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A Survey of Bacterial Respiratory Pathogens in Native and Introduced Mountain Goats (*Oreamnos americanus*)

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ABSTRACT: In contrast to broad range expansion through translocations, many mountain goat (*Oreamnos americanus*) populations have shown signs of decline. Recent documentation of pneumonia in mountain goats highlights their susceptibility to bacterial pathogens typically associated with bighorn sheep (*Ovis canadensis*) epizootics. Respiratory pathogen communities of mountain goats are poorly characterized yet have important implications for management and conservation of both species. We characterized resident pathogen communities across a range of mountain goat populations as an initial step to inform management efforts. Between 2010 and 2017, we sampled 98 individuals within three regions of the Greater Yellowstone Area (GYA), with a smaller sampling effort in southeast Alaska, US. Within the GYA, we detected *Mycoplasma ovipneumoniae* in two regions and we found at least two *Pasteurellaceae* species in animals from all regions. *Mannheimia haemolytica* was the only pathogen that we detected in southeast Alaska. Given the difficult sampling conditions, limited sample size, and imperfect detection, our failure to detect specific pathogens should be interpreted with caution. Nonetheless, respiratory pathogens within the GYA may be an important, yet underappreciated, cause of mountain goat mortality. Moreover, because of the strong niche overlap of bighorn sheep and mountain goats, interspecific transmission is an important concern for managers restoring or introducing mountain ungulates within sympatric ranges.

Key words: Bighorn sheep, disease, mountain goat, *Mycoplasma ovipneumoniae*, *Oreamnos americanus*, *Pasteurellaceae*, pneumonia.

At the time of European settlement of North America, mountain goats (*Oreamnos americanus*) were distributed from the mainland mountain ranges of southern Alaska, throughout the western Canadian Provinces and Territories, and into the northwestern US including Washington, Oregon, and western Idaho and Montana (Côté and Festa-Bianchet 2003). While mountain goats did not experience the level of overexploitation and reduction typical of other North American ungulates, wildlife management agencies included mountain goats in translocation programs during the early- to mid-1900s and expanded their distribution beyond known historical ranges (Côté and Festa-Bianchet 2003). Translocation efforts are considered a success, with introduced populations now established throughout the western US and Canada (Flesch et al. 2016). Nonetheless, in contrast to general range expansion through translocation, many populations show signs of decline. For example, today native populations in Montana (outside of Glacier National Park) are a third to a quarter of their estimated abundances in the 1940s (Smith and DeCesare 2017). Moreover, mountain goat abundance in British Columbia, Canada, and Washington state declined by at least half from the 1950s and 60s to the early 2000s (Mountain Goat Management Team 2010; Rice and Gay 2010).

The difficulty in studying mountain goats presents a number of challenges in documenting cause-specific declines, which can include anthropogenic causes or predation (Côté and Festa-Bianchet 2003). While driv-

ing factors are regionally specific, recent documentation of pneumonia in adult and kid mountain goats in Nevada (Wolff et al. 2014; Anderson et al. 2016) highlights the susceptibility of mountain goats to pneumonia pathogens typically associated with bighorn sheep (*Ovis canadensis*) epizootics (Blanchong et al. 2018; Cassirer et al. 2018). Given the broad distribution of respiratory pathogens in bighorn sheep (Butler et al. 2017), susceptibility of mountain goats to epizootics may be a more-widespread cause for concern. Moreover, where mountain goats are sympatric with bighorn sheep there is strong niche overlap (Lowrey et al. 2018) and potential for interspecific disease transmission (Wolff et al. 2016; Blanchong et al. 2018). Resident pathogen communities of mountain goats are poorly characterized yet have important implications for management and conservation of both mountain ungulate species. We evaluated mountain goat respiratory samples collected through multiple monitoring efforts in Montana, Wyoming, Idaho, and Alaska to regionally characterize the resident pathogen community across a diverse range of mountain goat populations as an initial step to inform management efforts.

Sampling efforts were conducted within three regions of the Greater Yellowstone Area (GYA), with a smaller sampling effort in southeast Alaska (Fig. 1). Mountain goats are considered nonnative in the GYA and grew from 170 individuals introduced in the mid 1900s to roughly 1,650 individuals in 2016 (Flesch et al. 2016). Sampling efforts in the GYA targeted three regions: the northeast GYA, including portions of Yellowstone National Park, Grand Teton National Park (GTNP), and the southwest GYA, including the Snake River Range of Wyoming and Idaho (Fig. 1). Mountain goats are sympatric with bighorn sheep in the northern GYA and GTNP but are considered allopatric in the southwest GYA. Historically, all populations in the GYA were broadly sympatric with domestic livestock. We provided a comparison with native populations that have never shared ranges with domestic livestock by sampling four populations in southeast Alaska (Fig. 1). While the southwest GYA is the presumed source of mountain goats colonizing GTNP (Lowrey et al. 2017), there is no other suspected connectivity between the four regions.

