

REPORT OF THE COMMITTEE ON WILDLIFE DISEASES

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The Committee met from 12:30-5:30 PM on October 21 at John Ascuaga's Hotel, Reno, Nevada. At least 109 people attended, including 44 committee members. Reports were provided concerning ongoing and emerging health issues involving wildlife and of interest to the United States Animal Health Association (USAHA) and its members. Summaries of the reports follow.

Avian influenza virus research studies

Dr. Justin Brown, Southeastern Cooperative Wildlife Disease Study (SCWDS) provided a summary to the committee on the collaborative research being conducted at SCWDS and the Southeast Poultry Research Laboratory, Agriculture Research Service (ARS), U.S. Department of Agriculture (USDA) on H5N1 highly pathogenic avian influenza (HPAI) virus transmission in wild birds. Specifically, he discussed two projects which evaluated: 1) the species-related differences in susceptibility and viral shedding among wild avian species in the Orders Anseriformes and Charadriiformes; and 2) the concentration of virus required to produce infection and death in wood ducks (*Aix sponsa*).

To evaluate the potential for H5N1 HPAI viruses to be maintained in wild avian populations, the morbidity, mortality, and extent and duration of viral shedding in eleven species of anseriforms and two species of charadriiforms were assessed after intranasal (IN) challenge with an Asian H5N1 HPAI virus. Species-related differences in morbidity, mortality, viral shedding, and viral distribution exist between the examined species. Based on these differences, the thirteen species were separated into four general categories of susceptibility: 1) 100 percent mortality within two days with viral antigen present in the endothelial cells throughout the body and/or parenchymal cells of numerous visceral organs and brain (black swans *Cygnus atratus*); 2) 100 percent mortality within 4 to 7 days with viral antigen located in the parenchymal cells of numerous visceral organs and brain (mute swans *Cygnus olor*, trumpeter swans *Cygnus buccinator*, and whooper swans *Cygnus cygnus*); 3) high morbidity and variable mortality with viral antigen primarily located in the parenchymal cells of the brain, adrenal gland, and pancreas (herring gulls *Larus argentatus*, laughing gulls *Larus atricilla*, wood ducks, bar-headed geese *Anser indicus*, and cackling geese *Branta hutchinsii*); and 4) no mortality or detectable viral antigen (mallards *Anas platyrhynchos*, blue-winged teal *Anas discors*, redheads *Aythya americana*, Northern pintails *Anas acuta*). As with previous studies on H5N1 HPAI virus infection in waterfowl, viral titers were higher in oropharyngeal (OP) swabs than cloacal swabs, and generally, titers were positively associated with the susceptibility of a species: the highest viral titers were excreted by the most susceptible species. The results from these experimental infection

trials indicate that H5N1 HPAI viruses are virulent for select wild avian species and this is consistent with field data from outbreaks of H5N1 HPAI throughout Eurasia. Based on this study, viral titers are lower in species that remain asymptomatic compared to those species that exhibit morbidity associated with H5N1 HPAI virus infection. This is consistent with the Eurasian active field surveillance results thus far, in which isolation of H5N1 HPAI virus from clinically healthy wild birds has been extremely rare. Taken together, these experimental and field data suggest that the wild avian species that are affected clinically are the primary species involved in the transmission and spread of H5N1 HPAI viruses in wild bird populations, as opposed to an asymptomatic avian host. Furthermore, these data suggest that an asymptomatic wild bird reservoir for H5N1 HPAI viruses may not exist and that epidemics in Europe during 2005-2006 likely represent spill-over events from domestic poultry into wild birds with limited persistence and transmission within the wild avian population.

In order to further examine the susceptibility of a “highly susceptible” wild bird species, the median bird infectious dose (BID₅₀) and lethal dose (BLD₅₀) of a H5N1 HPAI virus for wood ducks were determined after IN inoculation. The results of this study indicated that wood ducks have a low BID₅₀ and BLD₅₀ of 10^{0.95} EID₅₀ and 10^{1.71} EID₅₀, respectively. These infectious and lethal viral doses are less than those of the domestic chicken, traditionally considered one of the most susceptible avian species to H5N1 HPAI viruses, using the same H5N1 HPAI isolate. These results confirm that wood ducks are highly susceptible to H5N1 HPAI viruses and suggest that wild avian species that appear to be “highly susceptible” to H5N1 HPAI viruses based on field data or experimental infection trials, are truly sensitive to infection with these viruses.

