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MORTALITY DURING EPIZOOTICS IN BIGHORN SHEEP: EFFECTS OF INITIAL POPULATION SIZE AND CAUSE

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ABSTRACT: One of the most severe threats to bighorn sheep (*Ovis canadensis*) populations is disease. With the objective of projecting possible epizootic consequences to bighorn sheep population dynamics, we examined 23 epizootic mortality episodes from presumably known causes that occurred in the United States and Canada from 1942 to 2005. These outbreaks were correlated with population size using regression models. Epizootic origins were documented by considering contact with a "new" pathogen for the bighorn sheep population or pneumonic processes, presumably triggered by stress. We suggest mortality rates are negatively related to population size in a logarithmic function, and offer a model to estimate the percentage of disease-related mortalities for a given population size of bighorn sheep. From a disease dynamics perspective, we suggest a minimum population of 188 bighorn sheep would be required to insure long-term persistence in the presence of epizootic disease.

Key words: Diseases, epizootics, *Ovis canadensis*, population size.

INTRODUCTION

Bighorn sheep populations have decreased significantly in recent decades due mainly to habitat fragmentation and degradation, poaching, disease, urban development, and human recreational activities (Valdez and Krausman, 1999). The total population of bighorn sheep in Mexico (*Ovis canadnesis mexicana*, *Ovis canadnesis cremnobates*, and *Ovis canadnesis weemsi*) is estimated between 5,500 and 8,800 animals (Medellin et al., 2005) distributed in Sonora, Baja California, and Tiburon Island. Bighorn sheep were extirpated from Nuevo León in the 1930s and from Chihuahua (Heffelfinger and Marquez-Muñoz, 2005) and Coahuila around the 1970s (Espinosa et al. 2006). Although conservation efforts, including reintroduction programs, are occurring in Chihuahua (Cassaigne, pers. obs.) and Coahuila (McKinney and Delgadillo-Villalobos, 2005; Sandoval and Espinosa-Treviño, 2001), the vast majority of the Mexican populations comprise only a few dozen individuals (Dirección General de Vida Silvestre, unpubl. data).

Although there is a general understanding of the role diseases play in the survival of populations, in recent years this aspect has gained importance in the study, management, and conservation of wildlife. Disease has been considered the primary cause of many bighorn sheep population extinctions (Gross et al., 2000). Bighorn sheep are more susceptible than other sheep to a variety of pathogens that have been related to pneumonic epizootics with mortality rates of 25% to 100% (Onderka and Wishart, 1982; Jessup, 1985; Festa-Bianchet, 1988; Sandoval, 1988; Miller et al., 1991). The presence of domestic animals, especially domestic sheep (*Ovis aries*), adjacent to or in the same habitat as bighorn sheep increases the risk of transmission of pathogens that can be fatal for bighorn sheep (Ough and De Vos, 1986; Ramey et al., 2000). Additionally, animals that are restricted to small habitats or habitat fragments increase the possibility of retransmission of some diseases (Risenhoover et al., 1988) by remaining in contact with the sources of infection.

In addition to this increased susceptibility, several factors, including human activities, the presence of domestic and feral livestock, climate change, and population isolation that can lead to local overgrazing, can provoke chronic stress, which decreases immune response (Pruett, 2003; Kemenya and Schedlowskib, 2007). Stress is a key factor that can increase the risk of an epizootic outbreak. Finally, the forced isolation in which many bighorn sheep populations exist (Allen, 1980) promotes inbreeding depression. Many researchers have suggested that detrimental characteristics associated with this process, such as the loss of evolutionary adaptability and the increase of disease can substantially increase risk of local extinction (O'Brien and Everman, 1988; Mills and Smouse, 1994; Saccheri et al., 1998).

Considering these factors, the need to understand the possible impact of epizootics among bighorn sheep populations of differing sizes is apparent. Specifically, we should be asking whether smaller populations have greater mortality rates than larger populations, and whether this places them at greater risk of extinction. Smaller populations may experience more direct contact among individuals, resulting in faster transmission rates of pathogens. Also, being gregarious, bighorn sheep might also become more stressed when living in reduced numbers.

