



**Wyoming Game and Fish Department
2016-18 Respiratory Disease Surveillance in Bighorn Sheep
and Mountain Goats
October 2018**



Wyoming is home to over 6,500 bighorn sheep; over 80% of which comprise the largest population of native, migratory bighorn sheep in the lower 48 states. While the majority of populations occur in the northwestern corner of the state, other reintroduced herds are scattered in multiple locations across the state. In general, the health of Wyoming sheep herds is stable or increasing, and although periodic die-offs may occur, herds are resilient and rebound to previous population levels in a few years. One exception is the Whiskey Mountain herd which suffered an outbreak of respiratory disease in the early 1990's; causing a significant all age die-off in the herd that it has never recovered from.

The true cause of the Whiskey Mountain outbreak remains a mystery. Diagnostic techniques available at the time were limited and *Mycoplasma ovipneumoniae* hadn't yet been identified as a respiratory pathogen. As diagnostics improved over the years, the debate over which bacterial pathogen is the primary cause of respiratory disease has raged on. Although researchers have been unable to agree on which pathogens are responsible, most agree that *Mannheimia haemolytica*, *Mycoplasma ovipneumoniae*, *Bibersteinia trehalosi* and *Pasteurella multocida* are all pathogens of concern. In the past six years, new culture and diagnostic techniques have been developed to accurately identify bacterial pathogens; allowing us to document their presence in each population. Knowing the pathogen communities for each population is not only necessary when considering source and recipient herds for transplants, but may also allow us to determine if their presence can be linked to overall herd health. In addition to bacterial pathogens, sinus tumors have recently been identified as another concern associated with respiratory disease in bighorn sheep (Fox et al. 2010, 2015). These tumors have been documented in several of the State's bighorn populations.

Methods:

Between 2011 and 2018, the Wyoming Game and Fish Department (WGFD) Wildlife Health Laboratory sampled 848 bighorn sheep and 64 mountain goats. During the winters of 2016-18, nine bighorn sheep herd units and 19 sub-herds were monitored for respiratory pathogens (see figure 1). Two mountain goat herds were also monitored. Target herds were selected for surveillance based on sampling history, accessibility, health status (e.g. significant changes in lamb recruitment, high death loss, etc...), or the likelihood of serving as a potential source herd for future reintroductions/augmentations. Animals were captured by helicopter net-gunning, or darting with a CO₂ projector. Opportunistic sampling of animals submitted for necropsy (euthanized due to disease or found dead) and road-killed animals were also utilized. In addition, samples were collected from bighorn sheep that were lethally removed due to their

location outside of established bighorn sheep herd unit boundaries and near domestic sheep and goat operations. Numerous samples were collected from all animals including nasal, tonsil, and ear swabs, feces, and blood.

To ensure detection of bacterial pathogens associated with respiratory disease, several measures were adopted to optimize sample collection and preservation in the field. One of the primary steps was inoculation of bacterial culture media immediately after swabbing the tonsillar crypts. Culture plates were placed into a 37°C mobile incubator as soon as possible to ensure bacterial survival. To enhance detection, an additional tonsil swab was collected and placed into preservation media for inoculation of an additional culture plate within 8 hours of collection. Culture plates were examined every 24 hours while in the field, where suspect isolates were subcultured and purified for further identification. Laboratory analysis of field samples included classical bacterial culture and polymerase chain reaction (PCR) techniques. Bacterial cultures were analyzed with PCR for undetected isolates as well as for the presence of leukotoxin genes. Mycoplasma cultures from nasal swabs were enriched in Modified Tryptone Soya Broth, plated on growth media and analyzed with PCR. Fecal samples were submitted to the Wyoming State Veterinary Laboratory (WSVL) for parasitological analysis. Whole blood and serum samples were submitted to the WSVL for trace mineral analysis, as well as to Dr. Holly Ernest for genetic analysis. Remaining serum was banked for future serological testing as needed.

