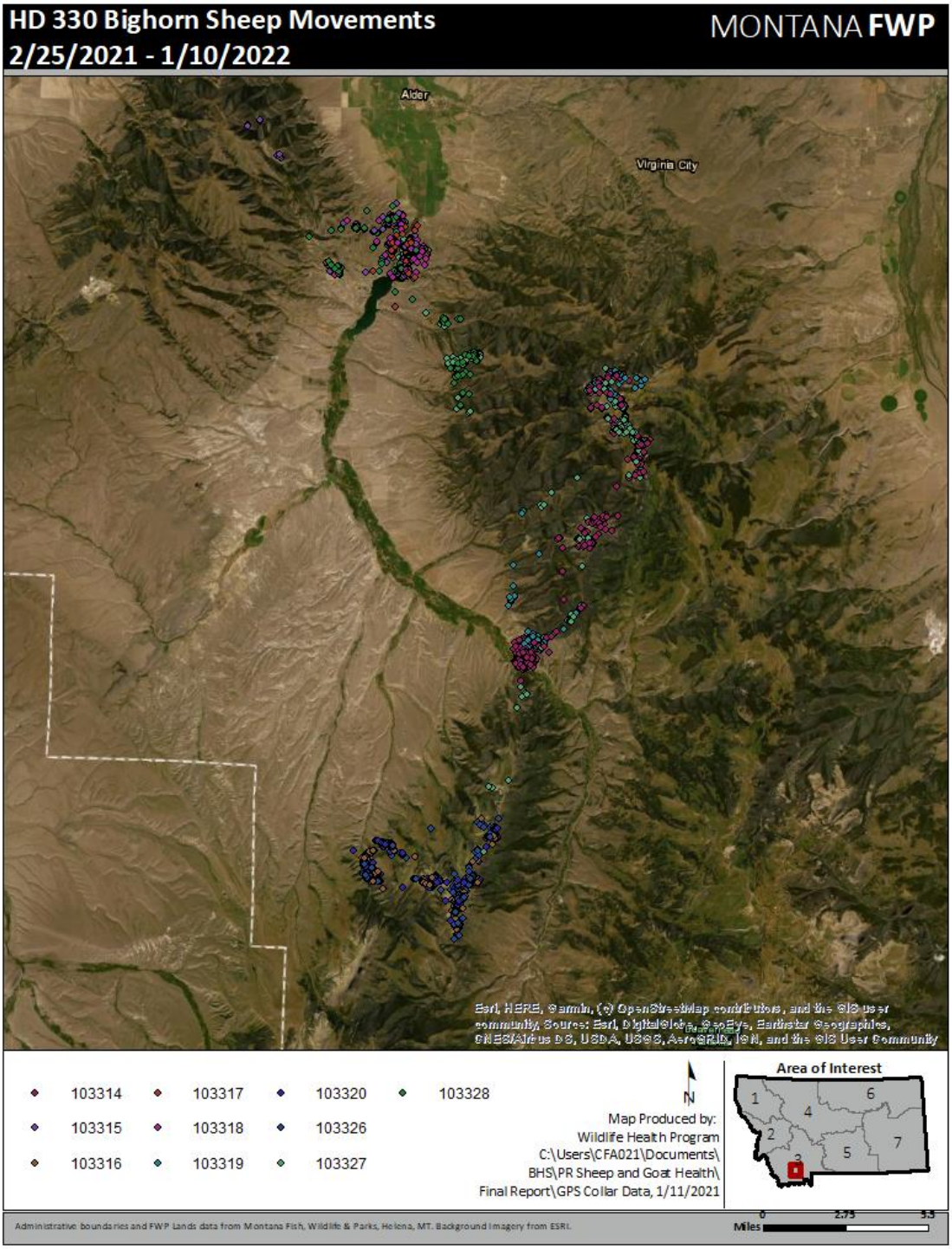


Figure 14. Map of HD 330 Greenhorn bighorn sheep GPS collar locations, February 2021-January 2022, color coded by animal.

HD 393 MG: Bridger Mountains

In December 2020, GPS collars were deployed on 12 mountain goats, including 8 nannies and 2 billies, in the Bridger Mountains to obtain home range and movement information and as part of a research project on goat habitat use and human recreation (Figure 15). These collars will continue to collect data for another 2-3 years.