National wild bird avian influenza surveillance – United States Department of Agriculture, (USDA) Animal and Plant Health Inspection Service (APHIS)-Wildlife Services

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

Prior to implementation, Congress appropriated APHIS \$71.5 million in emergency 2006 supplemental funding to address the threat of HPAI throughout the world. Wildlife Services was provided \$17 million to conduct both domestic and international activities regarding surveillance for HPAI in wild, migratory birds and developing capacity to respond to emergency events regarding wildlife and domestic animal health. Congress appropriated \$47.2 million for APHIS in 2007 to continue similar activities in support of the National Strategy for Pandemic Influenza, and WS received \$13 million to fund surveillance activities. Although the Federal FY08 budget currently has not been passed, surveillance activities continue.

Domestic surveillance is divided into two phases. The initial phase addresses early detection activities in Alaska and the second phase addresses subsequent HPAI detection activities in four major North American flyways. The plan for 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. All samples are submitted to the laboratories in the National Animal Health Laboratory Network (NAHLN) for initial screening using real-time, reverse transcription-polymerase chain reaction tests. Following these tests, matrix and H5/H7 positive samples are sent directly to the National Veterinary Services Laboratory (NVSL) for additional testing including virus isolation, subtyping, and molecular sequence characterization.

To date, over 109,000 wild birds and 60,000 environmental samples have been tested for HPAI through the APHIS-funded program. 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.

In June 2007, WS hosted six training workshops to review the current activities and better plan for fall sampling of wild, migratory birds. The workshops, attended by over 180 participants from State Wildlife Agencies, NAHLN laboratories, and WS, greatly improved communication among all partners and increased efficiency regarding surveillance for HPAI.

WS has implemented a reporting system to answer calls and inquires from the public regarding dead or sick wild birds. The toll-free number, 866-4-USDA-WS, has been published on the APHIS website to support public inquires and expedite calls. The calls are tracked through an on-line system to monitor any potential increases in dead or sick bird reports. To support avian influenza surveillance in wild birds, a protocol and decision tree were developed to triage reports of dead or sick birds.

To date, 32 presumptive positive and/or confirmatory test results for the low pathogenic H5N1 avian influenza have been reported from 13 States: Illinois, Maryland, Michigan, Montana, New York, Ohio, Delaware, South Dakota, Missouri, North Carolina, New Jersey, Pennsylvania, and Vermont. In all cases, genetic testing at NVSL ruled out the presence of the strain of HPAI that is circulating overseas. Because low pathogenic avian influenza detections from wild birds are common and pose no threat to human health, USDA transitioned to a new method of notifying the public online. In the event of a presumptive H5N1 test result involving a large number of sick or dead birds, or other circumstances that suggest the possibility of a highly pathogenic virus, USDA in coordination with the State Wildlife Agency, DOI, and HHS will issue a news release or conduct a technical briefing to notify the media and the public.

Avian Influenza in Wild Birds – U.S. Department of the Interior

Christine Bunck, National Wildlife Health Center, reported that interagency surveillance for the early detection of highly pathogenic avian influenza (HPAI) H5N1 in migratory birds began in the spring of 2006 and is continuing into the fall of 2007. The Policy Coordinating Committee of the U.S. Department of Homeland Security directed the U.S. Department of the Interior (DOI) and the USDA, in conjunction with U.S. Department of Health and Human Services, the Association of Fish and Wildlife Agencies, and the state of Alaska to develop an interagency plan for detecting the potential introduction of HPAI H5N1 in the United States. The plan was completed by March 2006 and implemented in the spring of 2006. The plan identified 5 approaches for surveillance in wild migratory birds:

1. Investigating morbidity and mortality events to determine the role (if any) of HPAI H5N1 in the event
2. Sampling apparently healthy migratory birds that were typically captured live and released
3. Sampling apparently healthy migratory birds killed during sport and subsistence hunts as well as management activities
4. Sampling sentinel migratory birds placed in various locations
5. Testing samples of water, soil or bird feces gathered from the environment at various locations where migratory birds congregate

DOI focused primarily on the first three of these approaches. DOI and its partners have conducted investigations of morbidity and mortality events throughout the Nation during 2006 season (1 April 2006 to 31 March 2007) and the 2007 season (1 April 2007 to 31 March 2008). Although live and hunter-harvested migratory birds were sampled throughout North America in both 2006 and 2007, DOI and its partners focused their efforts during the 2006 season on Alaska, the lower Pacific Flyway and the Pacific Islands, and expanded their efforts during the 2007 season to include the Central, Mississippi and Atlantic Flyways.