We captured mountain goats via ground darting, helicopter net-gunning, or helicopter darting between 2010 and 2017. All captures were conducted in accordance with Montana State University Institutional Animal Care and Use Committee (2011-17, 2014-32) and agency permits. Following extensive studies in bighorn sheep (Besser et al. 2013; Butler et al. 2017), we focused on the presence of *Pasteurellaceae* organisms (specifically leukotoxigenic and beta-hemolytic *Bibersteinia trehalosi*, *Mannheimia haemolytica*, and *Mannheimia* spp. as well as *Pasteurella multocida*) from tonsil swabs and *Mycoplasma ovipneumoniae* from nasal swabs. Sampling protocols varied between regions, but generally adhered to Butler et al. (2017). The protocols varied with respect to the transport media for swabs, the type of diagnostic test to identify pathogens, and the diagnostic laboratory that conducted the analyses. All samples were collected using sterile, polyester-tipped applicators. Transport media included Port-A-Cul™ tubes (BD, Sparks, Maryland, USA), tryptic soy broth with 15% glycerol (TSB; Hardy Diagnostics, Santa Maria, California, USA) vials, and immediate inoculation of Columbia blood agar culture plates (Hardy Diagnostics). The inoculated TSB vials were frozen as soon as possible after each capture and later shipped overnight on dry ice to prevent freeze-thaw cycles. We assessed the presence of pathogens using a combination of PCR and culture techniques. We delivered samples to the Washington Animal Disease Diagnostic Laboratory or the Wyoming Game and Fish Department Wildlife Health Laboratory for detection and identification of respiratory pathogens. We did not account for detection probability (Butler et al. 2017) and present our results as a minimum resident pathogen community within each region.

We sampled a total of 98 individuals across the four study regions. Due to local logistics and funding availability, there was notable

