REPORT OF THE COMMITTEE ON WILDLIFE DISEASES

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The Committee met on October 28, 2008 at the Sheraton Greensboro Hotel, Greensboro, North Carolina, from 8:00 a.m. to 12:00 p.m. There were 39 members and 54 guests present.

Mike Miller, Colorado Division of Wildlife, presented a time-specific paper titled the CAST Commentary – Pasteurellosis Transmission Risks Between Domestic and Wild Sheep. The paper in its entirety is included at the end of this report.

Working Group Report on Development of Best Management Practices for Grazing Domestic Sheep and Goats Where Contact with Bighorn Sheep May Occur
Walter Cook, Wyoming State Veterinarian, reported that the Working Group on Best Management Practices for Domestic Sheep Grazing on Public Land Ranges Shared with Bighorn Sheep met three times via conference call and shared numerous emails. The group will meet in person on October 28, 2008 at USAHA to continue work on the draft document. The group hopes to present the final document at the 2009 United States Animal Health Association (USAHA) Annual Meeting for publication in the proceedings.

Anthrax in Bison
Dave Hunter, Turner Enterprises, reported on bison and elk mortality due to anthrax in southwestern Montana during the summer of 2008. The first of two outbreaks occurred in an 18,000 acre pasture in which 298 bison died out of a herd of approximately 5,000 bison. Elk mortality totaled 16-20 bulls. Breeding bull bison also were hit particularly hard with 35 percent of them killed in the outbreak. Carcasses were burned in an air curtain incinerator or buried deeply with a back-hoe. A second outbreak subsequently occurred in bison located remotely from the initially affected herd. This outbreak lasted only one day during which 32 bison died. Follow-up information on the anthrax outbreaks will be provided at the 2009 USAHA Annual Meeting.

Elk, Brucellosis, and the Changing Environment
Neil Anderson, Montana Department of Fish, Wildlife, and Parks, reported on changing land ownership in Montana and the changing land use patterns in the Madison Valley near Yellowstone National Park (YNP). Many new landowners limit the elk hunting on their property entirely or restrict hunting to bulls only, resulting in a refuge effect among elk in the area. Consequently, elk movement patterns have changed with

the animals arriving in the private land areas from public land earlier, staying later, and largely avoiding the public lands during hunting season when pressure is high. *Brucella* antibody seroprevalence has increased over the last 20-30 years in elk in this area. The increased seroprevalence and the increased amount of time the elk spend on private land in proximity to cattle have increased the potential risk of brucellosis transmission from elk to cattle.

Bovine Tuberculosis in Minnesota Cattle and Deer

Bill Hartmann, Minnesota State Veterinarian, reported that after three years of surveillance of free ranging white-tailed deer in the area of where infection has been found in cattle herds, 24 out of 4,164 deer have tested positive for bovine tuberculosis (TB). All of these positive deer have been killed within a 164 square mile area. All positive deer were alive in 2005 when the first infected cattle herds were discovered suggesting that deer to deer transmission may not be occurring.

The approach to managing deer in this area is threefold; eliminating deer, banning recreational feeding and baiting and reducing the risk of transmission between cattle and deer. During the winter 2008 deer removal, 1,062 deer were taken out of this area and 6 were found infected with *Mycobacterium bovis*. This was done by a combination of special hunts, landowner permits, ground sharp shooting and aerial gunning. Both ground sharp shooting and aerial gunning were effective methods of removing deer. Aerial gunning being the most expensive. Feeding and baiting are both banned from this area and there are significant enforcement efforts in place. A cattle herd buyout is being implemented in this area: 45 of the 68 cattle producers in the area have signed contracts and must have all cattle gone by January 31, 2009. No cattle will be allowed back on the farms until the area is TB free. The remaining farms must construct deer proof fencing around their stored feed and winter feeding areas.

Hemorrhagic Disease in Wild and Captive Cervids

David Stallknecht, Southeastern Cooperative Wildlife Disease Study (SCWDS), presented an update on hemorrhagic disease (HD) in wild ungulates in the U.S. During 2007, there were numerous reports of HD and an unprecedented number of virus isolations (283) were made at SCWDS. Serotypes isolated during 2007 included epizootic hemorrhagic disease virus (EHDV)-1, EHDV-2, and EHDV-6, blue tongue virus (BTV)-10, BTV-11, and BTV-17. Based on reports of disease that were received from state fish and wildlife agencies during the winter and spring of 2008, there were two major outbreaks EHDV-2 in white-tailed deer in the eastern United States and BTV-17 in deer and pronghorn in the western United States. The EHDV-2 outbreak probably represented the most extensive orbivirus outbreak in U.S. history and it affected deer in some areas where HD does not historically occur.

To date in 2008, SCWDS has isolated EHDV-1 (Texas), EHDV-2 (Texas, Indiana), EHDV-6 (Texas, Kansas) and BTV-3 (Arkansas). The BTV-3 isolate was confirmed by National Veterinary Servcices Laboratory (NVSL). This is the third consecutive year that EHDV-6 was isolated and the second report of BTV-3; the first isolation of BTV-3 from white-tailed deer in the U.S. came from a wild deer in Mississippi during 2006. Sequence analyses of the 2006-2008 EHDV-6 isolates suggest that this virus may be derived from an EHDV-6/ EHDV-2 reassortment. The origin of this virus and BTV-3 are currently unknown but their repeated isolation suggests that they are now established in the U.S.