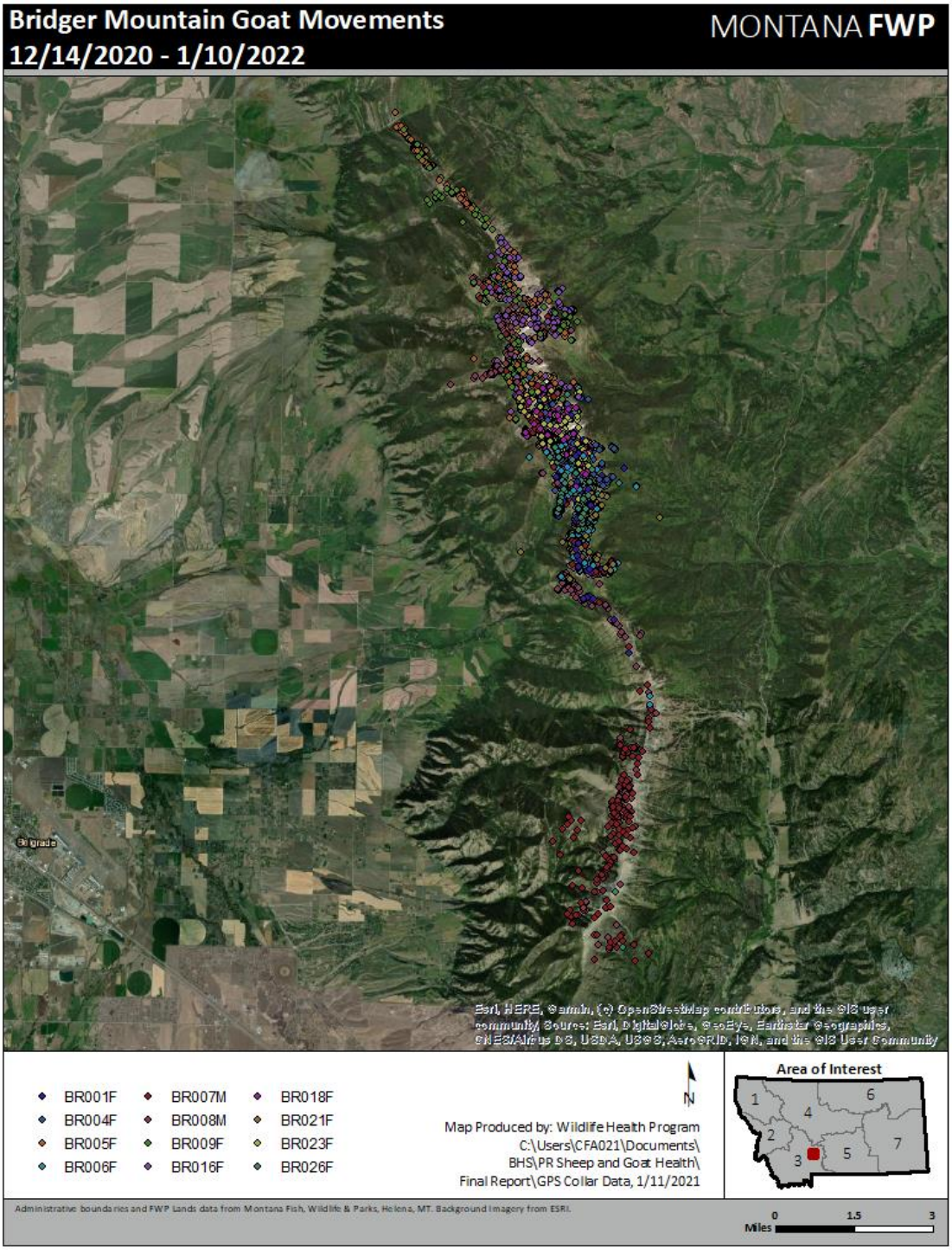


Figure 15. Map of HD 339 Bridger Mountain goat GPS collar locations, December 2020-January 2022, color coded by animal.

HD 441 BHS: North Fork Birch Creek – Teton

In 2021, 5 collars were deployed on 3 ewes and 2 rams to better understand the North Fork Birch Creek-Teton bighorn sheep herd's movements (Figure 16). Motivations for better understanding movement within this herd included (1) increasing survey efficiency, since sheep habitat within this range is patchy and difficult to survey and collars have already indicated that sheep are using habitats not included in previous surveys, (2) examining connectivity to neighboring sheep populations where known all-age die-offs have occurred, (3) to better understand the sexual segregation across space within this herd, and (4) to determine movements or proximity, if any, to a nearby domestic sheep population. These collars will remain deployed for the next 2-3 years.

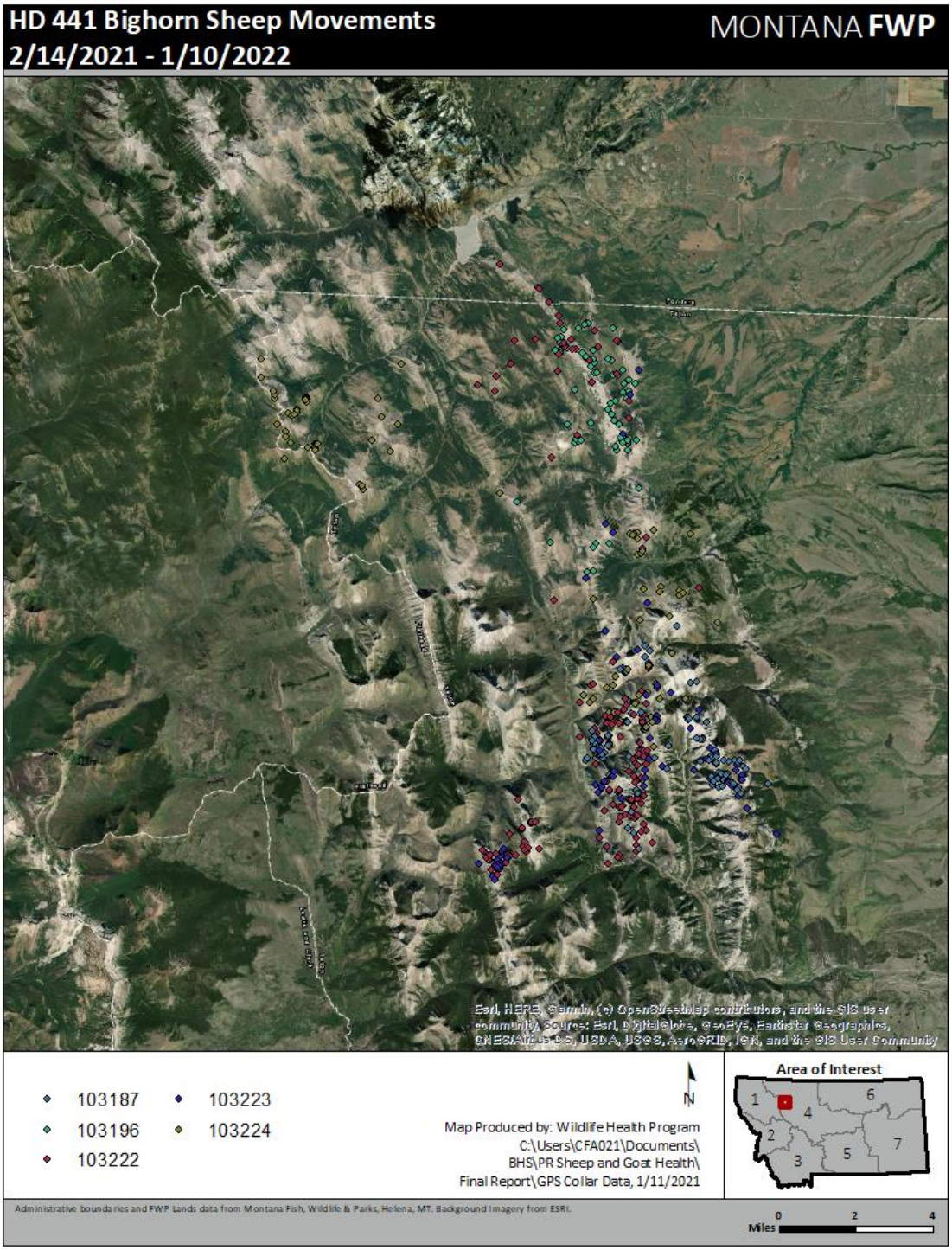


Figure 16. Map of HD 441 North Fork Birch Creek – Teton bighorn sheep GPS collar locations, February 2021-January 2022, color coded by animal.

Discussion

Between 2016 and 2021, Montana Fish, Wildlife and Parks conducted health assessments on 14 bighorn sheep herds (N = 465) and 3 mountain goat herds (N = 51) that FWP regional wildlife program managers prioritized for sampling to inform current or near-future management. Due to weather or difficult capture terrain, we were unable to conduct planned captures of bighorn sheep in the Pryor Mountains (HD 503) or mountain goats in the Big Belt Mountains (HDs 350 and 453). Many of our captures fell short of reaching desired sample sizes, due to small sheep or goat population sizes, weather, and difficult capture terrain, factors that remain significant challenges for assessing the health of small sheep or goat herds. Some of our larger sampling events occurred on populations being evaluated for, or being used as sources for translocations, including bighorn sheep populations in HD 199 (26 sheep translocated to the Tendoy Mountains in 2021), HD 302 (within-range translocation of 97 sheep), HD 482 (60 sheep translocated to the Beartooth Wildlife Management Area in 2016-2017 and 50 sheep translocated to the Little Belt Mountains in 2020), and HD 622 (20 sheep translocated to HD 122 in 2018).

