



United States Department of Agriculture

Forest Service

Rocky Mountain Research Station

General Technical Report RMRS-GTR-209

September 2008

A Review of Disease Related Conflicts Between Domestic Sheep and Goats and Bighorn Sheep

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Schommer, Timothy J.; Woolever, Melanie M. 2008. **A review of disease related conflicts between domestic sheep and goats and bighorn sheep.** Gen. Tech. Rep. RMRS-GTR-209 Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Research Station. 16 p.

ABSTRACT

Research shows that contact between bighorn sheep and domestic sheep and goats can lead to respiratory disease and fatal pneumonia in bighorn sheep. We reviewed experimental methods and evidence regarding respiratory disease in bighorn sheep relative to domestic sheep and goats based upon the contact hypothesis and categorized by experimental approach. Although efforts to identify organisms causing pneumonia in bighorn sheep following contact with domestic sheep have identified multiple bacteria species, the complete range of mechanisms/causal agents leading to epizootic disease events are not completely understood. However, based upon the effect of disease transmission, spatial and/or temporal separation between domestic sheep and goats and bighorn sheep is prudent when the management objective is to maintain bighorn sheep populations.

Keywords: *Ovis*, *Capra*, respiratory, disease, transmission

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INTRODUCTION

The purposes of this document are to: 1) review the science related to disease, particularly respiratory disease, in sympatric populations of domestic sheep (*Ovis aries*) and goats (*Capra hircus*) and bighorn sheep (*Ovis canadensis*) and 2) provide scientific foundation for the development of agency policy. For the purpose of this document, the terms pneumonia and respiratory disease are used interchangeably as are the terms bighorn sheep, wild sheep, and mountain sheep. Additionally, the organism called *Pasturella haemolytica* has been renamed *Mannheimia haemolytica*, but because much of the scientific literature uses the old nomenclature, the names should be considered synonymous.

Major bighorn sheep die-offs have been reported from the mid-1800s to present and have been known to occur in every western state (Martin and others 1996; Toweill and Geist 1999). Research shows that contact between bighorn and domestic sheep can lead to respiratory disease and fatal pneumonia in bighorns (Callan and others 1991; Foreyt 1989, 1992a, 1994; Foreyt and Lagerquist 1996; George and others 2008; Onderka and Wishart 1988). Therefore, the role that domestic sheep play in causing pneumonia in bighorn sheep is an important issue in multiple-use management (Foreyt and others 1994; Hurley 1999; Schommer and Woolever 2001; Schwantje and others 2006).

Presently, about 90 percent of Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*) and 20 percent of desert bighorn sheep (*Ovis canadensis nelson*) in the United States spend all or part of their lives on National Forest System lands. Although domestic sheep allotments on national forests in the western United States have declined greatly in number, they remain numerous in some areas. When domestic and wild sheep ranges overlap or are in close proximity, bighorn sheep advocates, whether from state agencies, non-governmental organizations, or tribes, express concern regarding the potential for contact between the species. Managers often struggle because they lack an understanding of the disease-related conflicts between domestic sheep and goats and bighorn sheep, or of how to develop potential solutions. An earlier document by Schommer and Woolever (2001) provided management guidance for national forests supporting bighorn sheep populations and this document has proven effective in aiding in the development of solutions across the western United States.

HISTORY

The original distribution of native sheep in North America extended north to the Brooks Range in Alaska, south to Baja California and the northern reaches of mainland Mexico, and east to western Texas and the badland and river break habitats immediately east of the Rocky Mountains in North and South Dakota and western Nebraska (Buechner 1960; Valdez and Krausman 1999). It is usually assumed that all suitable habitats were historically occupied.

The distribution of native sheep in Alaska and Canada remains essentially unchanged (Valdez and Krausman 1999). In contrast, many populations to the south have gone extinct, including all native populations in Washington, Oregon, and neighboring regions of southwestern Idaho, northeastern California, and northwestern Nevada (Buechner 1960). Toweill and Geist (1999) reported bighorn sheep extirpations from Arizona, New Mexico, Nebraska, Nevada, North Dakota, South Dakota, Utah, Oregon, and Washington. The states of California and Nevada lost an estimated 110 native populations (McQuivey 1978; Wehausen and others 1987; Wehausen and others in prep). Desert bighorn sheep were extirpated from the states of Coahuila, Chihuahua, and Nuevo Leon, Mexico and Colorado and Texas, USA. Populations in other western states of the United States and Mexico probably declined to less than 5,000 individuals (Toweill and Geist 1999). Although estimates of historical bighorn sheep numbers in pre-Columbian North America have been debated (Buechner 1960; Seton 1929; Valdez 1988), there is general consensus that population estimates of the Twentieth century are comparatively lower (Buechner 1960; Toweill and Geist 1999; Valdez and Krausman 1999).