For surveillance of live birds and hunter-harvested birds in Alaska, the following criteria were used to select priority species:

1. Contact with Asia or birds migrating directly from Asia
2. Contact with location(s) where H5N1 has been found
3. Habitats used in Asia
4. Population size in region of interest
5. Ability to obtain samples

These criteria were stepped down in the Pacific Islands and Flyways to identify priority species. In the lower 48 states, northern pintail, Pacific black brant, Wrangel Island snow geese and

lesser sandhill cranes were priority species. Additional species were added to the priority list for each flyway based on their contact with priority species in Alaska during the winter.

Cloacal and oral-pharyngeal swabs (cloacal swabs only in 2006) were collected from live and hunter-harvested birds; cloacal and tracheal swabs were collected from necropsied carcasses submitted from morbidity and mortality events. Swabs were screened for Avian Influenza (AI) at the U.S. Geological Survey (USGS), National Wildlife Health Center (NWHC) by matrix reverse transcriptase-polymerase chain reaction (RT-PCR) assay. AI-positive samples were then screened for H5 and H7 subtypes. Samples positive for H5 and H7 subtypes were sent to the USDA National Veterinary Services Laboratory for confirmation and further characterization. Swab samples were also inoculated into chicken eggs at the NWHC for virus isolation. Isolated viruses were characterized by sequence analyses at NWHC.

During the 2006 season, DOI and its partners tested samples from 27,295 migratory birds, representing 177 species and 11 orders of birds. Avian influenza was identified by matrix PCR in 741 (2.7 percent) of the birds, representing 26 species and two orders of birds. Positive prevalence rates ranged from 0.35 percent in dunlin to 10.05 percent in green-winged teal. These findings include the first identification of avian influenza in Aleutian tern, pectoral sandpiper, common eider, king eider, spectacled eider, Steller's eider, and glaucous gull.

As of October 11, 2007, 392 viruses have been isolated. Subtype information is currently available for 104 viruses and sequence information is available for 52 viruses. Subtyping and sequencing of samples from the 2006 season is continuing.

Thus far, hemagglutinin subtypes identified include H1-H8, H10, H11, H13, and H16. All nine neuraminidase subtypes have been identified. H5 has been identified in 23 birds and subtypes included 16 H5N2, 4 H5N3, and 3 H5N9. Co-infections of H5 with another hemagglutinin subtype were found in 20 percent of these birds. H5 viruses were identified in geese, mallards, gadwall, pintail, shovelers, and swans as well as several marine coastal species. H7 has been identified in 25 birds and subtypes include 17 H7N3, 1 H7N4, 1 H7N8, 4 H7N7, 1 H7N8 and 1 H7N9. H7 viruses were identified in mallards, teal, shovelers, pintails, geese, and eiders. Preliminary results of sequencing indicate that 8 of the 52 viruses sequenced so far contain RNA segments of Eurasian origin.

In the 2007 season, samples from 8,800 birds have been submitted as of October 11, 2007. These birds include 2,638 subsistence-hunted birds in Alaska; 5,761 live-captured birds in Alaska, the lower Pacific Flyway, Central Flyway, and Pacific Islands; and 401 carcasses from 54 mortality events throughout the Nation from April to October 2007. Details on mortality events can be found on the NWHC web site (<http://www.nwhc.usgs.gov>). Thus far, 134 of the 8,800 birds (1.5 percent) were positive for AI based on matrix PCR. We anticipate a total of >20,000 migratory birds will be tested at NWHC by the end of the 2007 season.

Results of DOI surveillance under the Interagency Strategic Plan, combined with those from USDA surveillance, for the 2006 and 2007 seasons can be viewed at the HPAI Early Detection Data System (HEDDS) found at <http://wildlifedisease.nbii.gov/ai/>.

***Mycoplasma ovipneumoniae* in bighorn sheep**

Dr. Donald Knowles, USDA-ARS, reported that utilizing 16S clone library analysis, conventional bacteriology, PCR, DNA sequencing and serology, a hypothesis was tested that primary infection with one or more currently unidentified agents precede *Mannheimia* or *Pasteurella* spp. infections associated with bronchopneumonia in bighorn sheep. Data from testing this hypothesis demonstrated that *Mycoplasma ovipneumoniae* was a major component of the bacterial flora of pneumonic lungs from bighorn sheep lambs.