Status of Chronic Wasting Disease (CWD) Final Rule and APHIS-VS Activities Related to CWD

Lee Ann Thomas, APHIS-VS, provided an update on VS actions related to CWD. In FY 2008 APHIS received approximately $17.68 million in appropriated CWD funding, including $1.5 million in congressional earmarks.

The new proposed supplemental rule for CWD is now in the clearance process. It focuses primarily on interstate movement requirements but also addresses a few provisions of the CWD herd certification program. The scheduled publication of this proposed rule is December 2008. The final rule should be published in 2009.

APHIS-VS tested more than 20,500 farmed and captive cervids for CWD in FY 2008 using immunohistochemistry. Rectal biopsy evaluation also continues.

On August 25, 2008, the NVSL confirmed CWD in a 3-year-old doe at a farmed white-tailed deer facility in Kent County, Michigan. This was the first confirmed case of CWD in Michigan. The remaining animals on the property were depopulated by Wildlife Services (WS) on August 26, 2008. The epidemiological investigation of this occurrence is continuing. The second positive herd for 2008 was discovered in Portage County, Wisconsin, and was confirmed on October 9, 2008. This is a captive

hunting preserve with about 150 white-tailed deer. The epidemiology is currently under investigation. At this time, in addition to this positive white-tailed deer herd in Wisconsin, four positive elk herds remain in Colorado. VS continues to offer indemnity and cover depopulation, disposal and testing costs for CWD-positive and exposed herds and trace animals.

In FY 2008, $5 million in cooperative agreements were made available to the state wildlife agencies. The tier system for funding state cooperative agreements that was developed in consultation with Association of Fish and Wildlife Agencies (AFWA) remained unchanged from FY 2007. However, more scrutiny has been focused on states that have not fully utilized their funding in past years. As a result, some states are receiving less than the full amount they are eligible for. Forty-eight states are receiving FY08 funding and two are extending their FY07 agreements. Some additional funds have also been made available to tier 1 states with additional needs. Final reports on the FY 2007 agreements are due 90 days after the agreement period ends. Thus, all are due before December 31, 2008.

VS is working to standardize procedures across all its programs. Templates are being developed for submitting cooperative agreement work plans and budgets. The CWD template is being used as one of the models, but it will probably be modified to some extent.

VS provided $600,000 to support tribal CWD activities in FY 2008. In addition to the ongoing cooperative agreement with the Native American Fish and Wildlife Society, a number of individual tribes will receive CWD assistance.

A workshop to explore the next generation of CWD surveillance strategies in wild cervids was held in Madison, Wisconsin in July, hosted by the United States Geological Survey (USGS), National Wildlife Health Center. This was a follow-up to the initial workshop held in 2002. A report from the workshop is being prepared and will be issued in 2009.

The agriculture appropriations bill for FY 2009 has not yet been passed by Congress. In the House of Representatives, the Agriculture Appropriations Subcommittee has marked up its bill but it has not been acted upon by the full Appropriations Committee and the bill's provisions have not been made available. The Senate Appropriations Committee has cleared its FY 2009 agriculture appropriations bill but it has not been voted on by the full Senate. The Senate bill provides $17.8 million for the CWD program, including $1.57 million in congressional earmarks. It does not appear to support the 40 percent state cost share in the President's FY 2009 budget. As in most recent years, we anticipate being on continuing resolution funding for some period at the beginning of FY 2009, possibly extending deep into the fiscal year. Once funding levels are clarified, we will continue to work with AFWA to assure an equitable distribution of the cooperative funding that is available.

Carnivorous Behavior Patterns in Deer

Harry W. (Pete) Squibb, Senior Wildlife Biologist/Consultant with Wildlife Solutions, and Brad Thurston,   reported on a small study they conducted to observe animals visiting carcasses and gut piles in the environment. They reported that during 2006-2007, 36 of 58 (62 percent) volunteers placed trail cameras on gut piles or carcasses to record the animal species that visited them. During 2007-2008, 28 of 42 (67 percent) volunteers placed cameras. During both survey periods a wide variety of birds and mammals were photographed at or near the sites.

Of particular interest was the seemingly high use of these sites by deer. Deer were photographed at 22 of the 36 sites (61 percent) in 2006-07 and 18 of the 28 sites (64 percent) in 2007-08. Activity of deer at these sites varied considerably. Most deer appeared to be interested or inquisitive. Observations and photos indicated three sites with deer actually feeding on carcasses in 2006-07 and one in 2007-08. One was a young deer feeding on a cottontail rabbit carcass set out to attract coyotes. In a series of pictures, the whitetail is clearly shown eating the legs and ears from the cottontail rabbit carcass. In one site deer were clearly observed eating portions of a wild turkey carcass. In a third location, deer were the only animals feeding on a skinned beaver carcass set out to photograph predators. In 2007-08 a whitetail buck was observed on video actively feeding on a gut pile. In the remainder of the sites with deer present it must be noted that deer were usually the first animals to investigate the site after camera placement.