Bighorn sheep recovery began during the 1960s in most western states and has continued to the present. State wildlife agencies have ongoing efforts in partnership with land management agencies that include transplanting sheep into unoccupied habitat, augmenting existing herds, and manipulating habitat. While success rates vary, herds found at peak population or in close proximity to domestic sheep tend to be more susceptible to die-offs (Monello and others 2001). Since most western state agencies have a policy of not re-establishing bighorns near domestic sheep operations, recovery of bighorn sheep into those vacant habitats is probably being limited. Even with the ongoing recovery efforts, current bighorn sheep numbers in the western United States are only a fraction of their original numbers. In 1999, Toweill and Geist estimated the population of all species in the contiguous United States at about 47,900 individuals, far fewer than historical estimates proposed by Seton (1929) and Buechner (1960).

Widespread bighorn sheep extirpations in North America are geographically coincident with regions where historically large numbers of domestic sheep grazed (Wehausen and others in prep). Researchers have long hypothesized that disease transferred from domestic sheep was a key factor in the widespread loss of bighorn sheep populations (Valdez and Krausman 1999; Wehausen and others in prep). For example, the first large-scale population losses in the nineteenth century were principally attributed to scabies introduced by domestic sheep. This conclusion was based largely on clinical evidence of scabies in bighorn sheep during die-offs and the fact that these scabies outbreaks closely followed the introduction of domestic sheep (Buechner 1960; Honess and Frost 1942; Jones 1950; Smith 1954). Further negative correlations between the presence of domestic sheep grazing and the health of bighorn sheep populations emerged in the

Twentieth century (Wehausen and others in prep). In Nevada, McQuivey (1978) noted a negative correlation between past domestic sheep grazing and the persistence of bighorn sheep populations. Additionally, an accumulation of considerable circumstantial evidence supports the hypothesis that bighorn sheep die-offs frequently follow contact with domestic sheep (Cassirer and others 1996; Coggins 1988, 2002; Foreyt and Jessup 1982; Goodson 1982; Martin and others 1996; Singer and others 2001). Finally, Monello and others (2001) concluded that bighorn herds are rendered vulnerable to pneumonia transmission of *Pasteurella* spp. from domestic sheep serving as reservoir hosts.

Although respiratory disease resulting in pneumonia is the most serious and devastating disease at a population level that is shared by domestic and bighorn sheep, other diseases and parasites, including but not limited to scabies, anaplasma, babesia, ovine parapox (contagious ecthyma), and infectious keratoconjunctivitis (pink eye), may be communicable (Jessup and Boyce 1993).

DISEASE REVIEW

An understanding of the disease-related conflicts between domestic sheep and goats and bighorn sheep is essential to the development of agency policy regarding management of these species.

Research concerning disease transmission when bighorn sheep come into contact with domestic sheep has been extensive over the past quarter century. The hypothesis that contact with domestic sheep results in pneumonia in bighorn sheep has been researched under a variety of experimental conditions. The following is a review and summary of the experimental methods and evidence relative to the hypothesis that bighorn sheep have a high likelihood of contracting fatal respiratory disease following contact with domestic sheep, characterized as the “contact hypothesis” (Wehausen and others in prep). Additional hypotheses that are refinements of the contact hypothesis are addressed (Wehausen and others in prep). The following summary of this information is categorized by experimental condition: 1) unplanned pen experiments; 2) planned pen experiments; 3) planned pen experiments with other species; 4) inoculation experiments; 5) research to identify bacteria strains causing fatal pneumonia; and 6) vaccination trials. A seventh section includes other pertinent disease information. A brief review of science panel conclusions follows the summary.