Wildlife/Livestock Disease Interactions – Finding Common Ground

Dr. Jim Logan, Wyoming Assistant State Veterinarian, reported that the significance of diseases involving wildlife and livestock has increased conflict between natural resource and livestock interests. The concerns are valid for the potential for disease transmission in either direction between wildlife and livestock. Domestic and wild species frequently share the same habitat and may share several pathogens. This interface creates many complex problems. Unfortunately, these problems

are not always easily solved scientifically and so remedy is sought through political and/or legal channels.

Diseases such as brucellosis in the Greater Yellowstone Area (GYA), Tuberculosis in Michigan, pseudorabies and swine brucellosis in feral swine, and avian influenza are some program diseases of concern to wildlife managers, livestock interests, and regulatory agencies. Other diseases such as bluetongue, vesicular stomatitis, rabies, malignant catarrhal fever, and fever ticks pose a threat to domestic and wild species. In addition, several foreign animal diseases could devastate naïve populations of wild and domestic animals.

The issues surrounding the bighorn sheep/domestic sheep disease interactions are many. There is controversy between wildlife managers and sheep producers regarding the pathogenesis of Bighorn sheep die-offs. Bighorn sheep die-offs have occurred in relation to the presence/proximity of domestic sheep and, conversely, die-offs have occurred in the total absence of domestic sheep. Certainly there are many contributing factors involved in the bighorn sheep die-offs.

It has been recognized at the Bighorn Sheep Disease Workshops that there are “knowledge gaps” and that there is still a need for further study and research to determine the etiology of the respiratory complex diseases associated with the die-offs. We know that *Pasteurella (Mannheimia)* species, viruses, and *Mycoplasma* species have been implicated. It is also known that factors such as stress, weather, parasites, other animals, and nutrition very likely play roles in pathogenesis.

Controversy also exists within this issue pertaining to the loss of grazing allotment opportunities for the domestic sheep industry. Historical grazing allotments are inextricably linked to base property values and mortgage-ability. When grazing allotment usage is curtailed, the viability of a ranch is jeopardized. This has the potential to negatively affect both the private sector rancher and the wildlife interests due to habitat and migration corridor loss if a ranch is subdivided and developed due to better economic opportunity than wool-growing.

Based upon the available literature, limited surveillance and limited research, the domestic sheep industry contends that it is premature to incriminate domestic sheep as the major cause of bighorn sheep disease and herd decline. It is time to encourage appropriate collaborative research and increased surveillance activities on which both wildlife and livestock interests can agree and on which policy decisions can be made.

Agriculture and wildlife interests share common risks/threats such as mutual foreign animal disease risk, loss of land/habitat to urban sprawl and land developments, and animal rights activism. It is imperative that we work together to preserve our common interests. Working together will require extensive cooperation, coordination, communication, and collaboration between several agencies and interest groups. It will also require respect for the responsibilities, authorities, skills, and livelihoods of all partners, and will help to develop trust. The domestic sheep industry asks for cooperation from wildlife interest groups and agencies, the United States Animal Health Association (USAHA), regulatory agencies, land management agencies, Agriculture Research Service (ARS) and Cooperative State Research Education and Extension Service (CSREES) to collaborate on focused efforts to enhance surveillance, diagnostics, epidemiology, and research involving domestic sheep/Bighorn sheep disease transmission, resulting in policy decisions based on the results of these efforts.

Recent Risk Assessments of Bighorn Sheep/Domestic Sheep Disease Interactions

Dr. Mark Drew, Idaho Departments of Agriculture and Fish and Game, reported that currently, bighorn sheep (BHS) populations are less than 5 percent of historic levels. Disease appears to be a major factor in BHS population dynamics, largely through pneumonia associated with *Pasteurella* spp., *Mycoplasma* spp., respiratory viruses, lungworms, and other factors. In general, disease is very difficult, if not impossible to control or manage in free-ranging populations.