This study was designed to determine the existence, type, and level of association between population size and mortality rate during epizootics in bighorn sheep populations. In addition, we estimate and suggest a minimum viable population size that considers disease, and evaluate possible risks of extinction of bighorn sheep populations related to epizootic events.

MATERIALS AND METHODS

We compiled reports from the literature documenting disease outbreaks that lasted 1–15 yr in bighorn sheep populations of known size in North America. To define an epizootic event, we used 30% as the defining mortality level. Among documented epizootics of free-ranging bighorn sheep populations that occurred in the USA and Canada, we used only those in which the initial population size, mortality rate, and presumed cause were reported. Mortality rates reported did not identify specific age or gender segments of the population. The time line we considered for the epizootic mortalities was as reported by the authors from the time when mortalities were first observed until the population was presumably no longer decreasing. From this analysis we identified two different potential origins of epizootics. The first were epizootics that originated from a suspected contact with a new or unknown pathogen to which bighorn sheep had no natural defenses. These included some *Pasteurella* and *Mannheimia* serotypes from domestic sheep and were considered as introduction of a new pathogen. Secondly, we considered epizootics that originated from pathogens that were most likely present in the population but disease may have been triggered by external stress. These were considered as stress-induced.

Scabies has been related to several epizootics but has also been detected in populations with no attributed mortalities (Sandoval, 1980; Welsh and Bunch, 1982; Boyce and Weisenberger, 2005). Therefore, we classified these epizootics based exclusively on the associated factors reported by the authors. If stress factors were described, we considered the epizootic as stress-induced, but if no other factor besides scabies was reported, we categorized it to be of new-pathogen origin. Epizootics where the possible origin seems to be related to both of the cited factors along with the presence of livestock were considered to be of mixed origin, and were considered only for the general analysis. Mortality percentages were graphed by the initial population size and a logarithmic regression line was fitted. This model was used because it stabilizes when a population is projected to infinity.

To calculate an estimated mortality rate for a specific population size, we converted the logarithmic model to a linear model to develop a more accurate estimation. The formulas obtained were applied to different hypothetical population sizes. Although the minimum viable population size for bighorn sheep is controversial, most researchers recommend a founder population of 41 to 125 animals (Berger, 1990; Ehrenfeld, 1994; Gross et al., 2000; Singer et al., 2000a, b, 2001). Management of the founder population may assist populations below that range to persist for the long term. However, for this analysis we considered 50 animals as the minimum size for which a bighorn population would be able to recover after an epizootic event.

RESULTS

Since the 1880s, at least 36″ epizootic episodes have been documented in bighorn sheep populations from the USA and Canada. From these we analyzed 23 that had the information necessary for our analysis (Table 1). From the 23 episodes, 13 originated from a new pathogen. Of these, 84% were pneumonias derived from contact with domestic sheep, 8% were suspected to have resulted from contact with domestic sheep, and 8% were scabies where the population apparently had not been exposed previously. We found eight cases of epizootics triggered by stress. Of these, three (37%) were related to changes in weather (and two [25%] of these three were complicated with scabies), 3 (37%) were related to close human activities including capture events, and the remaining two (25%) were related to multiple factors such as the presence of cattle, human activities, population peaks, or extreme weather conditions (e.g., prolonged droughts, extreme low temperatures). Two cases were considered of mixed origin (Aravaipa Canyon [Mouton et al., 1991] 1989 and Hells Canyon ram 1995 [Cassirer et al., 1996]) and were counted only in the total epizootics analysis. In the case of the San Andres epizootic (Sandoval, 1980), we considered only the first years of the epizootic (1976–78), in which the most severe decline was observed. This event might be analyzed in the future as a case of continuing stress plus the presence of psoroptic scabies, which, after a period of more than 20 yr (1976–97) resulted in the decline of a population of more than 200 sheep to a single ewe (Boyce and Weisenberger, 2005). The remaining epizootics were considered in their total period of decline (≤15 yr). All but two of the studies examined reported the duration of mortalities at ≤5 yr.