While this is a limited sample of data, the results indicate that deer show more interest in these sites than most wildlife professionals would normally expect. Initial observations from this study seem to indicate gut piles and carcasses of infected animals remaining in the woods could be a source of bovine TB and CWD for deer. This may be especially important in relation to localized deer populations. The results of this small survey and other incidental observations of whitetail deer around gut piles and carcasses have led some biologists and wildlife observers to question whether deer activity at and in the

close vicinity of these sites may serve as a possible transmission mode between animals in the wild. Due to the large number of mammals and birds known to actually feed on these gut piles and carcasses it is suggested further investigation be done to determine the risk of inter and intra species transmission of these and other potentially serious diseases in the wild.

Current Montana Brucellosis Situation

Marty Zaluski, Montana State Veterinarian, informed the Committee that in May 2007 the first brucellosis infected cattle herd was detected in Carbon County. In May 2008, a second infected herd was detected in Park County resulting in an official down-grade to Class A Brucellosis Status for Montana. December 2009 is the earliest that Class Free Status may be officially granted by APHIS.

The epidemiological investigation of the cases can be viewed at the Montana Department of Livestock Website www.liv.mt.gov. Cattle, bison and elk were investigated as potential sources. All source, contact, trace-out cattle tested negative, no Mexican-origin source was found, and wild, free-ranging elk are regarded as the most likely source.

The Committee also was informed of ongoing activities related to the Inter-agency Bison Management Plan, which is a multi-agency partnership that was formalized by a Record of Decision signed in December, 2000. Signing parties include U.S. Department of Interior, USDA-APHIS, USDA Forest Service, Montana Department of Livestock, and Montana Fish Wildlife and Parks. The two goals of the Plan are to prevent transmission of brucellosis from bison to livestock and to maintain a wild, free ranging bison population.

Wyoming Brucellosis Update

Walter Cook, Wyoming State Veterinarian, reported that the first brucellosis infected herd found was a 650 beef breeding cow herd near Daniel, Wyoming (Sublette County) in June 2008. Two reactors were detected at the local sale barn and a total of 39 reactors were found in the herd which was depopulated by early October 2008. The owner plans to repopulate after cleaning and disinfection (CD) and rest. The ranch is located near an elk feedground.

The second case was a market cattle identified (MCI) Reactor killed in Nebraska that was traced back to a 200 breeding cow herd in Bondurant, Wyoming (Sublette County). To date, half of the herd has tested negative. The other half of the herd is to be tested in early November. As with the other ranch, elk feeding occurred nearby.

Statewide, from October 2007 through September 2008, 87,227 brucellosis tests were conducted. This does not include out of state slaughter surveillance. State-wide testing at sale barns may get reduced in future. Change of ownership/movement testing continues in the area of concern, which is based on elk feedgrounds, wildlife seroprevalence and Enforceability.

Herd plans have been recommended by the Governor's Coordination Team and The Program Review Team. The area of concern is the primary focus and herd owners complete a questionnaire and undergo a risk assessment. The primary goal is to reduce the risk of *Brucella* transmission from wildlife to cattle.

Yellowstone National Park Brucellosis Management Program

Glenn Plumb, Yellowstone National Park (YNP), reported on bison populations, genetics, surveillance and vaccination in YNP. The overall goals of bison management in YNP are to preserve a wild bison population, prevent brucellosis transmission from bison to cattle, and reduce disease prevalence.

The park's bison population has increased since 2000, due to an increase in the northern population; the central population has declined. Annual survival is 83 percent when culling and slaughter are included, and 90 percent of seronegative pregnant cows have a full term pregnancy.

Goals of bison and brucellosis surveillance studies in YNP include:
1. estimate the abundance, demographic rates, and limiting factors for bison.
2. describe migratory and nomadic movements by bison in and out of park.
3. estimate genetic diversity and probabilities of conservation
4. estimate risks of transmission within and between species and areas.
5. estimate seroprevalence rates, culture rates, and cross-reactive agents.
6. determine rates of recrudescence.
7. determine factors influencing the vulnerability of bison to infection and transmission.
8. estimate the timing and percent of removals.

9. document bison use of zones outside the park and commingling with cattle.
10. estimate the effects of hazing or holding bison at capture pens.
11. determine the strength and duration of the immune response following syringe vaccination.
12. determine the strength and duration of the immune response following remote delivery vaccination.
13. document trends in prevalence and the effects of vaccination, other risk management actions, and ecological conditions on these trends.

Regarding vaccination, the following timetable has been proposed: internal agency review of Draft EIS in Winter 2008; draft EIS released for public comment – Spring 2009; content analysis and revision – Summer 2009; Internal agency review of Final EIS – Autumn 2009, and final EIS and Record of Decision – Winter 2010.