Bighorn Sheep (BHS) Pathogen Surveillance in Wyoming 2016 - 2018

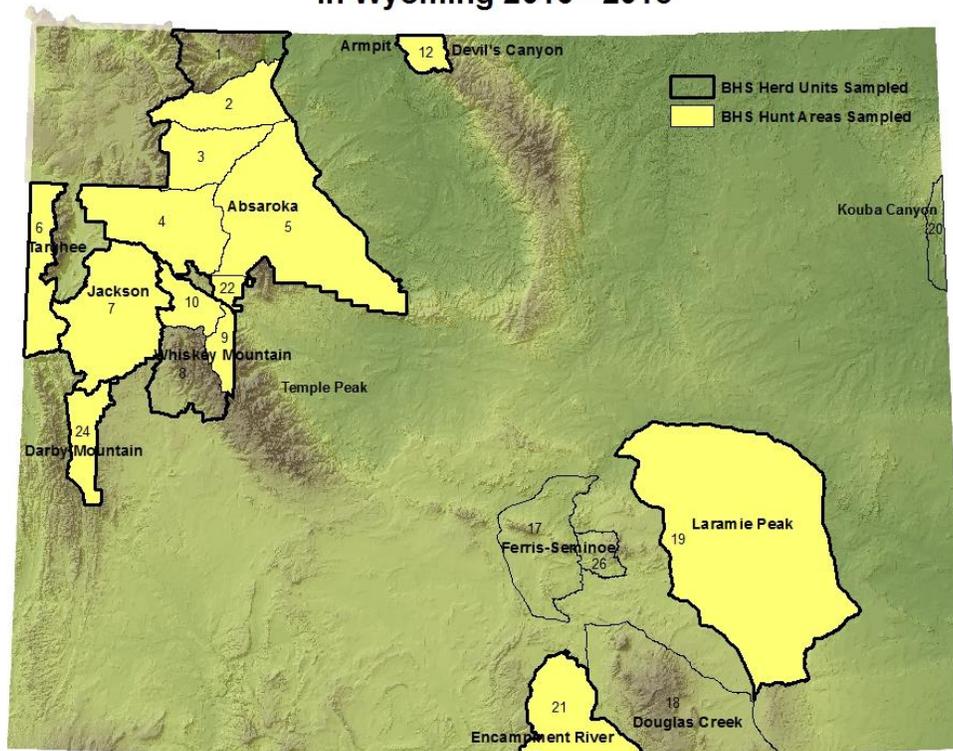


Figure 1. Location of bighorn sheep herds sampled for respiratory pathogens in 2016-18

Health surveillance activities also included examining hunter-harvested rams for sinus tumors, where taxidermists were asked to retain skulls once the horns were removed and submit to the WGFD Wildlife Health Laboratory for dissection. In addition, field personnel collected heads from targeted sheep (e.g. found dead or showing signs of severe rhinitis), and all animals that were lethally removed outside established bighorn sheep herd unit boundaries or submitted to the laboratory for disease testing were also examined.

In addition to disease surveillance, research into body condition of the Whiskey, Jackson and Absaroka herds was conducted through a cooperative study with Dr. Kevin Monteith of the University of Wyoming. The overall goal of this three-year project is to link body condition to the presence of respiratory pathogens and the overall health of the herd. Animals were captured in the late fall and again in the early spring to measure body fat and collect routine samples for respiratory pathogens and overall health. The initial phase of this project was completed in January of 2018, but based on preliminary findings, the study has expanded to forage evaluation and cause specific mortality of collared animals.

Another cooperative study with the University of Wyoming seeks to examine the DNA profiles of all state bighorn sheep herds. The objectives of this long-term study are to collect and analyze sufficient DNA profiles over time to ascertain a herd’s genetic diversity, as well as to identify if specific genetic markers exist that may influence tolerance of some respiratory pathogens. Mapping the genetic profiles of each herd would also allow managers to determine the source of “wondering” ewes and rams outside established bighorn sheep herd unit boundaries. This project is still progressing, and a publication has been submitted for publication to the Journal of Wildlife Management in the summer of 2018 (Love Stowell et al, in review)

In early 2015, complete blood counts were added to the diagnostic array of our bighorn sheep disease surveillance program. The goal was to determine if white blood cell counts (WBC) could be used as an indicator of active respiratory disease in a particular herd, and does a correlation exist between elevated WBC counts and low/ewe ratio in an infected herd? The final aspect was to assess if the presence of a particular respiratory pathogen could be linked to elevated WBC counts. This data was analyzed in part through the Rocky Mountain Veterinary Externship program as a wildlife disease project in 2018.

Results:

A total of 279 bighorn sheep were sampled from nine herd units and nine mountain goats from two herds in 2016-18 (see table 1 below).

Herd	Hunt Area	Number of Animals Sampled
Bighorn Sheep		
Absaroka	2-5, 22	53
Darby Mountain	24	8
Devil’s Canyon	12	67
Encampment River	21	5

Jackson	7	51
Laramie Peak	19	6
Targhee	6	18
Temple Peak	NA	12
Whiskey Mountain	8, 9, 10, 23	55
“Armpit”	NA	4
	Mountain Goat	
GTNP	NA	5
Palisades	2	4

Table 1: Total bighorn sheep and mountain goats sampled in 2016-18 by herd unit and hunt area

Bacterial respiratory pathogens were recovered from each of the herd units in both bighorn sheep and mountain goats. Sampling in the Absaroka, Jackson, and Whiskey Mountain herd units detected: *Mannheimia haemolytica* /*M. glucosida*, *Mannheimia spp* (*M. granulomatis*, *M. rumenalis*, or *M. varigena*), *B. trehalosi* with leukotoxin, *P. multocida*, and *M. ovipneumoniae*. Sixty-seven animals were captured in Devil’s Canyon for translocation to the Ferris and Seminoe Mountains. As with previous sampling of this herd, most pathogens, except *M. ovipneumoniae* and *B. trehalosi* with leukotoxin were detected. In addition, four rams were sampled in the Armpit area just west of Devil’s Canyon herd unit, with only *Mannheimia spp* identified. The Darby and the Targhee herds were tested for the first time in many years. *P. multocida* and *Mannheimia spp* were the only respiratory pathogens detected. Sample sizes for the Armpit and Darby herds were small and likely don’t represent the entire spectrum of pathogens in these populations.