All sampled herds exhibited evidence of exposure to at least one known respiratory pathogen, including *Pasteurellaceae* or *Mycoplasma ovipneumoniae*, with the exception of bighorn sheep HDs 101 and 122, for which we had insufficient sample sizes for pathogen detection. Serological testing for exposure to *Mycoplasma ovipneumoniae* remains the more sensitive tool for determining active or recent infection with the bacteria, and combined with PCR results, these tools indicated the presence of *Mycoplasma ovipneumoniae* infection in bighorn HDs 250, 301, 302, 330, 340, 441, 482 (in 2016, but not 2020), and 680 and in mountain goat HD 314. Bighorn HDs 102, 199, 622, and 482 (as of 2020), and mountain goat HDs 313, appear to be free from *Mycoplasma ovipneumoniae* infection. Opportunistic sampling of hunter-harvested bighorn sheep and mountain goats, particularly from HDs 482, 622, and 313 corroborate these observations (Appendix I, Table A1.2 & A1.3.). Natural or management-induced pathogen fade-out can occur (Spaan et al. 2021, Besser et al. 2021, Garwood et al. 2020, Almberg et al. 2021), and this is one plausible explanation for the disappearance of *Mycoplasma ovipneumoniae* from HD 482. Mountain goat HD 393 is also likely free of *Mycoplasma ovipneumoniae* based on serological results, but we failed to meet our target statistical power for PCR detection. Of these herds, all-age-die-offs related to respiratory disease have been documented in HDs 340 and 441.

Respiratory disease has been identified as one of the largest and most damaging health issues facing bighorn sheep, and the recent discovery that mountain goats harbor the same respiratory pathogens is also of great concern. However, the etiology of respiratory disease in bighorn sheep remains quite uncertain (Cassirer et al. 2018), and it is even less certain in mountain goats. The difficult nature of detecting pathogens and the incomplete scientific understanding of the disease expression process make concrete conclusions impossible, and translocation and other management decisions will necessarily be made under this uncertainty. At the same time, the sampling program and results we describe in this report are among the most rigorous and complete in any jurisdiction, and some general insights are possible.

There is significant scientific evidence that *Mycoplasma ovipneumoniae* is a necessary agent involved in pneumonia outbreaks (Besser et al. 2012, Besser et al. 2013, Cassirer et al. 2018, Butler et al. 2018). However, research has revealed substantial variation in morbidity, mortality, recruitment rates and herd performance in the presence of *Mycoplasma ovipneumoniae,* suggesting that other factors, including *Mycoplasma ovipneumoniae* strain type or co-infecting agents, are influential. Among 14 *Mycoplasma ovipneumoniae*-positive herds in Montana (n=7) and in Wyoming (n=7) (Butler 2017), at least half of the herds have exhibited adequate lamb recruitment and adult survival, and have recently been stable or increasing, despite some history of pneumonia epizootics. Conversely, we are unaware of populations that have a recent or more distant history of pneumonia epizootics in which *Mycoplasma ovipneumoniae* has not been detected, since diagnostic tools for *Mycoplasma ovipneumoniae* have become available. Based on the evidence accumulated to date, *Mycoplasma ovipneumoniae* is likely a necessary agent involved in pneumonia epizootics but may not be a sufficient indicator of a history, severity, or likelihood of pneumonia epizootics. Understanding the variation in response to infection with *Mycoplasma ovipneumoniae* continues to be the subject of ongoing study across the west.

Bacteria in the *Pasteurellaceae* family, particularly hemolytic strains or those that contain and express the Leukotoxin A gene, are thought to play important roles in respiratory disease, influencing patterns of morbidity and mortality (Dassanayake et al. 2010, Besser et al. 2012, Shanthalingam et al. 2014, Wood et al. 2016). Past work has indicated that detection probabilities are extremely low (0.12-0.36) for the majority of *Pasteurellaceae* using culture-based diagnostic methods (Butler 2017, Butler et al. 2017, Walsh et al. 2012). Our sampling effort attempted to accommodate these low detection probabilities by testing multiple tonsil swabs per animal by culture. While our detection probabilities remained low in many cases due to small sample sizes, we detected at least one of the respiratory pathogens of concern (e.g. *Pasteurellaceae*, the Leukotoxin A gene, or *Mycoplasma ovipneumoniae*) within each herd, except in HD 101 and 122 where samples sizes were extremely low (Figure 4 & 5). Our data, combined with historic data and results from previous studies (Butler et al. 2018) suggest widespread respiratory pathogen distribution across Montana's bighorn herds (Figure 6). As we have found in other herds, the detection of the leukotoxin gene did not always correspond with the detection of hemolytic activity of the bacteria (the ability of the bacteria to lyse red blood cells), which is assumed to be the sign of toxin expression (Fisher et al. 1999). This indicates that while the leukotoxin A gene is present in the *Pasteurellaceae* bacteria in all our tested herds, it is not always being expressed. How this relates to future risk of gene expression and associated hemolytic activity is unknown.

Serological data indicated relatively common exposure to *Anaplasma*, contagious ecthyma, epizootic hemorrhagic disease virus, and/or *Leptospiria*, and ubiquitous exposure to Parainfluenza-3. Although the *Anaplasma* serology test is designed to detect bovine exposure to *Anaplasma marginale*, the causative agent of bovine anaplasmosis, reactions in sheep may indicate spillover exposure or cross-reactions with other circulating *Anaplasma* species (Aubry & Geale 2010). This bacterial infection is transmitted via biting ticks or flies, and in cattle, can cause acute anemia and death (Underwood et al. 2015). Our understanding of the impacts of