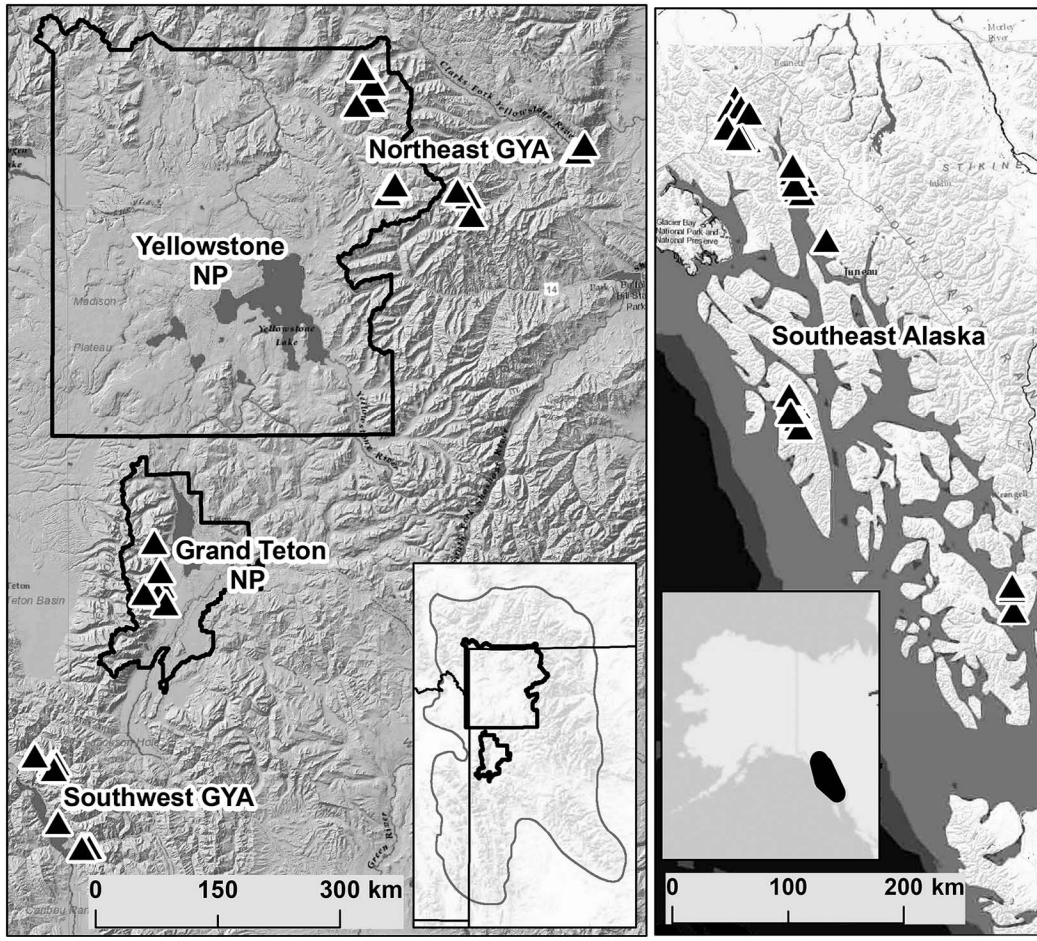

FIGURE 1. Greater Yellowstone Area (GYA; left) and southeast Alaska (right) study regions for a survey of bacterial respiratory pathogens in mountain goats (*Oreamnos americanus*). Triangles represent mountain goat capture locations 2010–17. With the exception of Grand Teton National Park (NP) and the southwest GYA, each study region was an isolated aggregate of individuals. While there were varying degrees of connectivity within each region, meaningful population-level inferences were not possible with the spatial and temporal resolution of our sampling efforts.

variation in the number of yearly samples collected (mean=9, SD=5.34, range=1–20). The PCR was the only diagnostic test used in all laboratory, year, and study area combinations for the detection of *M. ovipneumoniae* and had positive detections in the northeast and southwest GYA (Table 1). *Mycoplasma ovipneumoniae* was not detected in GTNP or southeast Alaska. With the exception of the southwest GYA, serology tests strongly agreed with the PCR results. The cause of discrepancy in the southwest GYA in 2013 was unknown, but could have been related to sample size, sample timing in relation to nasal shedding, or the PCR assay which had not been validated for mountain goats.

We detected *B. trehalosi* and *Mannheimia* spp. in all regions within the GYA. *Mycoplasma haemolytica* was detected in the northeast and southwest regions but not in GTNP. The southwest GYA was the only region where we detected *P. multocida* (Table 2). In contrast to the GYA, *M. haemolytica* was the only *Pasteurellaceae* species detected in southeast Alaska (Table 2). Because differentiating isolates or leukotoxins of *M. haemolytica* with

TABLE 1. Diagnostic summaries for *Mycoplasma ovipneumoniae* in samples from a survey of bacterial respiratory pathogens from mountain goat (*Oreamnos americanus*) populations in the Greater Yellowstone Area (GYA) and southeast Alaska. The sample size for each protocol (*n*), as well as detected (+) and not detected (–) results, are shown for PCR and serology diagnostic tests.

					Mycoplasma ovipneumoniae[d]					
					PCR			Serology		
Location[a]	Year	No. of individuals	Transport medium[b]	Laboratory[c]	*n*	+	–	*n*	+	–
NEGYA	2013	14	TSB	WADDL	14	3	10	—	—	—
			PC	WGF	13	1	12	—	—	—
	2014	7	TSB	WADDL	7	1	5	—	—	—
			Serum	WADDL	—	—	—	7	2	4
SWGYA	2013	13	TSB	WADDL	13	0	13	—	—	—
			Serum	WADDL	—	—	—	7	6	1
			PC	WGF	5	0	5	—	—	—
	2014	9	PC	WGF	9	9	0	—	—	—
	2015	4	PC	WGF	4	2	2	—	—	—
	2017	4	PC	WGF	4	2	1	—	—	—
GTNP	2014	5	PC	WGF	5	0	5	—	—	—
			Serum	WGF	—	—	—	5	0	5
	2015	4	PC	WGF	4	0	4	—	—	—
			Serum	WGF	—	—	—	4	0	4
	2017	5	PC	WGF	5	0	5	—	—	—
			Serum	WGF	—	—	—	4	0	4
SEAK	2010	19	PC	WADDL	19	0	19	—	—	—
	2014	14	TSB	WADDL	14	0	14	—	—	—
			Serum	WADDL	—	—	—	16	0	16

[a] NEGYA = northeast GYA; SWGYA = southwest GYA; GTNP = Grand Teton National Park; SEAK = southeast Alaska.

[b] TSB = tryptic soy broth with 15% glycerol; PC = Port-A-Cul.

[c] WADDL = Washington Animal Disease Diagnostic Laboratory; WGF = Wyoming Game and Fish Department Wildlife Health Laboratory.

[d] — = no test was performed.