Avian Influenza (AI) Virus Research Studies

Justin Brown, Southeastern Cooperative Wildlife Disease Study (SCWDS), provided a summary on the collaborative research being conducted at SCWDS and the Southeast Poultry Research Laboratory. This research evaluates the influence that different environmental factors have on the ability of AI viruses to remain infective on aquatic habitats utilized by wild aquatic birds. Specifically he discussed the results of experimental trials that determined the effect that pH, salinity, and temperature have on the ability of AI viruses to persist in water using a laboratory-based distilled water model system. Additionally, he also reported the results for similar laboratory-based trials that evaluated the persistence of several Asian lineage H5N1 highly pathogenic avian influenza (HPAI) viruses. The overall goal of these studies was to provide data to improve our understanding of AI transmission within wild aquatic bird populations, and potentially, better evaluate risks associated with movement and local transmission of these viruses from wildlife reservoirs to domestic animals (poultry).

The environmental stability of twelve wild bird-origin AI viruses in water was examined under natural ranges pH (5.8 to 8.6), salinity (0 to 30 parts per thousand (ppt)), and temperature (4 to 37° C) that occur in aquatic bird habitats. The viruses varied in their overall ability to remain infective in water, but consistent trends in response to the three abiotic variables were observed among the AI strains. The majority of AI viruses tested in this study were most stable in water, based on duration of infectivity, at colder temperatures (4° to 17° C), in slightly basic conditions (pH ranging from 7.4 to 8.2), and in fresh to brackish water (salinity ranging from 0 to 20 ppt). These results are consistent with previous laboratory-based trials that have evaluated AI persistence in water.

There is strong experimental and field evidence to suggest that migratory waterfowl can, and have, contributed to the transmission and spread of H5N1 HPAI viruses. A question that remains unresolved is whether these viruses are established in wild aquatic bird populations. A critical factor in evaluating the potential transmission and maintenance of H5N1 HPAI viruses in aquatic bird populations is the environmental stability of these viruses in water, but currently very little data exists on this topic. In order to evaluate the range of environmental fitness among H5N1 HPAI viruses we determined the persistence for fifteen different H5N1 HPAI strains in water under three salinities (0, 15, and 30 ppt), two temperatures (17 and 28° C), and a pH of 7.2, under laboratory conditions. The results of these trials indicate that, similar to the wild bird-origin AI viruses described above, different strains of H5N1 HPAI vary in their stability in water. The H5N1 HPAI viruses exhibited similar trends in response to salinity and temperature as were noted among the wild bird-origin AI viruses.

The results of this research suggest that the natural conditions of aquatic habitats impact the ability of AI viruses to remain infective in different environments. Specifically, pH, temperature, and salinity, at levels normally encountered in nature, can influence the stability of AI viruses in water. In addition to improving our understanding on AI transmission within wild aquatic bird populations, the viral response data presented herein provide general trends in viral persistence that are potentially applicable to improving existing surveillance efforts

Exotic Newcastle Disease Report and National Wild Bird AI Surveillance: U.S. Department of Interior (DOI), U.S. Geological Survey (USGS)

Dr. Scott Wright, USGS National Wildlife Health Center reported that beginning in mid July 2008, there were reports of dead double-crested cormorants in south central Minnesota. The birds were found on islands in lakes surrounded by agricultural areas. The National Wildlife Health Center detected avian

paramyxovirus from the birds and the National Veterinary Service Laboratory (NVSL) determined that the birds had virulent Newcastle disease virus. Additional outbreaks also occurred in northern Minnesota at the U.S.-Canada border. Officials in Canada were notified of the die-offs and began testing birds in Canada. There have been other outbreaks in cormorants reported in Connecticut and Missouri. These have been single birds well away from the larger outbreaks and there is not a clear idea how these birds were infected. Other species, white pelicans and ring-billed gulls have also been culture positive in multiple organs; however, there is no histologic evidence of disease. The last large long term die-off also occurred in the Midwest in 1992.

There have been over 61,000 birds tested in the DOI portion of the national AI surveillance program since the beginning of the program in 2006. No highly pathogenic avian influenza H5N1 Asian strain has been detected in North America. There have been many low pathogenicity viruses detected. These viruses have occurred at a prevalence rate of 2.3 percent. Nearly every H serotype and all N serotypes have been detected through virus isolation. At least 5 new species of waterfowl were found with low pathogenicity viruses. Through genetic sequencing of a portion of the viruses there is a higher rate of viruses with Asian lineage than with European lineage that have mixed with North American viruses detected in birds samples in Alaska.

There has been a collaborative effort with USDA to examine the efficiency of molecular tests used for the rapid detection if avian influenza viruses. This has led to a modification of the H7 test. There has also been an examination into the presence of avian influenza viruses in sediments in freshwater lakes in the Southeastern United States. Viruses were detected in the sediments but not water in lakes in Georgia, suggesting that the viruses can persist in water warmer than previously demonstrated in laboratory experiments.

National Wild Bird AI Surveillance: APHIS-Wildlife Services (WS)

Tom Deliberto, APHIS- WS, reported that as part of the government-wide National Strategy for Pandemic Influenza, USDA-APHIS, DOI, and state wildlife agencies provided leadership in conducting surveillance for the early detection of highly pathogenic avian influenza (HPAI) in wild birds. Within APHIS, WS was delegated the responsibility for plan development, implementation, and oversight. WS, in collaboration with State Wildlife Agencies, DOI, and U.S. Department of Health and Human Services (USHHS), and other entities such as the Southeastern Cooperative Wildlife Disease Study (SCWDS), developed An Early Detection System for Highly Pathogenic H5N1 Avian Influenza in Wild Migratory Birds, U.S. Interagency Strategic Plan (U.S. Strategic Plan).