The Payette National Forest (PNF) is located in west central Idaho and encompasses 2.3 million acres. The forest is managed for multiple use including timber production, livestock grazing, recreation, and wildlife. The southeast part of the Hells Canyon National Recreation Area is managed by the PNF. In 2003, the Payette National Forest Plan was developed, but the plan was appealed to the Washington, D.C., U.S. Forest Service (USFS) office based largely on lack of management strategies for bighorn sheep. In 2005, the USFS rejected the Payette National Forest Plan and remanded the plan back to PNF Supervisor for revision. The revision required three things for approval, any of which could result in adjustments to domestic livestock grazing allotments:

- Analysis of BHS viability in Hells Canyon Management Area of the Payette National Forest
- Compliance with applicable law and regulation, specifically the Hells Canyon National Recreation Act
- A supplemental Environmental Impact Statement (EIS) for the revised Forest Plan

In order to comply with the decision of the USFS, the Payette National Forest Supervisor initiated a process to gather the needed information. The process consisted of three steps:

- Review of scientific literature on disease transmission between domestic sheep (DS) and BHS and impacts of disease on BHS populations
- Evaluation of population data for BHS within and near the forest
- Expert panel assessment of risk of disease transmission from DS on grazing allotments to nearby BHS populations

The final report was released on February 6, 2006 and entitled Risk Analysis of Disease Transmission Between Domestic Sheep and Bighorn Sheep on the Payette National Forest. An additional meeting was called by the Payette National Forest Supervisor on November 2, 2006. A Science Panel was convened with two objectives: Clarify the science based concerns regarding the Risk Analysis of Disease Transmission between DS and BHS on the PNF; and allow panelists to provide additional science-based information regarding disease transmission and its risk of occurring on the Payette National Forest for consideration in conjunction with the risk analysis.

The members of the Science Panel represented a diverse group of wildlife and livestock veterinarians, and wildlife and domestic livestock researchers, all with diverse views on bighorn-domestic sheep health issues. At the end of the panel discussion, a set of six statements was developed and unanimously agreed by all panel members as best summarizing existing knowledge about disease transmission and risk in bighorn sheep. Since then, these statements have come to be regarded as potential common ground for further discussing bighorn-domestic sheep (and domestic goat) interactions and disease issues.

The "Payette Principles" are as follows:

- 1.a. Scientific observation and field studies demonstrate that "contact" between domestic sheep and bighorn sheep is possible under range conditions. This contact increases* risk of subsequent bighorn sheep mortality and reduced recruitment, primarily due to respiratory disease. * alternative wording suggested "can increase risk" (A. Rink)
- 1.b. The complete range of mechanisms/causal agents that lead to epizootic disease events cannot be conclusively proven at this point.
- 1.c. 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 potential for disease introduction and transmission.
4. Dispersal, migratory, and exploratory behaviors of individual bighorn sheep traveling between populations may exacerbate potential for disease introductions and transmission.
5. There are factors (e. g., 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, other bacteria, viruses, and other agents may occur in healthy, free-ranging bighorn sheep.

Since the Science Panel meeting, the Payette Principles have been used in numerous settings for discussions about bighorn sheep and domestic sheep disease issues. Subsequent products arising from these discussions include the Western Association of Fish and Wildlife Agencies' (WAFWA) "Recommendations for domestic sheep and domestic goat management in wild sheep habitat"; the American Veterinary Medical Association – "Policy on "Wildlife-livestock interactions" recommended by Animal Agriculture Liaison Committee; and the Council for Agricultural Science and Technology (CAST) – "Commentary on bighorn sheep/domestic sheep disease issue. In addition, two subsequent meetings were held to further discuss these disease issues – The BHS Respiratory Workshop at the University of California-Davis, Davis, California and the bighorn

sheep/domestic sheep Disease Risk Assessment Workshop held in conjunction with The Wildlife Society in Tucson, Arizona.

Dr. Mark Atkinson, Nevada Department of Wildlife reported that in April 2007, a two-day facilitated workshop was held at the University of California, Davis to review the issue of respiratory disease in bighorn sheep (*Ovis canadensis*). Participants representing a broad array of scientific disciplines from both the wildlife and domestic livestock fields convened to discuss current knowledge of respiratory disease, identify gaps in that knowledge and set priorities for future research. Break-out groups discussed the issues of study design, field experimentation, disease risk assessment and analysis, outbreak investigation and research needs. The resulting management and research priorities included issues of identification, characterization, ecology and epidemiology associated with the introduction of novel and/or virulent microorganisms into free-ranging bighorn sheep populations; investigation of social factors impeding acceptance and implementation of current research findings; and development of applicable quantitative risk assessments for bighorn and domestic sheep management. Guidelines for sample collection and analysis for herd health assessment and disease outbreak investigations also were developed and will soon be published.