In the total epizootics analysis a negative logarithmic relationship was found between population size before the epizootic (initial size) and the mortality in the epizootic (Fig. 1; r^2=0.4286, SE=16.03, P<0.01). When dividing epizootics by their origin, we found no relationship for the new-pathogen origin but a negative logarithmic relationship for the stress-induced origin (Fig. 2; r^2=0.8055, SE=14.9, P<0.01). In epizootics originated by stress, mortality rate was more predictable than when we considered total epizootics. For the estimated mortality rate related to a certain hypothetical population size, we used the equation obtained from the conversion of the logarithmic function to a linear model. Total epizootics estimations were based on the equation: $y=85.0890+(-0.06293x)$; r^2=0.4283; SE=4.84. Stress-induced epizootics estimations were based on the equation $y=83.6310+(-0.07055x)$; r^2=0.7839; SE=5.139.

To have a high probability of persisting, populations should consist of at least 173 animals to survive a stress-induced epizootic (Table 3) and 188 animals to survive a general epizootic (Table 2).

DISCUSSION

The relationship between percentage of mortality and population size suggests that future minimum viable population size (MVP) for bighorn sheep should be greater than conventionally reported to account for the high risk of disease. Usually MVP considers only genetic, demographic, and environmental factors (Primack, 2001), and disease is considered as natural and predictable. Bighorn sheep are more susceptible than other ovine species to certain pathogens. The population impact of an epizootic may be great enough to affect population persistence through reduced recruitment and continuing mortality that may occur for 3–5 yr (Jessup, 1985; Gross et al., 2000). Such impacts could result in the local extinction of a population. Gross et al. (2000) demonstrated that disease was the most

TABLE 1. Epizootics and mortalities reported in bighorn sheep (*Ovis canadensis*) in the USA and Canada.

Epizootic date, place	Initial population/ mortality (%)[b]	Associated disease/possible cause	Origin of epizootic	Reference
1881–85, Wyoming	U/U	Scabies	Unknown	Lange, 1980
1880–90, Montana	U/U	Scabies	Unknown	Lange, 1980
1870–80, Idaho	U/U	Scabies	Unknown	Goodson, 1982
1870–79, California	U/U	Scabies	Unknown	Lange, 1980
1900–20, Rock Creek, Montana	U/U	Not determined	Unknown	Goodson, 1982
1917–30, Rocky Mountain National Park, Colorado	U/U	Pneumonia	Unknown	Goodson, 1982
1916–22, Utah	U/U	Scabies	Unknown	Goodson, 1982
1925, Sun River, Montana	U/70	Not determined	Unknown	Goodson, 1982
1931, Colorado	U/U	Scabies	Unknown	Lange, 1980
1936, Oregon	U/U	Scabies	Unknown	Lange, 1980
1939, Kootenay National Park, British Columbia	U/U	Pneumonia	Unknown	Goodson, 1982
1942–50, Thompson Falls, Montana[a]	50/100	Contact with domestic sheep	New pathogen	Goodson, 1982
1950, Dinosaur National Monument, Colorado	U/100	Not determined	Unknown	Goodson, 1982
1965–70, Upper Rock Creek, Montana[a]	150/100	Pneumonia/contact with domestic sheep	New pathogen	Goodson, 1982
1965, Bull River, British Columbia[a]	250/97	Pneumonia/contact with domestic sheep	New pathogen	Goodson, 1982
1955–70, Big Hatchet, New Mexico[a]	125–150/84	Drought and other factors	Stress factors	Watts, 1979
1971, Black Gap Wildlife Management Area, Texas[a]	20/90	Pneumonia/stress when being released	Stress factors	Kilpatric, 1982
1976–78, San Andres National Wildlife Refuge, New Mexico[a]	200/67	Scabies/changes in weather	Stress factors	Sandoval, 1980
1980–81, Black Mountains, California and Nevada[a]	511/38	Scabies/drought, high population density	Stress factors	Welsh and Bunch, 1982
1980–81, Waterton Canyon, Colorado[a]	77/77	Pneumonia/human activities	Stress factors	Bailey, 1986
1981–82, Macquire Creek, British Columbia, Canada[a]	50/52	Pneumonia/contact with domestic sheep.	New pathogen	Goodson, 1982
1980, Lava Beds National Monument, California[a]	42/76	Pneumonia/capture stress	Stress factors	Blaisdell, 1982
1981, Mormon Mountains, Nevada[a]	600/50	Pneumonia/contact with domestic sheep	New pathogen	Jessup, 1981
1979–81, Methow Game Range, Washington[a]	14/93	Pneumonia/contact with domestic sheep	New pathogen	Foreyt and Jessup, 1982
1982, Wigwam, British Columbia, Canada[a]	300/50	Pneumonia/contact with domestic sheep	New pathogen	Goodson, 1982
1988, Warner Mountains, California[a]	65/100	Pneumonia/contact with domestic sheep	New pathogen	Weaver, 1989
1981, Latir Parks, New Mexico[a]	36/100	Pneumonia/contact with domestic sheep	New pathogen	Sandoval, 1988
1985, Sheep River Wildlife Sanctuary, Alberta[a]	250/54	Apparent pneumonia	Stress factors	Festa-Bianchet, 1988
1986, Lostine, Wallowa Mountains, Oregon[a]	97/70	Pneumonia/contact with domestic sheep	New pathogen	Coggins and Matthews, 1992
1988, Southeast Washington[a]	80/62	Scabies/contact with transplanted Rocky Mountain bighorn	New pathogen	Foreyt et al., 1990