Sixteen rams and three ewes were lethally removed due to their location outside established bighorn sheep herd unit boundaries (as per the Wyoming Bighorn/Domestic Sheep Plan) from the Baggs area (1), Chugwater (1), Buffalo (2), Lusk (3), Midwest (1), Newcastle (7), Thermopolis (1) and Rawlins (2-ewes) and Laramie (1 ewe). Culture results are not assigned to a specific herd due to the inability to link these “wandering” sheep to a specific population.

Mountain goats hosted the same pathogens as many of the bighorn sheep herds. The Palisades herd was infected with the full range of respiratory pathogens, whereas the fourteen goats sampled in Grand Teton National Park were relatively clean, carrying only leukotoxin positive *B. trehalosi* (see Table 2) and *Mannheimia spp*.

2011 - 2018 Wyoming Bighorn Sheep Pathogens by Herd Unit

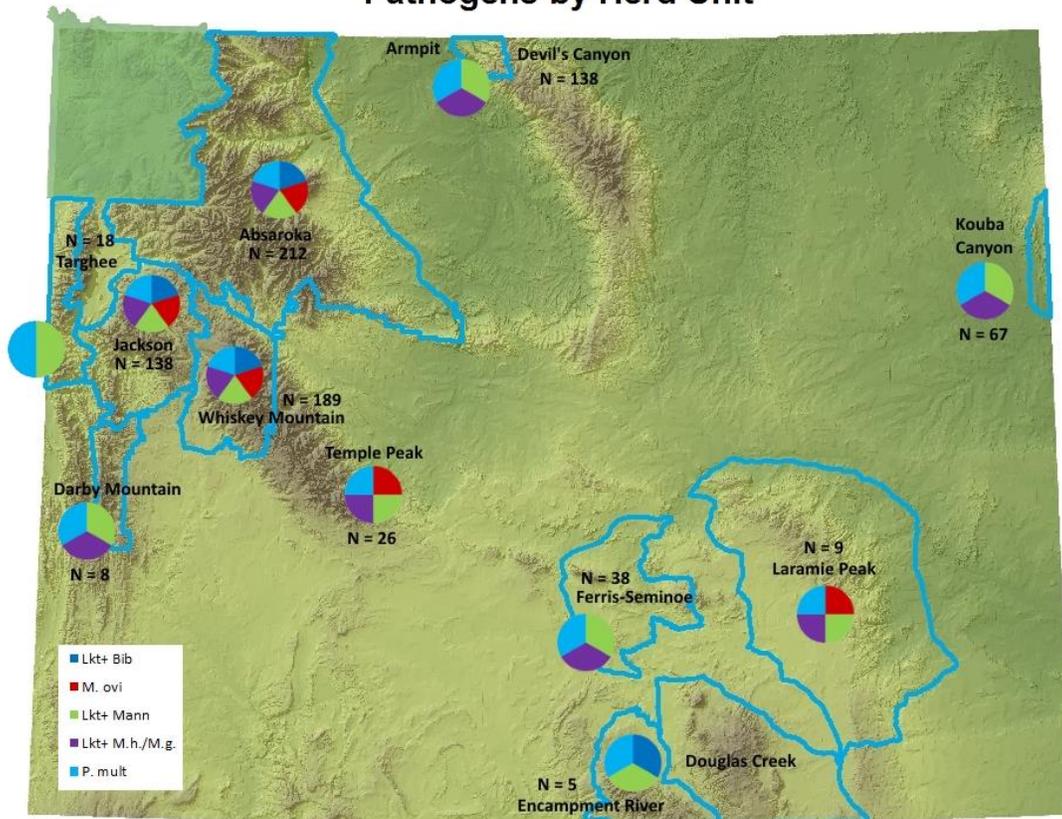


Figure 2. Graphic depiction of the distribution of respiratory pathogens in Wyoming's bighorn sheep herds 2011-2018

Bighorn Sheep

Herd Unit	HA	Sub Herd/Location	Total	Lkt+ <i>B. trehalosi</i>	<i>M. haemolytica</i>	<i>M. ovipneumoniae</i>	<i>Mannheimia spp</i>	<i>P. multocida</i>
Absaroka	1	Clarks Fork	19	X		X	X	X
	2	North Fork	78	X	X	X	X	X
	3	South Fork	63	X	X	X	X	X
	4	Younts Peak	8	X		X	X	X
	5	Meeteetse/Owl Crk	31	X	X	X	X	X
	22	Badlands	8	X		X		X
	22	Dennison	5	X		X	X	
Total Absaroka			212	X	X	X	X	X
Darby Mountain	24	Fish Creek Mtn	8		X		X	X
Devil's Canyon	12	Devil's Canyon	129		X		X	X
	12	Shell Canyon	5		X			
	12	Arm Pit	4				X	
Total Devil's Canyon			138		X		X	X
Encampment River	21	Encampment	5	X			X	X
Jackson	7	Gros Ventre	62	X	X	X	X	X
	7	NER	63	X		X	X	X
	7	Camp Creek	10	X		X	X	X
	7	Ramshorn	3			X	X	X
Total Jackson			138	X	X	X	X	X
Kouba Canyon	20	Kouba Canyon	67		X		X	X
Laramie Peak	19	Sybill Canyon	3			X		
	19	Iron Mountain	6		X		X	X
Total Laramie Peak			9		X	X	X	X
Seminole-Ferris	17	Seminole	36	X	X			