As a follow-up to this workshop, a one-day meeting focusing on information sharing and practical disease-risk assessment took place in Tucson, Arizona in late September, 2007. The goal of this meeting was to provide biologists, veterinarians, wildlife and wild land managers, domestic sheep producers and other interested parties, with the most current and relevant information pertaining to bighorn sheep health investigation and management. The 'Payette Principles' and the outcomes of the University of California Davis workshop and the Western Association of Fish and Wildlife Agencies (WAFWA) Wild Sheep Working Group were discussed. Several presenters addressed issues raised in the first workshop including the physical problems, costs and concerns of woolgrowers and collaborative approaches for conflict resolution. Participants also received detailed information about the value of performing quantitative disease risk assessment. Workshop details and proceedings are posted on the American Association of Wildlife Veterinarian's website <http://www.aawv.net> and at <http://www.mwvcrc.org/content/view/100/102/>.

A third workshop is scheduled to take place at the Foundation for North American Wild Sheep (FNAWS) 2008 Convention in Salt Lake City. The goals of this workshop are to identify common ground, best management practices and common sense solutions that will serve the conservation of bighorn sheep, while simultaneously promoting best use of public grazing land in the Western US.

Bovine Tuberculosis in Wild Deer in Minnesota

Dr. Linda Glaser, Minnesota Board of Animal Health, reported that bovine tuberculosis (TB) was identified in northwestern Minnesota in 2005 with a total of seven infected beef cattle herds were found and depopulated to date. With the identification of TB in cattle, the Minnesota Department of Natural Resources (DNR) initiated TB surveillance in free-ranging white-tailed deer within a 15 mile radius of any infected cattle farm during the 2005 hunting season. Since then, the DNR also has collected samples from over 6000 deer throughout the state; thirteen deer were positive for bovine TB. All infected deer were collected within five miles of infected cattle farms.

In 2006, after two consecutive years of TB surveillance in hunter-killed deer, the DNR identified a 'TB Management Zone' with a 'Core Area' of concern related to bovine TB in free ranging deer populations. The 'Core Area' encompasses a minimum two mile radius around all TB positive deer identified to date and includes five of the seven infected cattle premises. The habitat in this area supports deer densities of six to eight deer per square mile. It is primarily agricultural land used for cattle grazing and alfalfa production with forested public lands and wetlands managed for wildlife.

The DNR has initiated several measures to reduce potential disease transmission opportunities in this critical area in order to reduce the opportunity for deer to deer or deer to livestock transmission of bovine TB. These measures include:

- A recreational deer feeding ban in a 4000 square mile area around the 'TB Management Zone' effective in November 2006; baiting is already illegal in Minnesota.
- A contract with USDA-Wildlife Services to provide sharp shooters to collect deer in the "Core Area" from February through early April 2007; sharp shooters reduced the estimated deer population in this area by half.
- The DNR worked with eight producers to plan and construct deer-proof fencing of stored feed in 2007; an additional seven producers will have fences constructed next year.

- A new 'Bovine TB permit area' was created around the 'Core Area'. This permit area has special hunts, expanded bag limits, and issues free bonus permits in an effort to increase deer collected by hunters.

TB surveillance in deer collected during the hunting season from a 15 mile radius circle around infected cattle farms will be conducted again in 2007.

Brucellosis in Wildlife in Wyoming

Dr. Terry Kreeger, Wyoming Game and Fish Department reported that elk feedgrounds were begun by Wyoming in the early 20th century to mitigate elk starvation. As brucellosis concerns in cattle increased, the feedgrounds served to prevent commingling of cattle and elk. There are now 23 feedgrounds (22 state and 1 federal), feeding approximately 20,000 elk. Feedgrounds were designed to "shortstop" elk migration routes to prevent them from contacting cattle now occupying traditional elk winter ranges, but feedgrounds concentrated elk facilitating increased disease transmission. Brucellosis seroprevalence on feedgrounds is an order of magnitude higher than in non-feedground elk.

Elk vaccination for brucellosis began in 1985; currently 22 of 23 feedground elk calves are vaccinated annually with Strain 19 vaccine. Although seroprevalence data do not demonstrate statistical differences between vaccinated and unvaccinated elk, vaccination still may be effective in preventing abortions, even though the animals are seropositive. Developing winter habitat can decrease elk dependence on feedgrounds. Since 1990, over 70,000 acres have been improved, but such improvements require lots of time and money.