Unplanned Pen Experiments

The contact hypothesis has been tested numerous times in captive situations. Two tests were accidental in nature and, therefore, lacked any experimental design. However, because of the information garnered from those captivity situations, they still serve as tests of the contact hypothesis. One of the unplanned experiments occurred at Lava Beds National Monument, where a population of bighorn sheep was established in 1971 in a 5.4 km² enclosure (Blaisdell 1972). In 1980, nose-to-nose contact was observed through the enclosure fence between bighorn sheep and domestic sheep grazed on adjacent National Forest System lands. Bighorn sheep began dying of pneumonia 2 to 3 weeks later, and all 43 bighorn subsequently died (Foreyt and Jessup 1982). The second situation involved bighorn sheep in Washington that had been in a 2.5 ha enclosure for 10 months when domestic

sheep were added to the pen. Thirteen of 14 bighorn sheep died within 8 weeks of interspecies contact (Foreyt and Jessup 1982).

Planned Pen Experiments

Following the unplanned experiments, three independent research groups conducted 10 experiments designed to test the contact hypothesis using one to six captive bighorn sheep per trial. Five of these experiments used only domestic sheep (Foreyt 1989, 1990, 1994; Onderka and Wishart 1988) while contact in the other five (Callan and others 1991) involved a mixed flock of domestic sheep and hybrids of argali (*Ovis ammon*) and mouflon (*Ovis musimon*) sheep, the latter of which is the source of domestic sheep (Ramey 2000). The latter five trials also included treatments that attempted to control the resulting pneumonia in the bighorn sheep. All 23 bighorn sheep tested in these 10 trials died of respiratory disease following contact with domestic sheep or were euthanized when close to death. In every case, all the domestic and hybrid sheep remained healthy.

Two basic mechanisms have been hypothesized to explain the planned pen results: 1) contact results in transmission of microbes from domestic sheep to bighorn sheep that directly or indirectly leads to fatal pneumonia in the latter species and 2) introduction of another species into the pen creates a psychological effect on the bighorn sheep that results in a stress-related, compromised immune system that leads to respiratory disease unrelated to the transmission of different microbes (Wehausen and others in prep).

Planned Pen Experiments With Other Species

Planned pen experiments that put captive bighorn sheep in contact with other species do not support the stress hypothesis. Foreyt (1992a, 1994) and Foreyt and Lagerquist (1996) conducted eight independent contact experiments involving bighorn sheep penned with: 1) elk, white-tailed deer, and mule deer; 2) elk alone; 3) domestic goats; 4) mountain goats; 5) llamas; 6) cattle; 7) horses; and 8) steers. Of the 39 bighorn sheep tested in these experiments, only two died. One was an old female whose death was most likely due to a tooth abnormality that adversely affected her feeding ability. The other death was a bighorn sheep in the pen with the steers that died of pneumonia (Foreyt and Lagerquist 1996). These findings suggest that the presence of other species in pens itself is unlikely to lead to bighorn sheep deaths and that species other than domestic sheep are considerably less likely to transmit microbes fatal to bighorn sheep. This latter conclusion is consistent with a lack of historical observations or circumstantial data linking such species to bighorn sheep die-offs.

Recently, however, domestic goats have been implicated in fatal disease transmission to bighorn sheep. Some goats carry *Mannheimia* and *Pasteurella* species that have been identified in bighorn sheep disease events. DNA analysis conducted during a 1995 to 1996 Hells Canyon bighorn die-off revealed that a feral goat and two bighorn sheep shared a genetically identical *P. multocida* and *M. haemolytica* (Rudolph and others 2003; Weiser and others 2003). Since that time, other incidents involving domestic goats and bighorn sheep have been documented. An infectious keratoconjunctivitis (IKC) epizootic in bighorn sheep occurred in the Silver Bell Mountains, Arizona, in 2003 and 2004 (Heffelfinger 2004). That bighorn sheep population had been monitored for several decades prior to the incident, without evidence of IKC. Genetic investigation strongly suggests that

domestic goats transmitted IKC to native bighorn sheep (Jansen and others 2006). Contagious ecthyma was also transmitted to the previously native bighorn sheep in the same incident.

Inoculation Experiments

The hypothesis that specific strains of pneumophilic bacteria frequently carried by healthy domestic sheep are the cause of fatal pneumonia in bighorn sheep following contact between these species (Goodson 1982; Wehausen and others in prep) has been tested. In these experiments, captive bighorn sheep were inoculated with bacteria cultured from the respiratory tracts of domestic sheep. Both accidental and planned experiments have had similar results. The accidental experiment occurred when a lavage tube used to sample lung cells of domestic sheep was not fully sterilized before being used to obtain lung cultures from three captive bighorn sheep. Of the 10 original bighorn sheep in the herd, three died of pneumonia, as did three more bighorn sheep added to this herd during that time period (Foreyt 1990).