	17	Bennetts	2		X			
Total Seminoe-			38	X	X			
Targhee	6	Grand Teton	18			X	X	
Temple Peak	NA	Pine Bar	2		X		X	
	NA	Washakie Resivor	24			X	X	X
Total Temple Peak			26	X	X	X	X	X
Whiskey Mountain	10	Sheep Ridge	52	X	X	X	X	X
	10	Torrey Rim	98	X	X	X	X	X
	WRIR (9)	Dinwoody	39	X	X	X	X	X
Total Whiskey			189	X	X	X	X	X
Total			848					

Mountain Goats

Herd Unit	Hunt Area	Sub Herd/Location	Total	Lkt+ <i>B. trehalosi</i>	<i>M. haemolytica</i>	<i>M. ovipneumoniae</i>	<i>Mannheimia spp</i>	<i>P. multocida</i>
Beartooth	1		20	X	X	X		X
	2		0					
Total Beartooth			20					
Palisades	3	Alpine Canyon	30	X	X	X	X	X
GTNP	NA	Tetons	14	X			X	
Total			59					

Table 2. 2011-2018 Distribution of respiratory pathogens in Wyoming's bighorn sheep and mountain goat herds

Lungworm larvae (*Protostrongylus sp*) were detected in numerous fecal samples from all herd units, ranging from 0 to nearly 5,000 larvae per gram of feces (lpg), but the majority of lungworm burdens were considered low to moderate (<200 lpg). Trace mineral analysis was completed on blood samples collected from each herd unit. In comparison to domestic sheep, most herds were slightly low on serum concentrations of iron, zinc and molybdenum, but normal levels (or very close to) of manganese, copper and selenium (whole blood used for Se levels). The Kouba Canyon herd was the notable exception, with high levels of iron and selenium; populations in the Absaroka herd unit area 5 also had high levels of iron (see table 3). Unfortunately, trace mineral analysis on liver is rare and therefore sample sizes are generally too small to accurately compare levels of trace minerals in blood levels to levels in liver for most populations. Eleven liver samples were analyzed from the Kouba Canyon herd and were comparable in the elevated levels of iron and selenium.

Herd	HA	Average Herd Values – Serum or whole blood (Se)						Number Sampled	Average Herd Values – Liver						Number Sampled	
		Mn	Fe	Cu	Zn	Mo	Se		Mn	Fe	Cu	Zn	Mo	Se		
Absaroka	1	0.013	1.480	0.661	0.663	0.061	0.136	8								
Absaroka	2	0.009	1.036	0.701	0.509	0.053	0.121	41	3.6	299	84.9	154.0	0.960	0.13	1	
Absaroka	3	0.009	1.214	0.667	0.586	0.053	0.117	47	1.53	164.5	42.2	121	1.060	230	2	
Absaroka	5	0.007	2.335	0.604	0.793	0.050	0.277	10								
Absaroka	22	0.006	1.238	0.570	0.588	0.050	0.407	7	2.0	93.1	28.3	44.5	1.2	0.41	1	
"Armpit"	NA	<0.006	1.61	0.56	0.73	<0.05	0.50	4								
Darby Mountain	24	<0.006	1.14	0.59	0.64	<0.05	0.42	8								
Devil's Canyon	12	0.007	1.389	0.681	0.557	0.055	0.332	45								
Kouba Canyon	20						0.831	24	4.1	484.5	64.1	113.5	0.7	1.88	11	
Encampment River	21	0.006	1.206	0.813	0.720	0.050	0.216	5								
Jackson GV	7	0.011	1.311	0.665	0.583	0.06	0.340	46	3.1	296.0	65.5	96.0	1.2	0.62	3	
Jackson NER	7	0.01	1.393	0.652	0.578	<0.06	0.173	35	2.7	160.0	30.7	79.0	0.8	0.09	1	
Jackson – Ramshorn	7	<0.006	1.500	0.619	0.740	<0.05	0.275	3								
Laramie Peak	19	<0.006	1.299	0.695	0.608	<0.05	0.332	6								
Targhee	6	<0.006	1.338	0.641	0.721	<0.05	0.257	18								
Temple Peak	NA	0.009	1.352	0.831	0.573	0.053	0.266 (13)	23								
TWRC – (Absaroka)	NA	0.006	1.268	0.758	0.674	0.050	0.455	37	1.5	111.6	26.3	28.6	1.1	0.17	2	
Whiskey – Dinwd	9	0.011	1.347	0.585	0.621	0.050	0.182 (13)	19								
Whiskey – Sacaga	9	0.007	1.357	0.563	0.571	0.056	0.182 (7)	12								
Whiskey Sheep Rdg	10	0.012	1.386	0.792	0.606	0.068	0.186 (22)	33								
Whiskey Torrey Rm	10	0.011	1.429	0.722	0.591	0.087	0.162	32	2.2	63.4	20.3	40.3	1.1	0.26	6	
Normal Values		0.008-0.05	1.6-2.2	0.6-1.2	0.8-2	0.7	0.12-0.5		2-5	40-100	30-60	50-100	<2.0	0.25-1.0		