Anaplasma on wild ruminant health is extremely limited. Exposure to epizootic hemorrhagic disease virus (EHDV), transmitted via biting midges, was most common among bighorn sheep herds in the eastern part of the state (HDs 482, 622, 680), with limited exposure in southwestern herds (HD 301 and 340). These patterns are consistent with EHDV exposure patterns in other ruminant species across the state (Montana FWP, unpublished data), with high-mortality outbreaks being much more common in white-tailed deer populations in the eastern part of the state. EHDV can cause morbidity and mortality in bighorn sheep and mountain goats, although disease tends to be much less severe than in white-tailed deer (Ruder et al. 2015). Most infected individuals that recover are believed to clear the virus, so the risk of moving an actively or persistently infected individual is probably low, but unknown. Most herds have also been exposed to at least one serovar of *Leptospiria*, a pattern consistent with an observed widespread distribution of the bacteria across numerous species and the state (Montana FWP, unpublished data). We detected widespread exposure to contagious ecthyma across sampled herds. Contagious ecthyma, when introduced to naive sheep/goats, can cause debilitating sores to form on the lips, muzzle, udder, feet, or vulva of naive animals, in some cases leading to death. While sampled herds were asymptomatic, we have observed at least one severe outbreak in recent history (Gates of the Mountain) in which bighorn sheep were observed with large visible sores on their mouths. It is also possible that lesions in sampled herds were small or inconspicuous, or that they were more common in naïve lambs/kids, of which we sampled relatively few. All sampled herds were exposed to Parainfluenza-3, usually at high prevalences, suggesting widespread exposure but low morbidity and mortality. These rates are comparable to those found in other Montana bighorn sheep herds between 1990 – 1997 (Aune et al. 1998), although they are much higher than exposure rates reported in a large serosurvey of bighorn sheep in California from 1978-1990 (Clark et al. 1993).

Serological exposure to other respiratory viruses, including bovine respiratory syncytial virus, bovine viral diarrhea I & II, infectious bovine rhinotracheitis, and ovine progressive pneumonia, remained limited, consistent with earlier serosurveys of Montana bighorn sheep (Miller et al. 2011). Bovine viral diarrhea I & II (BVD) can cause gastrointestinal and respiratory disease, reproductive loss, and immunosuppression in cattle, and the viruses can infect a range of other domestic and wild ruminant species, including bighorn sheep and mountain goats (Wolff et al. 2016). While impacts to wild ruminants are not fully understood, absent or mild clinical signs to high-mortality outcomes have been documented (Fox et al. 2019). Bovine respiratory syncytial virus (BRSV) has been found to cause a range of clinical disease outcomes in bighorn sheep, ranging from no observable symptoms (Foryet et al. 1988) to pneumonia (Dassanayake et al. 2013). High seroprevalences of BRSV (and high titers) in HDs 482 and 680 in 2016 suggested recent and widespread infection, but by 2020, seroprevalence in HD 482 had dropped to near zero. We do not know how long titers to BRSV last, nor do we know the specificity of the serological test in bighorn sheep since the test is only validated for cattle, but if this represents a real dynamic and titers are short-lived, it is possible that an infection swept through these herds, and following high exposure, faded out from the population. Infectious bovine rhinotracheitis can cause upper respiratory tract infections in domestic sheep and goats, although impacts on wild sheep and goats remain largely unknown. Ovine progressive pneumonia, caused by a lentivirus, is a slow degenerative disease that can cause immune-

mediated lesions on organs, and can manifest in some older animals as ill-thrift, respiratory distress and mastitis (Brodie et al. 1998). It is widely distributed in domestic sheep, with one survey indicating prevalence of 49% among domestic sheep in the Rocky Mountains (Cutlip et al. 1992).

Brucella ovis, which can cause male reproductive lesions and occasional abortions or increased natal mortality in ewes, can cause disease in domestic sheep and goats (Burgess et al. 1985), as well as in bighorn sheep under experimental conditions (McCollum et al 2013). We were unable to find other references for *B. ovis* presence in mountain goats, despite two of our herds showing serological evidence of exposure. In mountain goat HD 393, where we observed a seroprevalence of 40% (95% CI: 20-64), it may be worth opportunistically examining the reproductive tracts of any harvested billies and monitoring the herd for any depressed reproduction.

We found that coccidia parasites were prevalent and widely distributed across herds. Most wild mammals are infected with one or more species of coccidian parasites at some point during their life, and it is generally assumed that these infections are harmless under natural, wild conditions (Duszynski & Upton 2001). Wild mammals can mount protective immunity to individual coccidian species. Coccidia-induced disease, known as coccidiosis, is generally only a health hazard in wild populations when unnatural crowding occurs or population density becomes very high, yielding extremely high transmission. Documented cases of clinical disease due to coccidiosis in wild mammals is rare in the literature. Determining true prevalence of coccidial infection in wild populations is difficult due to the very transient nature of infection and high variability in number of oocysts shed throughout the course of infection. Our testing is a survey for presence of various coccidia species.

Lungworms were once believed to be the primary causal agent for pneumonia and respiratory disease in bighorn sheep (Besser et al. 2013). As we have found among our surveyed herds in Montana, lungworm infestations are ubiquitous in most bighorn sheep populations, including those unaffected by pneumonia (Forrester and Senger, 1964; Festa-Bianchet, 1991). Experimental work, including infection challenges (Samson et al. 1987) and treatments with anthelmintics (Miller et al. 2000), have failed to show associations between lungworm infections, host survival, and pneumonia or respiratory disease (see Besser et al. 2013 for a review). More recent work suggests that lungworm presence has limited value in assessing herd health and likely causes little disease in wild populations (Festa-Bianchet, 1991).

Between 2018-2020, we detected three cases of *Psoroptes ovis* in bighorn sheep HD 250; this was the first time in recent history that this parasite had been confirmed in any of our Montana bighorn herds. When we revisited HD 250 in 2020, we found no further evidence of infection by *Psoroptes ovis*, suggesting that the infection within this herd is limited. *Psoroptes ovis* can cause mild to severe crusty or scabby lesions in the ears, and on the face, neck and torso. Severe infections can cause hearing loss, a decline in body condition and death, and in some cases *P. ovis* has been implicated in population-level declines of bighorn sheep (Boyce et al. 2005).

Trace element concentrations in all sampled herds appeared adequate according to previously published reference ranges in wild (Poppenga et al. 2012) and domestic sheep (Herdt & Hoff 2011), except for selenium and iron which were deficient in a number of herds. While low, it's not clear whether these levels are likely to cause problems in wild sheep. In domestic sheep, iron deficiencies can result in anemia, and selenium deficiencies have been implicated in muscular dystrophies, failure to thrive, poor reproduction, impaired immunity, and bone-marrow abnormalities (Poppenga et al. 2012, Flueck et al. 2012). Selenium levels appear consistently high in the eastern Montana herds we sampled (HDs 482, 622, and 680), likely indicating high selenium availability in the environment. Additionally, concentrations of molybdenum among goats in HDs 314 and 393 were below ranges reported for sheep, but, without published reference ranges for mountain goats, these may be normal values.