The initiative is divided into two phases. The initial phase addressed early detection activities in Alaska, and in particular, coastal areas that have the most potential for contact among Asian and North American birds. The second phase addresses subsequent HPAI detection activities in four major North American flyways. The plan for wild bird surveillance includes several interrelated components, including: the investigation of morbidity/mortality events, the sampling of live-captured birds, the deployment of sentinel species, environmental sampling; and sampling hunter-harvested birds.

WS developed a rating system designed to place more surveillance activities in locations that have a higher probability of detecting the virus. However, no state was excluded. The rating system was first developed internally using criteria such as migratory bird movements, historic avian influenza prevalence, wetland habitat and linear shoreline and geographic location. After the preliminary rating system was developed, WS sought input from each of the Flyway Councils and the Association of Fish and Wildlife Agencies. This input was incorporated into the WS, HPAI Implementation Plan, finalizing the process to support State Wildlife Agencies in sample collection efforts.

APHIS is collaborating with other federal agencies and state officials conduct surveillance in wild, migratory birds and cross training to improve surveillance strategies. To date, over 150,000 wild birds and 75,000 environmental samples have been tested for HPAI through the APHIS funded program. The DOI and others have tested approximately 50,000 wild birds to date. The current year's APHIS plan is to collect and analyze 50,000 wild birds and test 25,000 environmental samples through a targeted surveillance approach. Detailed information can be found in WS' Implementation Plan for HPAI Surveillance in Wild Migratory Birds in the United States. The targeted surveillance approach will provide a better protective measure for the early detection of HPAI by sampling high value species using live-wild bird and hunter-harvest methods. Additionally, environmental fecal sample collection will be focused in areas used by migratory birds. This targeted approach leads to cost efficiency by collecting smaller sample sizes while maintaining integrity of the science-based approach.

While targeted, surveillance using live wild birds, hunter harvested birds, and environmental sampling is an important component of the surveillance effort. Sampling morbidity/mortality events remains the most important sampling method in the program. It is recommended that all morbidity/mortality events in wild birds be evaluated for HPAI sampling, regardless of the species involved.

In partnership with all 50 State Wildlife Agencies, WS accomplished a majority of sampling during the 2007 fall migration and on wintering grounds of migratory birds, but efforts continued through the 2008 spring migration and on breeding grounds in Alaska. Surveillance activities are being increased during the current 2008 fall migration. Surveillance is conducted in all 4 major flyways - Pacific, Central, Mississippi, and Atlantic; all 50 States, Guam, and Puerto Rico; and other countries. Diagnostic testing of all wild bird samples collected in the U.S. is conducted through 47 National Animal Health Laboratory Network (NAHLN) laboratories and environmental samples are tested at WS, National Wildlife Research Center. Confirmatory testing of all samples is conducted at the NVSL.

Committee Business:

A single draft Resolution on wildlife immunocontraception was tabled until next year when the Committee hopes to be briefed on the status of research and licensing of products.

PASTEURELLOSIS TRANSMISSION RISKS BETWEEN DOMESTIC AND WILD SHEEP

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Introduction

Disease has contributed significantly to the decline of bighorn sheep (*Ovis canadensis*) populations throughout much of western North America, decreasing many native herds to less than 10% of their historical size and imperiling some populations and subspecies (Valdez and Krausman 1999). According to historical accounts (e.g., Grinnell 1928; Honess and Frost 1942; Shillinger 1937; Warren 1910), epidemics in some locations coincided with the advent of domestic livestock grazing in bighorn ranges, suggesting that novel pathogens may have been introduced into some bighorn populations beginning in the 1800s.

Native North American wild sheep species—bighorn sheep and thinhorn (Dall's and Stone's) sheep (*O. dalli*)—are very susceptible to pneumonia and particularly to pasteurellosis (Miller 2001). The generic term pasteurellosis is used here for disease (often respiratory) caused by bacteria in the family *Pasteurellaceae* but now classified in the genera *Pasteurella*, *Mannheimia*, or *Bibersteinia*. In some recent pneumonia epidemics in bighorns, the cause has been attributed to endemic respiratory pathogens or strains of *Pasteurellaceae* (Rudolph et al. 2007), and in other epidemics the cause has been attributed to *Pasteurellaceae* strains or other pathogens introduced via interactions with domestic sheep (*O. aires*; George et al. 2008). This Commentary reviews current knowledge on pneumonic pasteurellosis in domestic and wild sheep, the risks of transmission between these species, and approaches for lowering the overall risk of epidemics in wild sheep.

Pneumonic Pasteurellosis in Domestic Sheep

Respiratory disease is a serious problem in domestic sheep that can result in substantial economic losses. Pneumonia in domestic sheep is more common in lambs than in adults, and affected animals often die if not treated.