In 2003 and again in 2004, cattle herds in Wyoming were diagnosed with brucellosis. Epidemiologic investigations implicated infected elk and perhaps bison as the source of infection. Wyoming subsequently lost its federal "brucellosis free" status. Responding to the loss of free status, the governor of Wyoming convened the Wyoming Brucellosis Coordination Team and charged it with identifying issues, describing best management practices, and developing recommendations related to brucellosis in wildlife and livestock in the state. The goal of the Team was to reduce and eventually eliminate brucellosis in wildlife, and specifically address winter elk feedgrounds. After a year of meetings, the Wyoming Brucellosis Coordination Team developed several recommendations, the two most affecting wildlife were: (1) develop Brucellosis Management Action Plans (BMAPs) for each elk herd unit that has a feedground and (2) establish a five-year pilot project to reduce seroprevalence in the region where the first cattle brucellosis cases occurred. The operational definition of "reduction of seroprevalence" was the test and slaughter of feedground elk.

A large corral trap was constructed on the Muddy Creek feedground, the site of the first cattle exposure to brucellosis. The trap was monitored from a blind; when enough female elk were in the trap, the trap gates were remotely closed. Elk were herded into smaller alleyways and chutes for individual processing. Blood samples were taken from adult and yearling females; bulls and calves were ear-tagged and released. Bled elk were held overnight to run serology tests. A temporary laboratory ran serological tests on all cows and yearlings. Testing followed Uniform Methods and Rules (UM&R) criteria: card+, standard plate test+, rivanol+. If one or more result was positive, samples were tested by competitive enzyme-linked immunosorbent assay (cELISA). If the cELISA was positive, the animal was sent to slaughter. Fluorescence polarization assay also was done for validation purposes only. Females considered serologically negative were released. Seropositive elk were shipped to a USDA meat processor and packaged meat was donated to the public. At the processor, multiple tissues were taken for bacterial culture to compare with serologic results. In 2008, two feedgrounds (Muddy Creek and Fall Creek) will be tested.

2006-2007 Results of Test and Slaughter:

2006: 314 total captured; 2 mortalities (1 trap, 1 transit)

2007: 174 total captured; 1 trap mortality

2006: 171 adult and yearling females bled and tested

2007: 79 adult and yearling females bled and tested

2006: 58 (34%) seropositive

2007: 13 (16%) seropositive

2006: 18 (31%) culture positive
2007: 8 (44%) culture positive

Total 2006 costs were \$310,856 (\$5,911 per elk removed)
Total 2007 costs were \$293,319 (\$22,563 per elk removed)

Montana Brucellosis Situation, 2007

Dr. Marty Zaluski, Montana State Veterinarian, reported that the state experienced its first case of brucellosis in cattle since regaining its Class-Free Status in 1985. The index animal was a three year old beef cow that was given as a wedding present from an individual ranching in Emigrant, Montana to a daughter and son-in-law ranching in Bridger, Montana. The animal aborted as a 2 year old within a month of arriving in Bridger, and then again as a three year old. She was subsequently sold through a sale in Billings, Montana for use as an embryo transfer recipient. During export testing, she was found to be a reactor, and further testing revealed 6 additional reactor animals in the index herd. Epidemiological investigation revealed that exposure most likely occurred from elk co-grazing and co-mingling at the Emigrant herd, however, genetic fingerprinting of the *Brucella* strain was not conclusive

Montana is enhancing surveillance by two methods: First, Montana Department of Livestock (MDOL) is working with Montana Fish, Wildlife, & Parks to increase surveillance (blood and tissue) of hunter harvested elk in the area directly north of Yellowstone National Park. Second, MDOL is working with USDA-APHIS to assess risk of brucellosis in Greater Yellowstone Area (GYA) ranches and to enhance the number of herds with herd plans that include brucellosis testing, as well as adult brucellosis vaccination.

Yellowstone National Park Brucellosis Update

Dr. Glenn Plumb, Branch of Natural Resources, Yellowstone National Park, reported that Yellowstone National Park has an active brucellosis risk management program focused primarily on reducing the probability of wild bison commingling on common ranges used by domestic livestock. This management strategy is cooperatively implemented with USDA-APHIS, U.S. Forest Service, Montana Department of Livestock, and Montana Department of Fish, Wildlife and Parks. The action plan has been in place since December 2000.