It has been hypothesized that low selenium levels in bighorn sheep might explain the severity and persistence of respiratory disease within a herd (Coggins 2006, Rosen et al. 2009). However, it remains unclear whether observed low-selenium levels are problematic for bighorn sheep, as observations of overt signs of selenium deficiency are rare, vitamin E can alter selenium needs, and because of speculation that mountain sheep and goats may be adapted to low-selenium environments (Flueck et al. 2012). Selenium supplementation has not prevented all-age-die-offs (Coggins 2006) nor has the experimental evidence to date shown supplementation to have definitive effects on lamb production and survival or population growth (Cox 2006, Coggins 2006). Until additional experimental work is conducted with appropriate controls, the impacts of selenium on herd health, especially herds with respiratory disease, will remain unclear.

Adult female body condition indices and max fat measurements indicated good overall body condition for all herds that were measured, even for those measured later in February when fat stores are more likely to have been metabolized.

We detected high pregnancy rates among bighorn sheep herds sampled in February, consistent with those rates published for wild bighorn sheep and mountain goat populations (70-93%; Brundige et al. 1988, Berger 1991). Similarly, the mountain goats from HD 317 that we sampled in February exhibited high pregnancy rates, consistent with high parturition rates observed in other populations (55-90%; Hamel et al. 2010). Populations sampled in December (HD 250 in 2018 and HD 393 in 2020) exhibited very low pregnancy rates and were likely sampled too early to reliably detect pregnancy using Pregnancy-Specific Protein B in serum.

Management Implications

Given that bighorn sheep in HDs 250, 301, 302, 330, 340, 441, and 680 and mountain goats in HD 314 are infected with *Mycoplasma ovipneumoniae* and *Pasteurellaceae* with the Leukotoxin A gene, where possible, we would recommend against augmenting these herds or using them as sources for translocations. Susceptible bighorn sheep or mountain goats placed into a herd infected with respiratory infections may experience elevated mortality rates due to subsequent infection (Plowright et al. 2013) and are also likely to prolong the natural or spontaneous process of pathogen extinction (Almberg et al. 2021). Bighorn HDs 102, 199, 622, and 482 (as of

2020) and mountain goat HDs 313 appear to be free from *Mycoplasma ovipneumoniae* infection. Of these *Mycoplasma ovipnuemoniae*-free herds, bighorn sheep HDs 199, 622, and 482 are among our most robust populations, with no history of respiratory disease and consistently good body condition, suggesting these remain among our best options for source populations, particularly for reintroductions. Because all herds are infected with at least one pathogen of concern, augmentations must weigh benefits against the risk of mixing naïve and infected animals, which may lead to increased morbidity and mortality of translocated animals and/or trigger new disease outbreaks. Overall, we recommend rigorous monitoring of host and pathogen dynamics in herds following translocations to increase our understanding of the etiology of respiratory disease and better predict outcomes of management actions. Approaching translocations in an adaptive management framework, where management actions are preceded by predictive models then accompanied by detailed monitoring and updating of models based on monitoring data, should reduce uncertainty about the impact of pathogens on management actions and improve our ability to predict outcomes of management actions in the future given the ubiquitous distribution of pathogens we document here.

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Appendix I

Table A1.1. All captured mountain goats (MG) and bighorn sheep (BHS) will be screened for the following list of pathogens and parasites. This table also includes an assessment of the risk associated with each pathogen/parasite and an associated rationale, as well as the test types and laboratories employed for the screening. Testing laboratory abbreviations: WADDL=Washington Animal Disease Diagnostic Laboratory; FWP =Montana Fish, Wildlife, and Parks Health Laboratory; MVDL=Montana Veterinary Diagnostic Laboratory; MSU DCPAH=Michigan State University Diagnostic Center for Population and Animal Health.

Organism	**Risk category**	**Rationale**	**Test type and any limitations**	**Testing Laboratory**
Mycoplasma ovipneumoniae	High	Likely necessary, if not sufficient, for chronic or epidemic BHS pneumonia.	Serology—gives us most conservative metric of presence/absence from a herd. PCR—the proportion of actively infected individuals may be small and chronically infected individuals may shed intermittently, so a negative at the herd level may not give us as much confidence.	WADDL
Leukotoxin A+ *Pasteurellas*	High	Identified as a potentially important class of pathogens involved in respiratory disease.	PCR	WADDL
Hemolytic *Pasteurellas*	High	Identified as a potentially important class of pathogens involved in respiratory disease.	Culture	WADDL
Mannheimia haemolytica	Moderate	Sometimes identified in respiratory disease; exact role unknown.	Culture/PCR	WADDL
Bibersteinia trehalosi	Moderate	Sometimes identified in respiratory disease; exact role unknown.	Culture/PCR	WADDL
Pasteurella multocida	Moderate	Sometimes identified in respiratory disease; exact role unknown.	Culture/PCR	WADDL
Psoroptes ovis	High	Highly contagious and capable of causing chronic and extensive morbidity and mortality.	Parasitology	FWP/MVDL
Lungworm	Low	Depending on burden; low burdens are normal, high burdens may be problematic.	Parasitology	MSU DCPAH
Contagious ecthyma (Orf)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Brucella abortus	Low	Not generally considered a problem for sheep/goats.	Serology	MVDL

Brucella ovis	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Anaplasma	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Bovine respiratory syncytial virus (BRSV)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Bovine herpesvirus (IBR)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Parainfluenza-3 virus (PI3)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Ovine progressive pneumonia (OPP)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Bovine viral diarrhea (BVD I & II)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Bluetongue virus (BTV)	Moderate	Would not want to mix infected with naïve individuals.	Serology	MVDL
Epizootic hemorrhagic disease (EHD)	Low		Serology	MVDL
Leptospira (CAN, ICT, HAR, GRIP, POM serovars)	Low	Environmentally transmitted and widely distributed. Probably not a major concern.	Serology	MVDL

Table A1.2. Table of *Pasteurella* species detections by culture from tonsil swabs collected from bighorn sheep (BHS) and mountain goat (MG) mortalities due to hunter-harvest, road collisions, or found dead from other/unknown sources of mortality, 2016-2021. “N” denotes the number of individuals sampled, “HD” the species-specific hunting district from which the animal was sampled, and “Detections”, the number of each Pasteurella species detected. We note when no Pasteurella species were detected.