The planned inoculation experiments comprised six independent trials carried out by two different research groups using *Mannheimia haemolytica* cultures from domestic sheep (Foreyt and others 1994; Foreyt and Silflow 1996; Onderka and others 1988). Of the 13 bighorn sheep inoculated with those bacteria, 12 died of acute bronchopneumonia. Two groups of control bighorn sheep (five total) remained healthy, as did two groups of domestic sheep (nine total) that received the same inoculation doses as the bighorn sheep. Two of these inoculation trials (Foreyt and Silflow 1996; Onderka and others 1988) included experiments in which the source of the *M. haemolytica* inoculum was from healthy bighorn sheep. The three bighorn sheep used in the two trials showed no clinical signs of disease after the inoculations, nor did the seven domestic sheep similarly inoculated.

Foreyt and others (1996) also carried out an inoculation trial of three Dall's sheep (*Ovis dalli dalli*). Two of these sheep received a *Mannheimia haemolytica* strain (A2) from domestic sheep that was known to be fatal to bighorn sheep, while the other received a strain not considered pathogenic. The sheep receiving the non-pathogenic strain remained healthy. The other two developed bronchopneumonia and one died and the other was euthanized prior to death.

Research to Identify Microbial Strains Causing Fatal Pneumonia

The results of the various contact and inoculation trials support the occurrence of microbial transmission (Wehausen and others in prep). With sufficient diagnostic tools, it should be possible to identify the specific microbe(s) that causes fatal pneumonia in bighorn sheep. However, the goal of identifying all specific pathogenic organisms has proven elusive (Rudolph and others 2007; Wehausen and others in prep). First, multiple bacterial species have been implicated as disease agents. While *Mannheimia haemolytica* (especially the A2 strain) has been cultured from many bighorn sheep dying of pneumonia following experimental contact with domestic sheep, one set of experiments attributed the deaths to *Pasturella multocida* (Callan and others 1991). Additionally, some strains of *M. haemolytica* are now recognized as a separate species, *P. trehalosi*. Second, traditional methods used to differentiate strains of *M. haemolytica* by biotypes and serotypes (Dunbar and others 1990a,b; Queen and others 1994) have lacked adequate resolution. Previously undescribed serotypes have been found

in bighorn sheep (Dunbar and others 1990a) while other strains could not be identified using these methods (Dunbar 1990a; Silflow and others 1994; Sweeney and others 1994; Ward and others 1997), rendering these classification methods unsatisfactory for epidemiological investigations of this phenomenon (Jaworski and others 1993).

To overcome limitations of traditional methods, additional diagnostic tools have been applied to *Mannheimia haemolytica* and *Pasturella trehalosi* in attempts to identify strains responsible for bighorn sheep deaths. These methods include: 1) binary classification as hemolytic or non-hemolytic (Ward and others 2002; Wild and Miller 1991, 1994); 2) variation in surface proteins (Ward and others 1990); 3) assays of toxicity relative to peripheral neutrophils (Silflow and others 1993; Silflow and Foreyt 1994; Sweeney and others 1994); 4) DNA fingerprinting to identify different genetic forms (Foreyt and others 1994; Jaworski and others 1993; Snipes and others 1992; Ward and others 1997; Weiser and others 2003); and 5) culture-independent PCR-based methods and sequence-based phylogenetic analyses of multiple DNA loci (Kelley and others 2006; Safaei and others 2006). While DNA fingerprinting has been useful for investigating the transmission of bacterial strains between different species and individuals (Ward and others 1997), all of the above five methods appear to lack predictive power relative to identifying strains involved in fatal pneumonia in bighorn sheep.

Vaccination Trials

Vaccinations have been investigated as a potential solution but are not viewed as a viable management option for bighorn sheep. First, vaccination would be required annually and second, the difficulty vaccinating wildlife is exacerbated by the steep rocky terrain that bighorn sheep inhabit.

Ward and others (1999) investigated immunologic responses of bighorn and domestic sheep to a vaccine for three strains of *Mannheimia haemolytica*. They found that the vaccine produced only a moderate and transient immunologic response. Miller and others (1997) and Kraabel and others (1998) tested a vaccine for three different *M. haemolytica* strains on captive bighorn sheep. The sheep were challenged with a *Pasturella trehalosi* vaccine cultured from the lungs of free-ranging bighorn sheep during a pasteurellosis epizootic. Control and vaccinated bighorn both developed acute pneumonia, but the vaccinated bighorn sheep experienced lower mortality (30 versus 80 percent).