Pasteurellosis in domestic sheep often is described as a disease complex (Alley,Ionas, and Clarke 1999; Donachie 2007; Gilmour and Gilmour 1989) and generally is thought to result from invasion of the lung by *Pasteurellaceae* following a compromise of the respiratory tract. The initiating insult can be from respiratory infection by mildly pathogenic agents such as parainfluenza-3 (PI-3) virus, adenoviruses, respiratory syncytial viruses (RSV), *Chlamydia pecorumi*, and *Mycoplasma ovipneumoniae*, as well as from mechanical irritants such as dust (Alley, Ionas, and Clarke 1999; Brogden, Lehmkuhl, and Cutlip 1998; Donachie 2007) and lungworms. In most instances, these insults alone do not result in significant epidemics with high morbidity or mortality; however, when these and other stressors are compounded by infection with *Pasteurellaceae*, the result can be increased disease and death.

The effects of psychological, physiological, and physical environmental stressors are believed to be important components of pasteurellosis in many domestic ruminants (Brogden, Lehmkuhl, and Cutlip 1998; Carroll and Forsberg 2007; Donachie 2007; Gilmour and Gilmour 1989). Although the effects of

stressors are difficult to measure, some indicators including increased body temperature, heart rate, and plasma cortisol have been correlated with disease (Carroll and Forsberg 2007; Knowles et al. 1995).

Physiological response to stressors (collectively called "stress") includes suppression of the immune system; consequently, prolonged stress may increase susceptibility to pathogens and to morbidity and mortality. Environmental stressors most commonly associated with pasteurellosis in livestock include heat, cold, wind chill, crowding, mixing with new animals, poor ventilation, handling, and transport (Brogden, Lehmkuhl, and Cutlip 1998; Carroll and Forsberg 2007; Knowles et al. 1995). Other predisposing factors, such as lack of sufficient energy or protein, inadequate colostrum consumption, specific vitamins, or certain minerals, also may compromise immunity further (Carroll and Forsberg 2007).

Pasteurella multocida, *Mannheimia haemolytica*, and *Bibersteinia trehalosi* (all formerly in the genus *Pasteurella*) are the three most commonly isolated bacterial agents from pneumonias that result in high rates of illness, morbidity, and mortality in domestic sheep (Brogden, Lehmkuhl, and Cutlip 1998; Donachie 2007; Gilmour and Gilmour 1989). Early treatment with antibiotics effective against *Pasteurellaceae* generally stops a pneumonia outbreak, suggesting that these bacteria are important in the disease process. *Pasteurellaceae* are common inhabitants of the tonsils and oropharynx of a variety of healthy domestic and wild species (Gilmour, Thompson, and Fraser 1974; Jaworski, Hunter, and Ward 1998). In domestic sheep, *Pasteurellaceae* are believed to be opportunistic bacteria that colonize the lung after some predisposing insult (Brogden, Lehmkuhl, and Cutlip 1998). Some *Pasteurellaceae* strains make products (including leukotoxin and endotoxin) that exacerbate disease in the host after colonization of lung tissue (Ackermann and Brogden 2000; Gilmour and Gilmour 1989) and result in increased morbidity and mortality.

The diversity of commensal and disease-associated *Pasteurellaceae* further complicates the epidemiology and control of pasteurellosis. Serotyping and phenotyping based on variations in fermentation patterns (Angen et al. 1999; Frank 1982; Jaworski, Hunter, and Ward 1998) and gene sequencing (Angen et al. 1999; Jaworski et al. 1993; Kelley et al. 2007) have been used to distinguish among *Pasteurellaceae* strains. Studies using these approaches have shown that domestic sheep may carry numerous strains of *Pasteurellaceae* (Jaworski, Hunter, and Ward 1998; Ward et al. 1997).

Most *Pasteurellaceae* of sheep are obligate bacteria that die rapidly in the environment outside a living host (Dixon et al. 2002). Environmental sources such as water and soil are not thought to be important in maintaining or spreading these bacteria; consequently, transmission is most likely to occur through direct contact among animals. Because many healthy domestic sheep carry strains associated with disease (Jaworski, Hunter, and Ward 1998), transmission of a specific pathogenic *Pasteurellaceae* strain may not be necessary for a disease outbreak to occur. In some instances, however, mixing individuals from different sources and possibly carrying different strains of *Pasteurellaceae* seems to precipitate outbreaks (Gilmour and Gilmour 1989).

Pasteurellosis in Wild Sheep

As in domestic sheep, *Pasteurellaceae* commonly are associated with pneumonia epidemics in bighorn sheep (Miller 2001), and pasteurellosis frequently results in both all-age die-offs and persistent high rates of pneumonia in lambs (Cassirer and Sinclair 2007; Monello, Murray, and Cassirer 2001). Thinhorn sheep also are susceptible to pneumonia (Black et al. 1988; Foreyt, Silflow, and Lagerquist 1996; Jenkins et al. 2007), but epidemics have not been reported in free-ranging populations.