HD	Species	N	Pasteurella Species	Detections
100	BHS	2	None Detected	NA
100	MG	1	None Detected	NA
102	BHS	1	None Detected	NA
121	BHS	1	None Detected	NA
124	BHS	6	Pasteurella spp.	1
210	BHS	2	None Detected	NA
213	BHS	1	Bibersteinia trehalosi	1
270	BHS	1	None Detected	NA
301	BHS	7	Bibersteinia trehalosi	4
301	BHS	7	Mannheimia haemolytica	2
302	BHS	2	None Detected	NA
303	BHS	1	Bibersteinia trehalosi	2
313	MG	2	None Detected	NA
314	MG	3	Mannheimia haemolytica	1
314	MG	3	Mannheimia sp.	1
315	BHS	6	Bibersteinia trehalosi	3
315	BHS	6	Mannheimia ruminalis	1
315	BHS	6	Mannheimia sp.	2
315	BHS	6	Pasteurella multocida	1
323	MG	4	None Detected	NA
325	MG	1	None Detected	NA
328	MG	1	None Detected	NA
329	MG	3	None Detected	NA
330	BHS	3	Bibersteinia trehalosi	1
330	BHS	3	Mannheimia sp.	1
361	MG	1	None Detected	NA
415	MG	1	None Detected	NA
421	BHS	1	None Detected	NA
422	BHS	3	None Detected	NA
423	BHS	4	None Detected	NA
424	BHS	3	None Detected	NA
441	BHS	1	None Detected	NA
453	MG	1	None Detected	NA
482	BHS	2	Pasteurella spp.	1
514	MG	1	None Detected	NA
620	BHS	2	None Detected	NA
622	BHS	29	Bibersteinia trehalosi	2
622	BHS	29	Mannheimia glucosida	1
622	BHS	29	Mannheimia ruminalis	2
622	BHS	29	Mannheimia varigena	1
622	BHS	29	Pasteurella spp.	3
680	BHS	15	Mannheimia ruminalis	1
680	BHS	15	Mannheimia varigena	1

Table A1.3. A summary of results from (1) *Mycoplasma ovipneumoniae* PCR testing of nasal swabs, (2) Leukotoxin A PCR testing of the primary streak zone of cultured tonsil swabs, and (3) *Mycoplasma ovipneumoniae* serology from bighorn sheep (BHS) and mountain goat (MG) mortalities due to hunter-harvest, road collisions, or found dead from other/unknown sources of mortality, 2016-2021. "N" denotes the number of individuals sampled, "HD" the species-specific hunting district from which the animal was sampled, and "Detections", the number of positive samples. Prevalence and 95% confidence intervals are provided but are most meaningful for hunting districts with large sample sizes.

HD	Species	Pathogen & Test	N	Detections	Prevalence	Lower 95% CI	Upper 95% CI
100	BHS	Mycoplasma ovipneumoniae PCR	3	0	0	0	0.56
100	BHS	Pasteurella Leukotoxin A PCR	2	0	0	0	0.66
100	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
100	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
102	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
102	BHS	Pasteurella Leukotoxin A PCR	2	1	0.5	0.09	0.91
121	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
121	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
122	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
122	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
123	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
124	BHS	Mycoplasma ovipneumoniae PCR	8	0	0	0	0.32
124	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
124	BHS	Pasteurella Leukotoxin A PCR	4	1	0.25	0.05	0.7
142	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
203	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
203	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
203	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
210	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
210	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
210	BHS	Pasteurella Leukotoxin A PCR	2	1	0.5	0.09	0.91
212	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
213	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
213	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
213	BHS	Pasteurella Leukotoxin A PCR	1	1	1	0.21	1
216	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
240	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
250	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
270	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
301	BHS	Mycoplasma ovipneumoniae PCR	18	3	0.17	0.06	0.39
301	BHS	Mycoplasma ovipneumoniae Serology	1	1	1	0.21	1
301	BHS	Pasteurella Leukotoxin A PCR	10	5	0.5	0.24	0.76
301	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
301	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
302	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
302	BHS	Pasteurella Leukotoxin A PCR	1	1	1	0.21	1
303	BHS	Mycoplasma ovipneumoniae PCR	3	3	1	0.44	1
303	BHS	Pasteurella Leukotoxin A PCR	3	1	0.33	0.06	0.79
304	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
312	MG	Mycoplasma ovipneumoniae PCR	3	0	0	0	0.56

313	MG	Mycoplasma ovipneumoniae PCR	7	0	0	0	0.35
313	MG	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
313	MG	Pasteurella Leukotoxin A PCR	2	0	0	0	0.66
314	MG	Mycoplasma ovipneumoniae PCR	7	1	0.14	0.03	0.51
314	MG	Pasteurella Leukotoxin A PCR	3	1	0.33	0.06	0.79
315	BHS	Mycoplasma ovipneumoniae PCR	9	4	0.44	0.19	0.73
315	BHS	Pasteurella Leukotoxin A PCR	8	2	0.25	0.07	0.59
316	MG	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
321	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
323	MG	Mycoplasma ovipneumoniae PCR	8	0	0	0	0.32
323	MG	Pasteurella Leukotoxin A PCR	4	0	0	0	0.49
325	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
325	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
326	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
327	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
328	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
328	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
329	MG	Mycoplasma ovipneumoniae PCR	6	0	0	0	0.39
329	MG	Pasteurella Leukotoxin A PCR	3	0	0	0	0.56
330	BHS	Mycoplasma ovipneumoniae PCR	3	0	0	0	0.56
330	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
330	BHS	Pasteurella Leukotoxin A PCR	2	1	0.5	0.09	0.91
331	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
340	BHS	Mycoplasma ovipneumoniae PCR	11	3	0.27	0.1	0.57
340	BHS	Mycoplasma ovipneumoniae Serology	1	1	1	0.21	1
340	BHS	Pasteurella Leukotoxin A PCR	2	0	0	0	0.66
350	MG	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
361	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
362	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
381	BHS	Mycoplasma ovipneumoniae PCR	1	1	1	0.21	1
393	MG	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
393	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
413	BHS	Mycoplasma ovipneumoniae PCR	4	0	0	0	0.49
415	MG	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
415	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
421	BHS	Mycoplasma ovipneumoniae PCR	6	1	0.17	0.03	0.56
421	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
422	BHS	Mycoplasma ovipneumoniae PCR	11	0	0	0	0.26
422	BHS	Pasteurella Leukotoxin A PCR	3	0	0	0	0.56
423	BHS	Mycoplasma ovipneumoniae PCR	6	0	0	0	0.39
423	BHS	Pasteurella Leukotoxin A PCR	3	0	0	0	0.56
424	BHS	Mycoplasma ovipneumoniae PCR	9	0	0	0	0.3
424	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
441	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
453	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
453	MG	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
455	BHS	Mycoplasma ovipneumoniae PCR	2	0	0	0	0.66
455	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
482	BHS	Mycoplasma ovipneumoniae PCR	27	0	0	0	0.12
482	BHS	Mycoplasma ovipneumoniae Serology	4	0	0	0	0.49