Cassirer and others (2001) conducted experiments with free-ranging and captive bighorn sheep to test the efficacy of vaccines against *Mannheimia* spp. and *Pasteurella* spp. to reduce mortality of adults and lambs. Vaccinated females suffered notably higher lamb mortality.

Only two vaccination trials have used strains of *Mannheimia haemolytica* derived from domestic sheep as the post-vaccination challenge. Foreyt and Silflow (1996) inoculated two bighorn sheep twice with a non-lethal cytotoxic strain of *M. haemolytica*, and 6 weeks later, they inoculated them with a lethal cytotoxic strain (A2) from domestic sheep. The non-lethal strain provided no significant protection, and both bighorn sheep died of pneumonia. Foreyt (1992b) tested an experimental bacterin-toxoid vaccine for three *M. haemolytica* strains, using three treatment and three control bighorn sheep. After contact with domestic sheep, five of the six bighorn sheep, including the three vaccinated, died of pneumonia. There was no evidence of any protection from the vaccine.

OTHER PERTINENT DISEASE INFORMATION

Microbial Transmissibility

Although malnutrition, harsh weather, and other stressors may exacerbate susceptibility to disease, viruses, parasites, and bacteria can weaken or kill bighorn sheep. Bacteria, primarily *Mannheimia* spp. and *Pasteurella* spp., have led to massive, all-age die-offs of bighorn sheep in every western state (Martin and others 1996) and have been reported as the primary cause of bighorn sheep population declines throughout North America (Hurley 1999; Schwantje 1988; Wehausen and others in prep). Of the numerous pathogens affecting bighorn sheep, *M. haemolytica* has been viewed as the most prevalent respiratory pathogen that frequently leads to pneumonia and death (Foreyt 1995; Garde and others 2005; Martin and others 1996). *Pasteurella multocida* can also be important in the pneumonia complex. Some of the most recent and yet to be published work indicates that a *Mycoplasma* spp. bacteria may consistently be involved in bighorn sheep respiratory disease deaths (Cassirer, personal communication) in some locations. Black and others (1988) reported that a captive herd of Dall's sheep contracted *Mycoplasma ovipneumonia* infections after contact with domestic sheep. The pathology and epidemiology of *Mycoplasma*-induced pneumonia in sheep are somewhat different from those caused only by highly pathogenic bacteria. A review of *Pasteurella*-related pneumonia can be found in Frank and others (2004). An overview of the many pathogens of concern and the risks associated with them can be found in Garde and others (2005).

All ungulates, except llamas, carry some strains of *Mannheimia haemolytica* (Foreyt 1995). Bighorn sheep appear to be behaviorally attracted to domestic sheep and goats, but not to cattle or llamas. Since *Mannheimia* spp. and *Pasteurella* spp. bacteria transmission requires very close (less than 60 ft) contact or transfer of mucus through coughing or sneezing, it is more likely to occur between bighorn sheep and domestic sheep or goats (Dixon and others 2002) that are behaviorally attracted to one another.

Bighorn sheep appear to be more susceptible to respiratory disease than are domestic sheep. Dubay and others (2002) and Miller (2001) suggested that bighorn sheep did not co-evolve with the same set of pathogens as domestic sheep because of an evolutionary distance between them. Hiendleder and others (2002) estimated this distance at 5.63 million years. In addition, bighorn sheep immune response cells have a reduced capacity to kill bacteria compared to domestic sheep immune function (Dubay and others 2002; Frank and others 2004; Silflow and others 1993). This observation provides a very plausible reason why bighorn sheep may die of bacterial respiratory disease and pneumonia when in contact with domestic sheep while the domestics show no signs of disease.

Bighorn sheep die-offs due to pneumonia have occurred without any known association with domestic sheep (Foreyt 1989; Goodson 1982; Onderka and Wishart 1984; Rudolph and others 2007; Ryder and others 1994). However, when contact between wild sheep and domestic sheep and goats is documented, the severity of the wild sheep die-off is typically more pronounced (Aune and others 1998; Martin and others 1996). George and others (2008) documented that contact with a single domestic ram coincided with a 50 percent die-off in three interconnected herds.