Pasteurellaceae alone seem to have a more severe effect on wild sheep than on domestic sheep in experimental situations. Wild sheep experience high morbidity and mortality after being intratracheally or intradermally inoculated with relatively high doses (10^4 organisms) of field strains or attenuated strains of *M. haemolytica* from domestic sheep or cattle (*Bos taurus*), or with *B. trehalosi* strains originating from other wild sheep (Foreyt, Silflow, and Lagerquist 1996; Foreyt, Snipes, and Kasten 1994; Onderka, Rawluk, and Wishart 1988). The resulting pathology from experimental inoculations of wild sheep varied among strains used, but all strains caused some form of pneumonia. The observed differences in susceptibility to experimental and natural pasteurellosis between domestic and wild sheep are thought to result from differences in pulmonary host defense mechanisms and greater vulnerability of phagocytes to leukotoxin that apparently increase overall susceptibility to pasteurellosis (Foreyt, Silflow, and Lagerquist 1996; Silflow, Foreyt, and Leid 1993; Silflow et al. 1989).

Pasteurellaceae have been isolated from both healthy and pneumonic wild sheep (Jaworski, Hunter, and Ward 1998; Jenkins et al. 2007; Kelley et al. 2007; Rudolph et al. 2007). Although field investigations often are complicated by delays in detecting cases and by sample availability, two broad epidemic

patterns in bighorns have emerged. In some bighorn epidemics, endemic respiratory pathogens including *Pasteurellaceae*, PI-3, RSV, and *M. ovipneumoniae*, as well as lungworms (*Protostrongylus* spp.), with or without other environmental stressors, are believed to have contributed to disease (Rudolph et al. 2007; Spraker et al. 1986). These outbreaks resemble the patterns described in some pasteurellosis epidemics in feedlot lambs (Gilmour and Gilmour 1989). Other epidemics, however, are believed to have been initiated by introductions of novel respiratory pathogens into bighorn populations (Foreyt and Jessup 1982; George et al. 2008). These patterns resemble some pasteurellosis epidemics reported in domestic sheep, particularly feedlot lambs, after transportation and mixing of different groups in confinement settings (Gilmour and Gilmour 1989). Thus, both endemic and introduced pathogens are believed to contribute to contemporary pasteurellosis epidemics in bighorn sheep.

Risks to Wild Sheep Associated with Domestic Sheep Interactions

Based on evidence from empirical studies and field observations, interactions between wild sheep and domestic sheep increase the probability of mortality and reduced lamb survival in wild sheep populations, primarily because of respiratory disease (USDA–Forest Service [FS] – 2006). Interactions between wild sheep and domestic goats (*Capra hircus*), although not as widely reported, seem to pose comparable risks (Garde et al. 2005; Jansen et al. 2006). Similarities in social behavior and physiology between wild and domestic sheep (and, to a lesser extent, goats) probably create a natural attraction that fosters intimate contact between these species.

Pneumonia in wild sheep developed after contact with domestic sheep in captive conditions (Black et al. 1988; Callan et al. 1991; Foreyt 1989; Onderka and Wishart 1988). Moreover, relationships between the onset of some pneumonia epidemics in wild sheep and the concurrent presence of domestic sheep on bighorn ranges have been described (George et al. 2008; Monello, Murray, and Cassirer 2001). Whether introduced *Pasteurellaceae* strains, introduced virulence factors, or other introduced pathogens contribute to precipitating these epidemics remains unclear (Besser et al. 2008; George et al. 2008; Kelley et al. 2007).

Quantifying the risk of interspecies disease transmission between wild sheep and domestic sheep in a natural setting is problematic. Movements of wild sheep may influence the potential for pathogen introductions and transmission from domestic to wild sheep, as may the proximity, duration, movements, management, seasonality, reproductive status, and straying rates of domestic sheep grazing in occupied wild sheep habitats. The increased risk of a pneumonia epidemic in a wild sheep population associated with domestic sheep interaction seems to be the product of the probabilities of multiple events, namely: interactions of sufficient duration and proximity to transmit one or more pathogens; pathogen shedding by the domestic sheep; the ability to transmit an infectious dose to one or more wild sheep; the survival of newly infected wild sheep; and, further shedding and secondary transmission. Seasonal or environmental factors also may somehow modulate the probability of epidemics occurring (Cassirer and Sinclair 2007; George et al. 2008), and the risk attributable to interactions between these species probably is additive and may vary widely among wild sheep populations. Indeed, a common *Pasteurellaceae* strain or other agent directly linking bighorn epidemics to either domestic sheep interactions or to emergence of endemic pathogens has not been demonstrated to date, and thus unequivocal evidence for either process remains elusive. Consequently, the magnitude of such risks may be assessed best on a case-by-case basis (Clifford et al. 2007; Garde et al. 2005). Further work is needed to understand better the magnitude of potential risk to wild sheep arising from interactions with domestic goats, cattle, and other wild ruminant species, as well as potential influences of seasonal and environmental factors on these risks.