482	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
500	BHS	Mycoplasma ovipneumoniae PCR	3	0	0	0	0.56
501	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
501	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79
502	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
503	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
514	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
518	MG	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
620	BHS	Mycoplasma ovipneumoniae PCR	4	0	0	0	0.49
620	BHS	Pasteurella Leukotoxin A PCR	2	0	0	0	0.66
622	BHS	Mycoplasma ovipneumoniae PCR	40	0	0	0	0.09
622	BHS	Mycoplasma ovipneumoniae Serology	1	0	0	0	0.79
622	BHS	Pasteurella Leukotoxin A PCR	28	8	0.29	0.15	0.47
680	BHS	Mycoplasma ovipneumoniae PCR	59	0	0	0	0.06
680	BHS	Mycoplasma ovipneumoniae Serology	12	2	0.17	0.05	0.45
680	BHS	Pasteurella Leukotoxin A PCR	17	7	0.41	0.22	0.64
690	BHS	Mycoplasma ovipneumoniae PCR	1	0	0	0	0.79
690	BHS	Pasteurella Leukotoxin A PCR	1	0	0	0	0.79

Appendix II: Neck Measurements for Collar Fitting

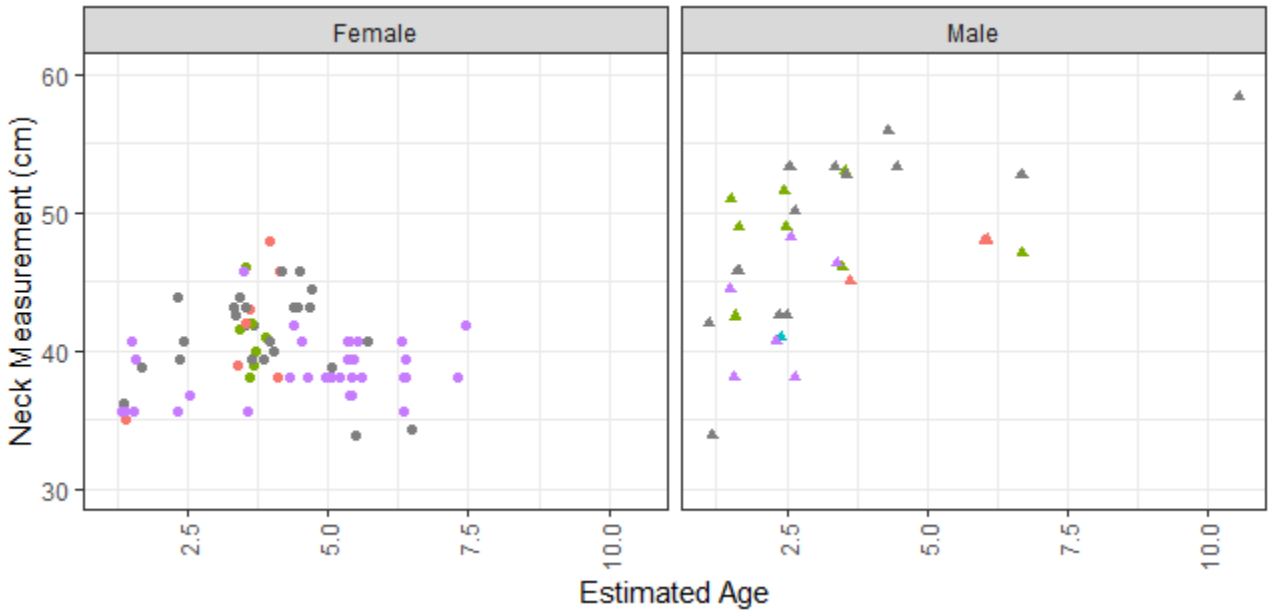

Figure A2.1. Plot of bighorn sheep neck measurements by estimated age, stratified by sex, and color-coded by herd. Data are from HDs 441, 330, 250, and 482.

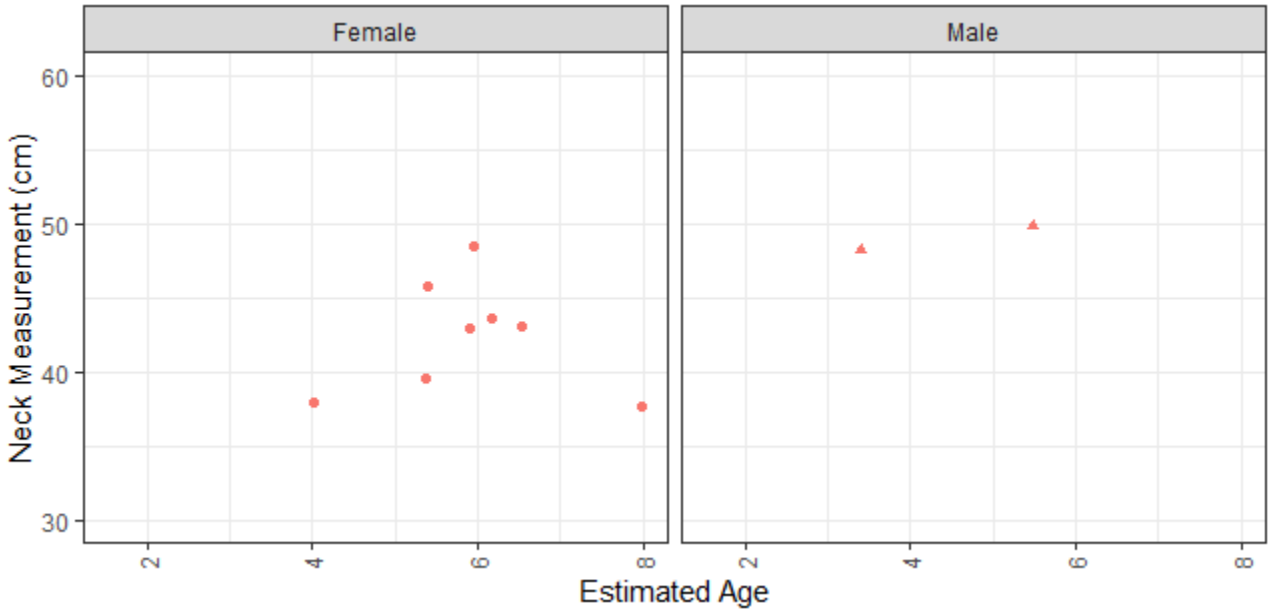

Figure A2.2. Plot of mountain goat neck measurements by estimated age, stratified by sex, and color-coded by herd. Data are from HD 393.