Table 3. Average blood and liver values for Wyoming’s bighorn sheep sub-herds

During the past five years of sinus tumor surveillance, 106 skulls have been examined (see table 4), with 24 of those showing gross signs of sinus tumors and three skulls that lesions suggestive of sinus tumors, but could not be confirmed. Herd units where tumors have been documented include Absaroka, Jackson, Laramie Peak, and Whiskey Mountain.

Herd	HA	Total Sampled	Suspect	Positive
Absaroka	1	9	0	4
Absaroka	2	14	0	6
Absaroka	3	16	0	6
Absaroka	4	12	0	1
Absaroka	5	11	0	3
Absaroka	22	5	0	1
Darby Mountain	24	1	0	0
Devil’s Canyon	12	7	0	0
Ferris/Seminole	26	1	0	0
Ferris/Seminole	17	1	0	0
Kouba Canyon	20	1	0	0
Encampment River	21	1	1	0
Jackson	7	3	1	0
Laramie Peak	19	7	0	1
Targhee	6	1	0	0
Temple Peak (Wind River Indian)	NA	4	0	0
Whiskey Mountain	8	2	1	0
Whiskey Mountain	9	3	0	1
Whiskey Mountain	10	7	0	1

Table 4. 2015-2018 Statewide sinus tumor surveillance in bighorn sheep

Pregnancy rates were determined for ewes captured as part of our surveillance efforts over the past five years (see table 5 and 6). The vast majority of females sampled were pregnant, with an overall pregnancy rate of 92.1%. A few subherds demonstrated very high pregnancy rates (e.g. Dinwoody, Devil’s Canyon, and Kouba Canyon), but some average below 90% (e.g. South Fork, Gros Ventre, NER, Sheep Ridge, and Torrey Rim subherds). In 2016/17, pregnancy rates in the Jackson unit were 68.8% (n=16) compared to 100% in previous years (2013/14 (n=9), 2015/16 (n=18)) and 91.7 in 2014/15 (n=12). Pregnancy rates in the Absaroka herd had been steadily declining from 2014 to 2017, but, like many of the other herds in the State, appeared to recover in 2018. Unfortunately, yearly sample sizes for many of the herds are insufficient to draw meaningful conclusions, but these warrant further monitoring.