DNA fingerprinting was used to investigate the origin of bacteria leading to death in bighorn sheep (Foreyt and others 1994; Jaworski and others 1993). Bacterial DNA isolated from dead bighorns originated in domestic sheep and had not been present in bighorn sheep before they were exposed. The source of DNA was *Mannheimia haemolytica* (Biotype A, Serotype 2). Research at a variety of facilities (Washington State University, Department of Agriculture, Edmonton, Canada, and Caine Veterinary Center) has shown that specific types of *M. haemolytica* and *Pasturella multocida* can be transmitted between bighorn sheep and domestic sheep (Foreyt 1989, 1990, 1992a; Hunter 1995a; Onderka and Wishart 1988).

In free-ranging conditions, domestic and bighorn sheep association will likely result in bighorn sheep deaths without adversely affecting domestic sheep. Determination by DNA fingerprinting of a shared *Mannheimia haemolytica* between domestic sheep and bighorn sheep indicates that the bacteria was transmitted between these two species under field conditions (Hunter 1995b; Hunter and others in prep).

Demographic Effects

Martin and others (1996) summarized over 30 cases where bighorn die-offs are believed to have resulted from contact with domestic sheep. In many cases, over 50 percent of the bighorn herd died. Domestic sheep always remained healthy.

When respiratory disease occurs in a population of bighorn sheep, mortality normally occurs in all age classes. Research indicated that lambs born in bighorn sheep herds that experienced a pneumonia episode usually died before 3 months of age (Foreyt 1990). Passive colostrum immunity protects lambs early in life, but when immunity wanes at 6 to 8 weeks of age, they die from pneumonia. Further, surviving ewes generally experienced low lamb survival rates for 3 to 5 years after the initial episode (Coggins and Matthews 1992; Foreyt 1990, 1995; Garde and others 2005; George and others 2008; Hunter 1995a; Ward and others 1992). Thus, it appears that ewes surviving pneumonia remain infectious for several years and transfer the bacteria to their lambs. Because low lamb survival rates usually continue for 3 to 5 years, population recovery can be delayed. Further, Hunter and others (in prep) reported that various *Pasteurella* strains can remain resident in bighorn sheep for months or years after contact with domestic sheep. These infected bighorns may become asymptomatic reservoirs of potentially lethal organisms.

Models have predicted that disease originating from domestic sheep and goats is a problem for mountain sheep. Epps and others (2004) noted that the presence of domestic sheep grazing allotments was negatively correlated with mountain sheep population persistence. Proximity of domestic sheep as a factor in the dynamics of mountain sheep populations is a major consideration in the models constructed by Gross and others (1997, 2000). Clifford and others (2007) quantitatively evaluated the degree of risk between domestic and bighorn sheep for Sierra Nevada bighorn sheep (*Ovis canadensis californiana*).

No published reports could be found that document fenced or free-ranging bighorn sheep herds remaining healthy when living directly with domestic sheep herds.

Pertinent Findings

Legal

The disease related conflict between domestic sheep and bighorn sheep was tested in the United States District Court (Oregon) in 1995. The following summarizes United States Magistrate Judge Donald C. Ashmanskas' findings: "Scientific research supports a finding that when bighorn sheep intermingle with domestic sheep, large numbers of bighorn sheep die. While the exact reason for this result may be in question, it is clear that the die-offs occur. An incompatibility exists between the two species, and there is no way to avoid the incompatibility other than to keep the domestics and the bighorns separate" (Ashmanskas 1995).

Payette Science Panel Findings and Recommendations

A science panel was convened in November 2006 to provide additional science-based information regarding disease transmission and the associated risks for the Payette National Forest. Although focused specifically on the Payette risk analysis, the panel's conclusions are applicable to all areas where domestic sheep or goats and bighorn sheep co-exist. The panelists, who were scientists from the livestock and wildlife disease communities, focused on disease and mortality concerns and jointly developed the following statements¹ (USDA Forest Service 2006):