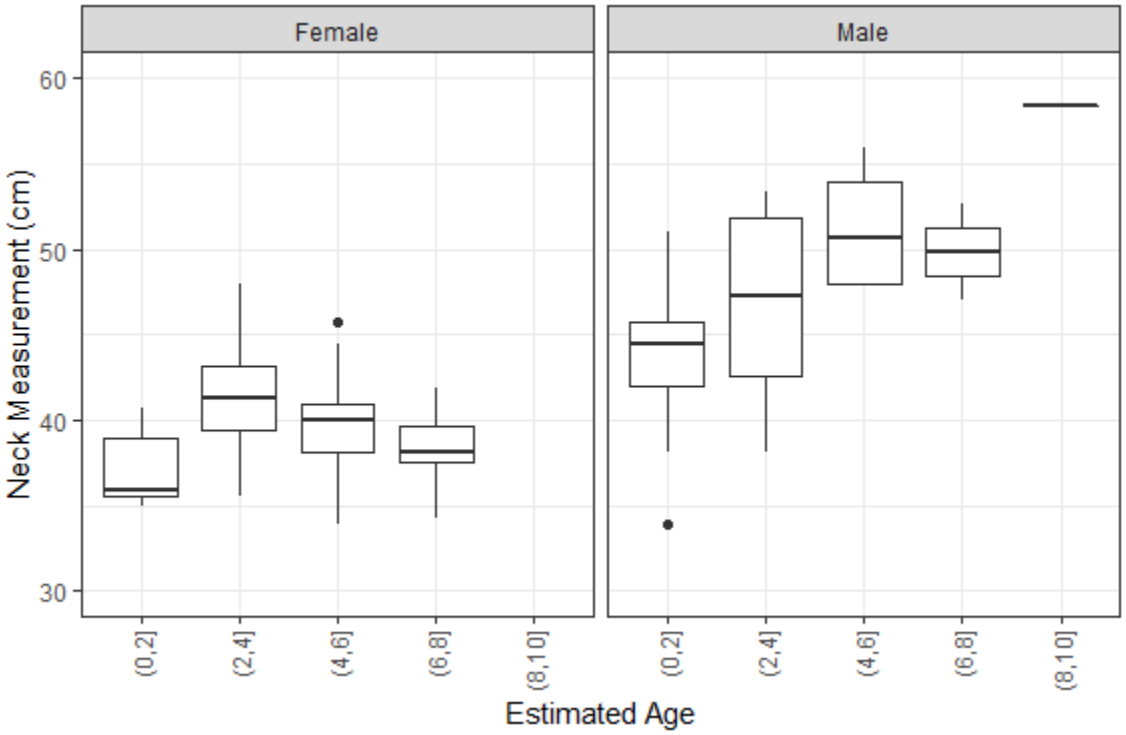

Figure A2.3. Boxplot of bighorn sheep neck measurements by estimated age and stratified by sex. Data are from HDs 441, 330, 250, and 482.

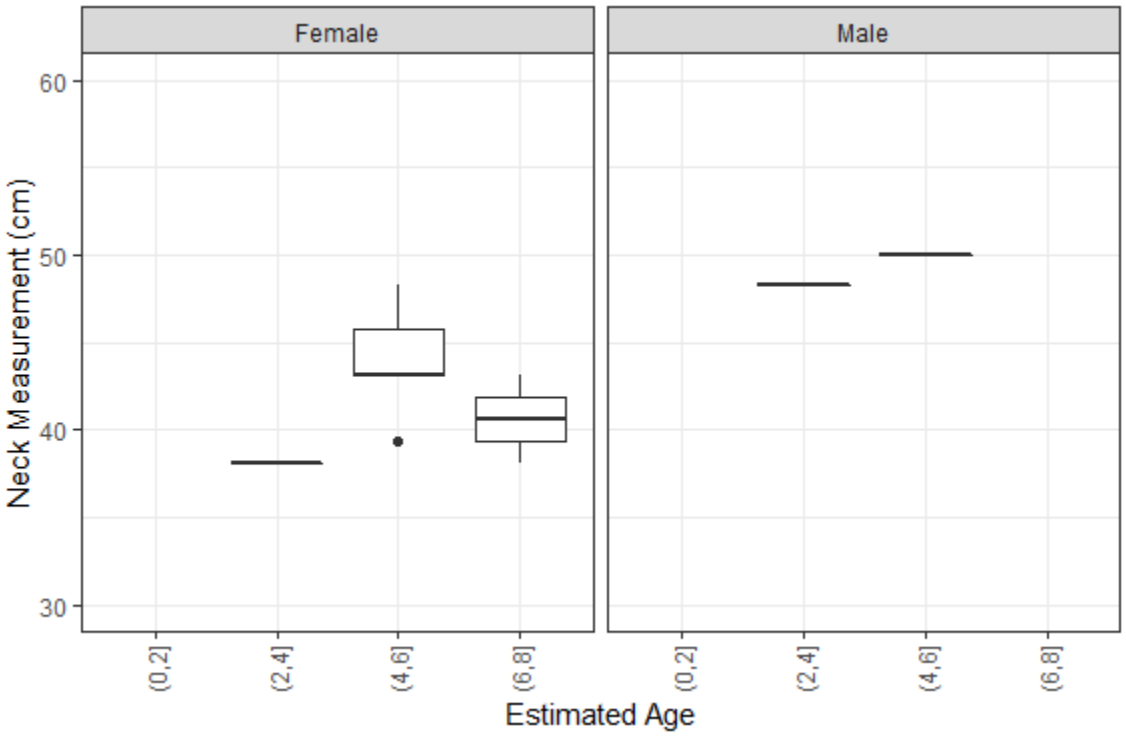

Figure A2.4. Boxplot of mountain goat neck measurements by estimated age and stratified by sex. Data are from HD 393.

Table A2.1. Summary of neck measurements from bighorn sheep and mountain goats, by sex and age class (lambs are <1 year old; yearlings are between 1 and 2 years old; adults are >2 years old), with sample sizes (N), medians, means, lower and upper 95% confidence intervals, and the minimum and maximum neck sizes in centimeters.

Species	Sex	Age Class	N	Median Neck Size (cm)	Mean Neck Size (cm)	Lower 95% CI (cm)	Upper 95% CI (cm)	Minimum Neck Size (cm)	Maximum Neck Size (cm)
Bighorn Sheep	Female	Lamb	1	36.0	36.0	NA	NA	36.0	36.0
Bighorn Sheep	Female	Yearling	8	35.9	37.1	32.8	41.3	35.0	40.6
Bighorn Sheep	Female	Adult	79	40.6	40.9	31.7	50.2	33.9	73.2
Bighorn Sheep	Male	Lamb	1	42.0	42.0	NA	NA	42.0	42.0
Bighorn Sheep	Male	Yearling	8	45.1	43.8	32.8	54.8	33.9	51.0
Bighorn Sheep	Male	Adult	23	48.3	48.6	38.2	58.9	38.1	58.4
Mountain Goat	Female	Adult	8	43.2	42.4	35.2	49.5	38.1	48.3
Mountain Goat	Male	Adult	2	49.1	49.1	46.7	51.5	48.3	50.0