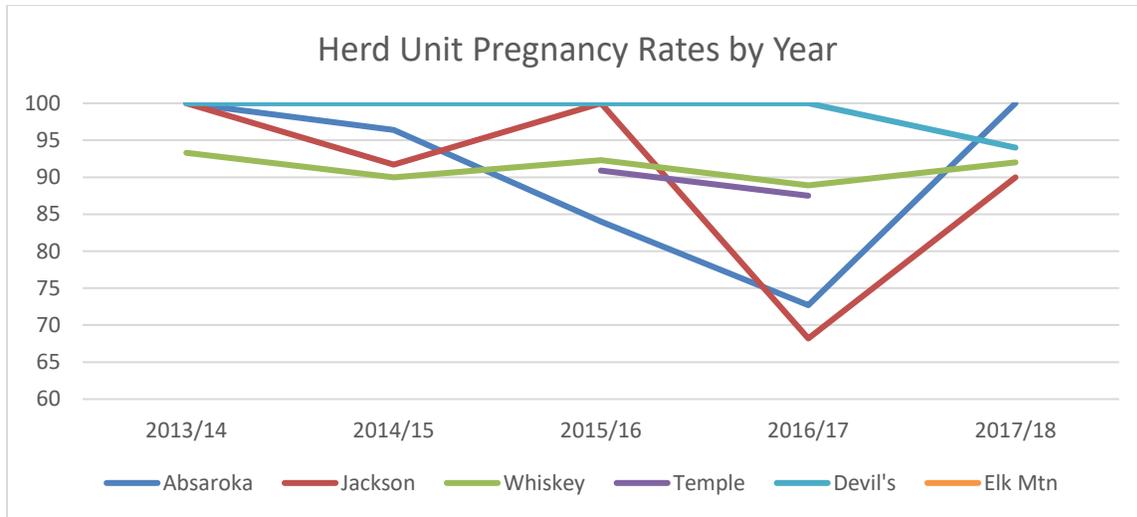


Table 5: Herd unit pregnancy rates from 2013 through 2018

Herd Unit	HA	Sub Herd/Location	Total Sampled	Total Pregnant	Percent Pregnant
Absaroka	1	Clarks Fork	10	9	90%
	2	North Fork	35	32	91.4%
	3	South Fork	45	39	86.6%
	4	Younts Peak	0	0	N/A
	5	Meeteetse/Owl Crk	20	19	95%
	22	Dennison/Badlands	8	8	100%
Total Absaroka			118	107	90.7%
Darby Mountain	24	Fish Creek	6	6	100%
Devil's Canyon	12	Devil's Canyon	82	81	98.8%
	12	Shell Canyon	4	4	100%
	12	Arm Pit	0	0	N/A
Total Devil's Canyon			86	85	98.8%
Elk Mountain	20	Elk Mountain	20	20	100%
Encampment	21	Encampment	5	5	100%
Jackson	7	Gros Ventre	27	24	88.9%
	7	NER	33	29	87.9%
	7	Camp Creek	3	3	100%
	7	Ramshorn	2	2	100%
Total Jackson			65	58	89.2%
Laramie Peak	19	Sybille Canyon	2	2	100%
	19	Iron Mountain	5	5	100%
Total Laramie Peak			7	7	100%
Seminole-Ferris	17	Seminole	6	3	50%
	17	Bennetts	2	2	100%
Total Seminole-Ferris			8	5	62.5%
Targhee	6	Grand Teton	6	4	67%
Temple Peak	NA	Washakie Reservoir	19	17	89.5%
Whiskey Mountain	10	Sheep Ridge	20	18	90.0%
	10	Torrey Rim	37	32	86.4%
	WRIR (9)	Dinwoody	22	22	100%
Total Whiskey Mountain			79	72	91.1%
Total			419	386	92.1%

Table 6: 2014-17 Average bighorn sheep pregnancy rates by subherd

Over the course of three years, a total of 361 whole blood samples were collected from multiple herds across the state and analyzed for complete white blood cell counts.

Sheep from the Absaroka, Devils Canyon, Jackson, Temple Peak, and Whiskey Mountain herds had elevated WBC counts in comparison to sheep housed at the CPW research facility which are respiratory pathogen free (see figure 3). Most of these herds with elevated WBC are also known to be affected by respiratory disease. The Absaroka herd had 19% of the animals with elevated WBC, 16% were documented in the Jackson herd, and 35% of the Whiskey Mountain herd had WBC counts above 7,000/*ul* (see figure 4).

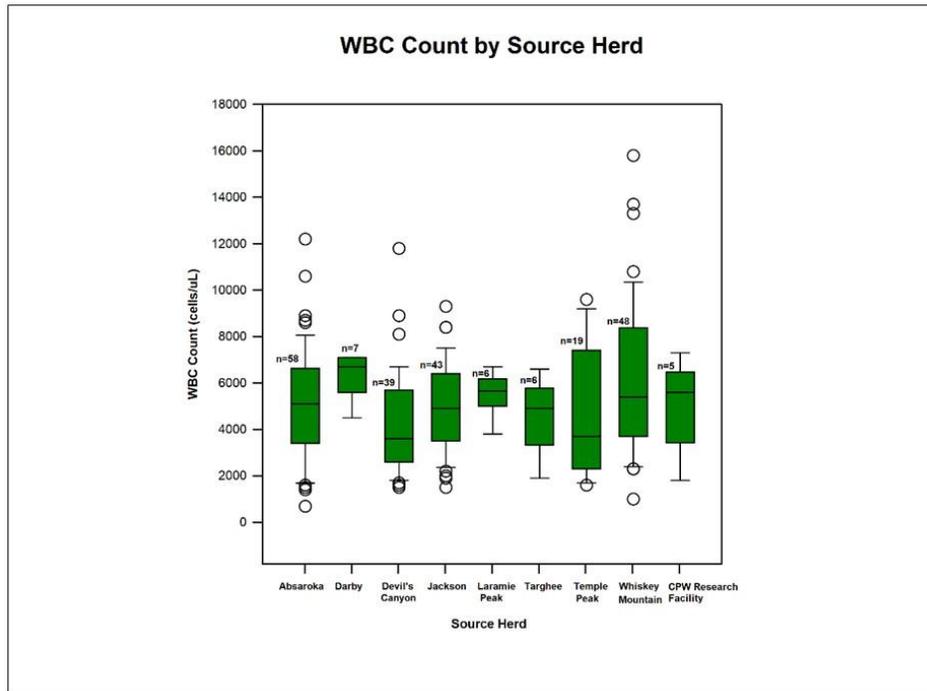


Figure 3. White blood cell (WBC) count for several Wyoming BHS herds. Colorado Parks and Wildlife (CPW) captive sheep are shown as a reference for animals not infected with respiratory disease pathogens.

When comparing WBC counts between years, the Temple Peak and Devil's Canyon herds demonstrated a marked increase in 2017 from the 2016 levels (see figure 4). A respiratory disease outbreak was documented in the Washakie Rim population of the Temple Peak herd during the spring 2017 capture. White blood cell counts increased from an average of 2,700 in 2016 to 7,550 in 2017. *Mannheimia haemolytica/glucoisida*, *P. multocida*, and *M. ovipneumoniae* were all detected in 2017, but absent in 2016, suggesting a recent exposure event for this herd. Unfortunately, the 2016 sample size was limited to 12 animals, making pathogen detection probability less than certain. The Devils Canyon herd also experienced an increase in WBC counts in 2017; but no new pathogens were detected during the subsequent 2017 or 2018 surveillance efforts.