TABLE 1. Continued.

Epizootic date, place	Initial population/ mortality (%)[b]	Associated disease/possible cause	Origin of epizootic	Reference
1989, Aravaipa Canyon, Arizona[a]	195/59	Blue Tongue-EHD[b]/ drought, cattle presence	Mixed origins	Mouton et al. 1991
1990–91, Whiskey Mountains, Dubois, Wyoming[a]	600–900/30–40	Pneumonia/cold temperatures	Stress factors	Ryder et al., 1992
1992–93, East Range, Nevada	U/U	Not determined	Unknown	Martin et al., 1996
1992–93, Desatoya Range, Nevada	U/U	Pneumonia	Unknown	Martin et al., 1996
1995, Hells Canyon, Washington and Oregon	700/50–75	Pneumonia/presence of cattle, goats, domestic sheep	Mixed origins	Cassirer et al., 1996
1997–2000, Kenosha and Tarryall Mountains, Colorado	250/50	Contact with domestic sheep	New pathogen	George et al., 2008
2005, Custer State Park, South Dakota[a]	200/75	Contact with domestic sheep	New pathogen	Freeman, 2006

[a] Epizootic analyzed for this study.

[b] U = unknown; EHD = epizootic hemorrhagic disease.

important factor influencing bighorn sheep population dynamics and in a similar study, Singer et al. (2001) suggested 292±82 animals as the minimum population size that would be able to recover from an epizootic. In the state of Sonora (excluding Tiburon Island) there are 46 bighorn ranges, which have been divided into seven wildlife management system units (SUMAS; Dirección General de Vida Silvestre, unpubl. data). These SUMAS are connected bighorn sheep ranges where these populations may have contact. Considering that populations have genetic flow between them, at least three of these units do not have populations above 188 animals. Our results indicate that 188 is the minimum population size that would not be at risk of extinction following an epizootic event.

Causes of bighorn population extinctions often can be associated with additional factors that are independent of stress or disease. Predation, for example, may be important, especially to smaller populations. Our analyses were based on historical epizootics and these complex factors are present today. The information derived from these historic events were based on authors' knowledge of the initial population sizes and remaining numbers after the epizootic event, as well as the possible associated cause. Some of this information may not be as accurate as recent estimates. However, we consider that their observations were reliable for estimating a general mortality rate of the populations being studied.

Additional factors beyond population size should be considered. Current estimates of bighorn sheep populations in Mexico frequently are based on aerial survey data. Complex aspects such as population dynamics, probability of contact with domestic animals, inbreeding level, genetic flow among populations, and suitable habitat patch sizes are largely unknown. Many bighorn populations in Mexico are isolated and the loss of genetic variability can reduce population fitness through decreased reproductive ability and reduced immunologic capacity (Munson, 1993). These effects can increase mortality during an epizootic, increasing

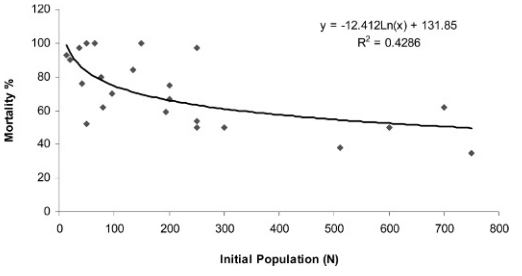

FIGURE 1. Negative logarithmic relationship found between initial population size and mortality in the analysis of total bighorn sheep epizootics (1942–2005).