Mannheimia glucosida is currently not possible, an unknown number of *M. glucosida* detections may have been misclassified as *M. haemolytica*. Lastly, there were no observed mountain goat die-offs in any region over the sampling period.

There was notable variation in pathogen detection within and among years (Tables 1, 2), which we attributed to low detection probability (Butler et al. 2017) and small annual sample sizes. Careful measures were taken to handle all samples according to protocols that optimized pathogen recovery and survival; however, mountain goats present challenging sampling conditions in rugged terrain at high elevations. Given the difficult sampling conditions, limited sample sizes, and imperfect detection, our failure to detect specific pathogens should be interpreted with caution. Moreover, recent sampling efforts suggest that nasal swabs are more effective than are swabs of tonsillar crypts for detecting *P. multocida*, an important bacterial respiratory pathogen (Weiser et al. 2003; Wood et al. 2017), but were not included in our sampling methods. Nonetheless, our results indicate a resident pathogen community containing both *M. ovipneumoniae* and *Pasteurellaceae* within the northeast and southwest GYA. Although multiple *Pasteurellaceae* species were detected in GTNP, we did not detect *M. ovipneumoniae* in the 14 animals sampled. Not surprisingly, southeast Alaska had the fewest

TABLE 2. Diagnostic summaries for *Pasteurellaceae* in samples from a survey of bacterial respiratory pathogens mountain goat (*Oreamnos americanus*) populations in the Greater Yellowstone Area (GYA) and southeast Alaska. The total number of individuals sampled within a year as well as the sample size for each protocol (*n*) is shown.

						Cultures				PCR[g]		
Location[a]	Year	No. of individuals[b]	Transport medium[c]	Laboratory[d]	*n*	*Bibersteinia trehalosi*[e]	*Mannheimia* spp.[e]	*Mannheimia haemolytica*[f]	*Pasteurella multocida*	LKt A *Bibersteinia*	LKt A *Mannheimia* spp.	LKt A *Mannheimia haemolytica*[f]
NEGYA	2013	14	TSB	WADDL	14	0	0	9	0	—	—	—
			PC	WGF	12	0	0	0	0	4	0	6
	2014	6	TSB	WADDL	6	0	1	2	0	—	—	—
SWGYA	2013	14	TSB	WADDL	14	0	0	3	1	—	—	—
			PC	WGF	5	0	1	0	2	—	—	—
	2014	9	PT/PC	WGF	9	0	0	2	0	4	2	3
	2015	1	PT/TSB	WGF	1	0	0	0	0	—	—	—
	2017	4	PT/PC	WGF	4	0	0	0	0	0	0	2
GTNP	2014	5	PT/PC	WGF	5	0	0	0	0	2	0	0
	2015	4	PT/PC	WGF	4	2	0	0	0	2	0	0
	2017	5	PT/PC/TSB	WGF	5	0	1	0	0	0	1	0
SEAK	2010	20	PC	WADDL	20	0	0	1	0	—	—	—
	2014	13	TSB	WADDL	13	0	0	0	0	—	—	—

[a] NEGYA = northeast GYA; SWGYA = southwest GYA; GTNP = Grand Teton National Park; SEAK = southeast Alaska.

[b] A total of 95 animals were tested for Pasteurellaceae species.

[c] TSB = tryptic soy broth with 15% glycerol; PC = Port-A-Cul; PT = plated.

[d] WADDL = Washington Animal Disease Diagnostic Laboratory; WGF = Wyoming Game and Fish Department Wildlife Health Laboratory.

[e] Only beta-hemolytic strains are summarized.

[f] Because differentiating isolates or leukotoxins (LKt) of *M. haemolytica* with *M. glucosida* is currently not possible, an unknown number of *M. glucosida* detections may have been misclassified as *M. haemolytica*.

[g] — = no test was performed.

detections of *Pasteurellaceae* and no detections of *M. ovipneumoniae*.

Little is known about diseases in mountain goats; however, recent findings in Nevada highlight their susceptibility to respiratory disease (Wolff et al. 2014; Blanchong et al. 2018). With a number of mountain goats populations in decline regionally, respiratory disease may serve as an important yet previously underappreciated cause of mortality. Moreover, because of the strong niche overlap of bighorn sheep and mountain goats (Lowrey et al. 2018), characterizing the respective pathogen communities should be an important prerequisite to establishing new sympatric populations or understanding the potential for interspecific transmission on existing sympatric ranges (Wolff et al. 2016). These dynamics highlight the challenges associated with managing sympatric mountain ungulates and the importance of characterizing local pathogen communities to inform the management and conservation of both species.

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