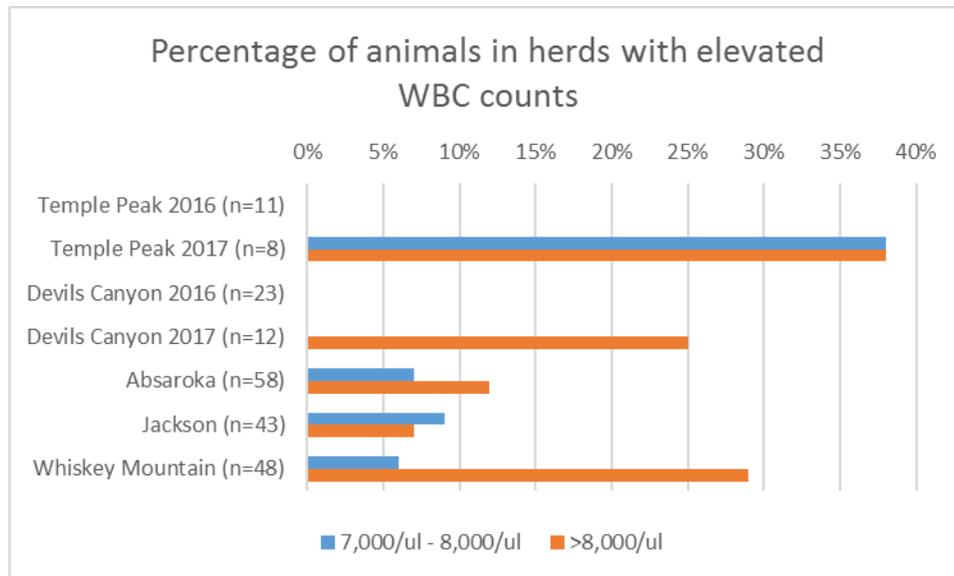


Figure 4. Percentage of animals within herds that have elevated WBC counts between 7,000/*ul* and 8,000/*ul* (blue) and above 8,000/*ul* (orange).

Discussion:

Advances in diagnostic techniques for respiratory pathogens have resulted in significant improvement in both the isolation and identification of bacterial respiratory pathogens by the WGFD Wildlife Health Laboratory. The Absaroka and Whiskey Mountain herds host a full suite of known bacterial respiratory pathogens. The Jackson herd also hosts a full suite of respiratory pathogens, and unfortunately, *M. haemolytica* was identified for the first time in this herd in 2016, suggesting that either this pathogen is present in very low numbers that have been difficult to detect during previous surveillance efforts, or this pathogen was introduced either through natural sheep or anthropogenic movements.

When examining the distribution of respiratory pathogens statewide, the Darby Mountain herd, the Shell Canyon sub herd of the Devil’s Canyon unit, and the Targhee unit stand out as having relatively few pathogens. Unfortunately, samples sizes are too small in the Targhee and Shell Canyon herds to consider these herds clean and further surveillance is required to accurately determine pathogen populations and how they might influence herd health.

The Devil’s Canyon herd has been a source herd for the Seminoe/Ferris herd for the past three years. The Seminoe herd was sampled (n=36) prior to the supplementation, and found to only carry *M. haemolytica*. Pathogen communities in the Seminoe/Ferris are expected to reflect the Devil’s Canyon herd; containing most respiratory pathogens except *M. ovipneumoniae*. The Kouba Canyon herd has not been sampled since 2013/14, but also had most pathogens but *M. ovipneumoniae* and Lkt+ *B. trehalosi*. Initially, *M. haemolytica* was identified in this population, but further testing using 16S genetic sequencing, more accurately identified this as *M. glucosida*.

Trace minerals are elements that are required in very small dietary amounts that are required for normal health, growth, reproduction, and immune function. The trace mineral values in the liver are generally thought to most accurately reflect the nutritional status of an

animal; however, when sampling live animals, whole blood and serum are often used instead. Correlating trace mineral levels in the blood to true nutritional status in the animal can be challenging. In general, both blood and liver trace mineral levels in our bighorn sheep herds are very close to, or within published ranges for domestic sheep (Puls, 1994) as well as bighorn sheep in California (Poppenga et al., 2012). Notable exceptions are high liver iron, zinc and selenium levels in several sheep from Jackson and Kouba Canyon herd units. Unfortunately, samples sizes where both blood and liver levels of trace minerals are available for an individual herd unit are small, with most values being derived from blood. Blood and liver mineral levels in captive bighorn sheep at the Thorne Williams Wildlife Research Center (TWRC) are very similar to our free-ranging populations. While these values are similar to those recorded for domestic sheep, they don't align exactly (TWRC captive, and free-ranging sheep tend to have lower Fe, Zn and Mo levels – see table 3). The TWRC herd is fed high quality diet of hay and pellets with a mineral supplement included, as well as having free access to both loose and block mineral supplements. We suspect that trace minerals are not limited in these animals and they may better reflect optimal levels of these elements.