TABLE 2. Relationship between initial population size and the predicted mortality caused by epizootic events (see Materials and Methods for explanation of predictive model). For long-term persistence following an epizootic event (estimated remaining population ≥50), a minimum initial population size of ≥188 animals is required.

Initial population	Expected mortality (%)	Estimated remaining
20	80	4
50	82	9
150	75	37
188	**73**	**50**
200	72	56
250	69	77
300	69	102
500	53	235

the probability of population extinction. Although there are studies of the health status of bighorn sheep populations, there is insufficient information from serologic or mortality studies of Mexican bighorn sheep populations to fully understand the pathogens potentially associated with disease-related declines in these populations. The potential for disease transmission following translocations among resident populations is a factor rarely considered in Mexico. In many Wildlife Management and Utilization Units in Mexico, bighorn sheep are kept in proximity to cattle (2–5 km) and in some cases they are separated only by fences (Cassaigne, pers. obs.). Even though there is no direct contact between bighorn sheep and domestic animals, many diseases can be indirectly transmitted by vectors. Goats have been observed near two important bighorn sheep areas in Sonora State and may be associated with population declines in those areas (Lee, 2004). Goats or cattle are present near bighorn sheep habitat and, in addition to increased potential for disease transmission, interactions with goats or cattle may also increase stress. Bissonette and Steinkamp (1996) reported avoidance of habitat by bighorn sheep when livestock were present. During an epizootic in Sierra del Viejo, Sonora, Mexico, the bighorn population decreased from 126 sheep in 1993 to 17 in 2003 (Lee, 2004). Specific causes for this decline are unknown and need to be understood to support management decisions related to Mexico's bighorn sheep recovery program.

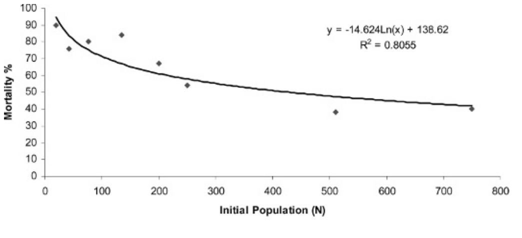

FIGURE 2. Negative logarithmic relationship found between initial population size and mortality in bighorn sheep epizootics induced by stress factors (1942–2005).

TABLE 3. Relationship between initial population size and predicted mortality caused by epizootic events originating from stress factors (see Materials and Methods for explanation of predictive model). For long-term persistence following an epizootic event, a minimum population size of 173 animals is required.

Initial population	Expected mortality (%)	Estimated remaining
20	82	3
50	80	10
150	73	40
173	**71**	**50**
200	69	62
250	66	85
300	62	114
500	48	260

Our suggested disease-based MVP size of 188 animals does not imply that smaller populations cannot survive after facing an epizootic event, but populations below that number may have lower probabilities of recovery and long-term persistence, and would probably require more intensive and costly management. On the other hand, populations above 188 animals also could become extinct, since additional factors such as inbreeding, habitat patch sizes, fragmentation, predation, and environmental conditions can increase mortality during an epizootic. Minimizing stress factors and avoidance of close contact with domestic sheep would decrease the probability of an epizootic; however, no bighorn sheep population can be considered entirely without risk.

Based on 2004 bighorn sheep population estimates by the wildlife department (Dirección General de Vida Silvestre, unpubl. data) in Sonora, our minimum population numbers suggests that only 42% of existing bighorn sheep would persist in the long term. The situation in the USA and Canada could be similar due to the fragmentation and isolation of many populations (Valdez and Krausman, 1999).

Information related to disease and population dynamics is needed to conserve and recover bighorn sheep populations in Mexico. Results from this study suggest that individual populations should be managed to exceed 170 animals but the causes and population factors (e.g., genetic variability, stress associated with livestock contact, increased disease transmission on shared habitats with domestic animals) associated with epizootics need to be better defined to continue to refine and understand disease risks as they relate to long-term bighorn sheep management.

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