Strategies for Minimizing Risk of Interspecies Disease
Transmission and Managing Wild Sheep Health

Available data suggest that interactions between wild and domestic sheep carry some inherent risk of precipitating pneumonia in wild sheep under range conditions (USDA–FS 2006). Given the limitations of today's tools, the most practical approaches identified thus far for minimizing this risk involve simply preventing interspecies interactions that could result in respiratory pathogen transmission between wild and domestic sheep (Western Association Fish and Wildlife Agencies [WAFWA] – 2007). Incomplete knowledge about the epidemiology and some details of processes contributing to the risk of interspecies disease transmission, however, remains an obstacle to consensus on acceptable and "best" management approaches.

To achieve effective separation (i.e., separation sufficient to minimize opportunities for pathogen transmission [WAFWA 2007]), herdsmen and wildlife managers can actively discourage wild sheep from approaching or commingling with domestic sheep, and vice versa. Domestic sheep should be monitored closely and herded to prevent straying and should not be left unattended in wild sheep habitats. In some instances, truck transport may be the best means for moving domestic sheep through critical wild sheep habitats. Similarly, wild sheep that have contacted domestic sheep should not be left to commingle with other wild sheep. On common public lands, land management agencies, wildlife agencies, and domestic sheep producers with grazing leases should develop and agree on plans for handling interactions between the species, with emphasis on preventing interactions that could result in respiratory pathogen transmission between domestic and wild sheep. Ideally, similar plans also should be established between private landowners and wildlife managers where wild sheep may stray onto private land.

The risk of interspecies pathogen transmission may be decreased further by ensuring that domestic sheep grazing in wild sheep habitats are healthy and by removing ill sheep of either species. As vaccines and therapeutics for the prevention and control of infection or disease caused by *Pasteurellaceae* in domestic or wild sheep become available, producers and wildlife managers should seek practical ways to use them. In some instances where these approaches are not effective, one species or the other may need to be given management priority in, or excluded from, a particular range (WAFWA 2007).

Although seemingly simple, the latter approach has several potential consequences, including lack of rangeland available to one or the other species, economic impacts, and limitations on restoration efforts. Not all pasteurellosis epidemics in bighorn sheep can be attributed to contact with domestic sheep (USDA–FS 2006). Because some potentially pathogenic *Pasteurellaceae* and other pathogens are endemic in some wild sheep populations, wildlife managers should examine the implications of interactions between different herds of wild sheep. In doing so, the benefits of outbreeding and genetic diversity must be weighed against the increased risk of disease transmission (WAFWA 2007). In certain instances, wild sheep may need to be maintained at herd densities that minimize dispersal to help lower the risk of pathogen spread.

Augmenting wild sheep herds with individuals from other herds also poses a risk for moving pathogens. Consequently, wildlife managers should recognize the potential for moving pathogens via translocations and should monitor wild sheep herds routinely for pathogens of concern, using only healthy herds as source stock. Protocols for sampling, testing for transplant, and responding to disease outbreaks should be standardized to the extent possible and reviewed and updated as necessary. Moreover, data should be shared and interagency and interdisciplinary communications should be encouraged to develop better strategies for improving overall herd health.

Research Needs

Current understanding about causative agents and the factors allowing these agents to lead to pasteurellosis epidemics in wild sheep is incomplete. Previous work, however, provides some clarity for future research directions. Further study of mechanisms underlying the increased susceptibility of wild sheep to respiratory diseases, as compared with domestic sheep and cattle, could aid in developing and refining approaches for improving and maintaining herd health. For developing better disease prevention and control strategies, more information is needed concerning host genetics and immune responses, virulence mechanisms, pathogen transmission dynamics, and the epidemiology of the diseases. The full influence and potential for control or mitigation of other factors such as environmental stressors and nutrition, which seem important in pasteurellosis epidemics in domestic ruminants, also need to be understood better for wild sheep.

Developing methods that decrease the occurrence or severity of pneumonia and pasteurellosis in either domestic or wild sheep, including the development and use of vaccines, immunostimulants, or long-acting therapeutic agents, might lead to advances in managing all impacted species. Outcomes of such research could help decrease risks posed by interspecies interactions, or decrease wild sheep susceptibility to pathogens. In developing biologic and therapeutic agents as tools, the research should focus not only on safety and efficacy of the products, but also on the potential for practical use in free-ranging populations.

Conclusions

Although the authors acknowledge that the current understanding about pasteurellosis in wild and domestic sheep is incomplete, respiratory disease clearly is a serious problem in both. Because the

onset of some pneumonia epidemics in bighorn sheep has been associated with the presence of domestic sheep on native range, and because other outbreaks seem to have resulted from pathogens already endemic in affected wild sheep herds, accurately quantifying the risk of interspecies disease transmission in range conditions is problematic. Consequently, a broad approach to population health management currently may be the most practical way to decrease the overall likelihood of epidemics in wild sheep populations. Such an approach includes, but does not rely solely on, practices that prevent interactions between wild and domestic sheep that could result in respiratory pathogen transmission. Preventing contact between wild and domestic sheep, better monitoring of exchanges and interactions between wild sheep populations, and managing population and habitat quality all have some value in improving and maintaining the overall health of wild sheep populations and preventing pneumonia epidemics. Ongoing and planned research also is likely to provide a better understanding and new tools that may further improve approaches for wild and domestic sheep health management on native ranges.

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