Sinus tumors were initially discovered in Colorado bighorn sheep herds (Fox et al., 2010), and subsequently identified in Wyoming's Clark's Fork sub-herd of the Absaroka unit in 2015. Sinus tumors are known to harbor respiratory disease pathogens (Fox et al., 2015), and are also likely responsible for impaired respiratory function. The discovery of sinus tumors in the Absaroka, Jackson, Laramie Peak, and Whiskey Mountain herd units is alarming. Sinus tumors are likely an under-documented contributor to respiratory disease in bighorn sheep and additional surveillance and research is needed to fully understand the distribution and effect they may be having on populations.

While most pregnancy rates nearly returned to normal in 2017/18, the 2016/17 levels for the state's bighorn sheep populations were the lowest seen in the past four seasons. Unfortunately, samples sizes are small, but the Jackson herd unit had the lowest pregnancy rate in the state at 68.8%, with both the Gros Ventre and National Elk Refuge subherds having low rates of 71.4% and 57.1% respectively. The Sheep Ridge subherd of the Whiskey Mountain unit was also low at 66.7%, whereas the Torrey Rim and Dinwoody subherds were 100%. Reasons for low pregnancy rates in some subherds are unknown, but the severe winter of 2016/17 may have influenced some pregnancies. Pregnancy rates for the state's mountain goat herds are not listed in this report due to discrepancies between test results and field observations of kids and nannies.

Over the past seven years of surveillance of the state's bighorn sheep herds, pathogen communities have been well documented in most of our sheep populations. The majority of these pathogens were recovered from apparently healthy animals, which may indicate the biotypes are not highly pathogenic to adults; however, their relative impact on lamb mortality is unknown. While core native populations in the Absarokas and Jackson appear to be stable, periodic documentation of respiratory disease in adults does occur. This suggests that respiratory disease due to these pathogens does occur at some level within these populations and significant

mortality could occur given the right circumstances/conditions. Efforts are currently underway to broaden our understanding of biotypes and how they may be used to assess the risk or likelihood of respiratory disease in a particular herd. Biotypes of *M. ovipneumoniae* are currently being researched by Dr. Tom Besser of Washington State University, while the Wildlife Health Laboratory and the Dr. Kerry Sondgeroth of the University of Wyoming is exploring Pasteurellaceae biotyping using MALDI-TOF and whole genome sequencing.

One cooperative research project that assessed which sampling/testing protocols are best at recovering and identifying bacterial pathogens was completed in 2017. This cooperative study with Montana State University examined the minimum number of animals that must be sampled in a herd to detect pathogens that occur at low prevalence as well as determining the expected prevalence of a particular pathogen within a population. A manuscript detailing this two-year study was published in PlosOne in July of 2017 (Butler et al., 2017)

Utilizing white blood cell counts as an indicator of active respiratory disease in a herd is useful. Elevated WBC counts were documented in the Temple Peak outbreak where *M. ovipneumoniae* and *Pasteurella* were recently documented. In addition, there appears to be a correlation to elevated WBC counts in those herds that have a history of respiratory disease (i.e. Jackson, Absaroka, Whiskey Mountain). But, because WBC counts can increase for multiple reasons, including capture (Kock et al., 1987), an increase should be evaluated with caution. The Devil's Canyon herd is an example, where an increase in WBC counts was observed in four of the twelve animals sampled, but no new respiratory pathogens were recovered in the two subsequent samplings in 2017 and 2018.

It should be noted that WBC counts for healthy Wyoming BHS were far below published values for captive Rocky Mountain BHS (6,668 – Woolf and Kradel, 1969), Dall Sheep (7,600 – Foreyt et al., 1983), and Desert BHS (7,100 – Borjesson et al., 2000). The average WBC counts across all herds excluding Whiskey Mountain and Temple Peak was 4,791 *ul* from a total of 172 samples (add range). By individual herd unit, Jackson averaged 4,981, Devils Canyon 4,253, Absaroka 5,032, and Temple peak was 2,700 prior to the 2017 outbreak. Even when you examine the Whiskey Mountain BHS, the average WBC counts of all animals below 7,000 *ul*, was 4,135 (65% of the population)

As surveillance efforts continue, we continue to build on our knowledge and understanding of the influence these bacterial pathogens have on the overall health of our bighorn sheep herds. Future surveillance efforts in free ranging herds will continue in 2019 with the overall goal of thoroughly mapping respiratory pathogens across all state populations. In addition, we are collaborating with Dr. Kevin Monteith of the University of Wyoming to monitor the body condition of many of our herds to explore how nutritional condition relates to carrying capacity, lamb survival, and herd resilience. Preliminary findings suggest the decreased resilience of the Whiskey Mountain herd may be associated with their poor condition of summer range. Efforts are currently underway to further evaluate this herd and determine if management actions can be taken to increase overall herd health.

Acknowledgements

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