- 1a) Scientific observation and field studies demonstrate that "contact" between domestic sheep and bighorn sheep is possible under range conditions. This contact increases the risk of subsequent bighorn sheep mortality and reduced recruitment, primarily due to respiratory disease.
- 1b) The complete range of mechanisms/causal agents that lead to epizootic disease events cannot be conclusively proven at this point.
- 1c) Given the previous two statements, it is prudent to undertake management to prevent contact between these species.
- 2) Not all bighorn sheep epizootic disease events can be attributed to contact with domestic sheep.
- 3) Gregarious behavior of bighorn sheep and domestic sheep may exacerbate the potential for disease introductions and transmission.
- 4) Dispersal, migratory, and exploratory behaviors of individual bighorn sheep traveling between populations may exacerbate the potential for disease introduction and transmission.
- 5) There are factors (for example, translocation, habitat improvement, harvest, weather, nutrition, fire, interspecies competition, and predation), some that can be managed and some that cannot, that can influence bighorn sheep population viability.
- 6) *Pasteurellaceae* and other bacteria, viruses, and other agents may occur in healthy, free-ranging bighorn sheep.

¹ References to domestic sheep also apply to domestic goats.

Western Association of Fish and Wildlife Agency Findings

In January 2007, the Western Association of Fish and Wildlife Agencies (WAFWA), a group of 23 state and provincial wildlife agencies from the western United States and western Canada, established a Wild Sheep Working Group (WSWG). Comprised of bighorn sheep managers and veterinarians, WSWG was requested to provide a comprehensive, west-wide assessment of all facets of wild sheep management. The following conclusions from their June 21, 2007 final report, which WAFWA unanimously endorsed in July 2007, are relevant to this disease overview:

- 1) Over the past 30 years, there has been a steadily increasing body of anecdotal and empirical evidence underscoring the potential risk of disease transmission from domestic sheep and goats to wild sheep.
- 2) There is a preponderance of evidence, taken collectively from a wide variety of observations, that indicates significant risk of disease transmission from domestic sheep and goats to wild sheep exists.
- 3) Effective separation (both temporal and/or spatial) between wild sheep and domestic sheep and goats should be a primary management goal of state and provincial agencies responsible for wildlife management.
- 4) We concur with statements developed and adopted by the interdisciplinary Payette National Forest Science Panel (listed above).
- 5) We recognize that it is impossible to achieve zero risk of contact or disease transmission: however, we also recognize there are many ways to work proactively toward minimizing or eliminating interaction between these species.
- 6) We developed management guidelines for use by all agencies, organizations, domestic producers, and private land owners.

CONCLUSIONS

The scientific literature and expert panels support the conclusion that bighorn and domestic sheep/goats should not occupy the same ranges simultaneously or be managed in close proximity to each other if maintenance of a bighorn sheep population is a management objective. The literature is clear regarding the high probability of bighorn sheep dying of pneumonia following contact with domestic sheep. Efforts to identify organisms causing pneumonia in bighorn sheep following contact with domestic sheep have identified many potentially pathogenic bacteria of multiple species, but the specific mechanisms/causal agents that lead to epizootic disease events are not completely understood.

MANAGEMENT IMPLICATIONS

Pressing resource management decisions cannot wait for a complete understanding of all aspects of respiratory disease processes in bighorn sheep. In landscapes where management objectives include the maintenance or enhancement of bighorn sheep populations, the risk of potential of disease transmission between domestic sheep/goats and bighorn sheep must be addressed. The available information supports creating spatial and/or temporal separation between domestic sheep/goats and bighorn sheep as a prudent management technique to manage the risk of disease transmission.

(Callan and others 1991; Coggins 1988, 2002; Coggins and Matthews 1992; Desert Bighorn Council 1990; Festa-Bianchet 1988; Foreyt 1989, 1990, 1992a, 1992b, 1994, 1995; Foreyt and Jessup 1982; Foreyt and others 1994; Garde and others 2005; Goodson 1982; Hunt 1980; Hunter 1995a; Hunter and others in prep; Jessup 1980, 1982, 1985; Kistner 1982; Martin and others 1996; Onderka 1986; Onderka and Wishart 1988; Pybus and others 1994; Ward and others 1997; Wishart 1983). Recent disease incidents involving domestic goats have resulted in the same conclusion (Garde and others 2005; Heffelfinger 2004; Jansen and others 2006).

ACKNOWLEDGMENTS

The authors are extremely grateful to Dr. John Wehausen for his generous contributions to the historical perspective and disease overview sections. His research-orientated approach of isolating questions and hypotheses and categorizing past research by experimental conditions provided increased clarity to a very complex problem. We thank the four reviewers who conducted blind reviews under a process overseen by Rocky Mountain Research Station.

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