Seasonal climate variability is a significant ecological driver in the Yellowstone ecosystem causing all native ungulate populations to shift from high elevation summer ranges to lower elevations as snow accumulates in the mountains. The majority of the bison population uses ranges within the park on a year around basis. Portions of the population migrate variable distances, in response to population density and winter severity, to find suitable winter habitats to survive the long cold winters. Bison tend to migrate later than other species and in some years migratory movements outside the National Park can be up to 30 percent of the population. Bison winter range overlaps with livestock range. To reduce the risk of brucellosis transmission from wild bison to domestic livestock, interagency partners actively haze bison away from livestock and when necessary capture and cull portions of the wild bison population. These actions keep the wild bison population within the primary conservation area established by the interagency management plan. The active management period generally runs from October through the winter and ends in June when the bison population returns to high elevation summer range.

During winter 2006-2007, risk management activities were successful in preventing brucellosis transmission from Yellowstone bison to livestock. One hundred twenty five hazing events were conducted to keep bison within the primary conservation area. Nine individual bison were culled because they persistently moved outside the conservation area onto spring livestock ranges. Yellowstone National Park is evaluating the feasibility of remote vaccination of the bison population. An ongoing environmental impact study is showing that the current program to vaccinate young (non-reproducing) bison only during years when risk management operations capture and release individuals will do little to reduce disease prevalence. Uncertainty about the duration of vaccine protection, the effects of vaccinating pregnant animals and the comparability of experimental trials

with expected results in wild populations are driving new efforts to initiate field studies in association with an expanded vaccination program that was directed in the 2000 management plan.

Yellowstone Wildlife Health Program

Plumb reported that wildlife, domestic animals and humans share a large and increasing number of infectious diseases. The continued globalization of society, human population growth, and associated landscape changes will further enhance interfaces between wildlife, domestic animals, and humans, thereby facilitating emergence and resurgence of infectious diseases. Further, habitat loss and other human-caused stresses on ecosystems have reduced the ability of many wildlife populations to recover following declines. The increasing challenges of zoonotic diseases has given new attention to the century-old concept of “the one medicine” because of the need to address these diseases across species if their economic, social and other impacts are to be effectively minimized. The wildlife component of this triad has received inadequate focus in the past. Disease emergence and resurgence has reached unprecedented importance for the sustainability of desired population levels for many wildlife populations and for the long-term survival of some species.

At Yellowstone National Park, the following wildlife diseases are currently, or have the potential to, determine the outcome of the park’s conservation mandate: brucellosis (bison & elk), hantavirus (small mammals), whirling disease (trout), West Nile Virus (birds), chronic wasting disease (elk & deer), Johne’s disease (bison), and highly pathogenic avian influenza (waterfowl and mammals). In response, Yellowstone National Park formed a new partnership with Montana State University and University of California-Davis Wildlife Health Center in 2007 to create the Yellowstone Wildlife Health Program (YWHP), a long term research program focused on understanding and solving priority wildlife health problems in Yellowstone National Park.

With government and private sector funding, the Yellowstone Wildlife Health Program will design and implement a long term wildlife health assessment program to monitor and evaluate wildlife diseases and health indicators; a subcomponent of the Vital Signs Monitoring Program; design and implement a disease surveillance program for priority wildlife disease threats; manage and conduct research on urgent and emergent wildlife disease and ecosystem health issues; prioritize and offer competitive grants for research projects pertaining to wildlife disease and health assessment; provide on-site wildlife veterinary services, including veterinary support for animal handling activities and disease outbreak investigation, including field evaluation, necropsy and specimen sampling; establish and manage an on-site wildlife disease diagnostics and research field laboratory; and facilitate graduate and post-doc research projects on wildlife disease and health.

The Yellowstone Wildlife Health Program (YWHP) operational design includes:

- Program Coordinators—each of the three principle program partners has designated a program coordinator. It is the responsibility of the Program Coordinators to coordinate research and facilitate cooperative efforts involving the three institutions and other program partners;
- Scientific/Stakeholder Advisory Committee - the YWHP will establish a scientific and stakeholder advisory committee to provide guidance to the program; provide a forum for scientific issues and assess the relevance and priority of research efforts among various research and stakeholder communities;
- Resident Ecosystem Health Field Director—a wildlife veterinarian/ecosystem health specialist will be based in the park to manage the Wildlife Health Program and to provide wildlife veterinary support services. The program may hire additional researchers and staff as needed if funding is available;
- Competitive Grants Program for Wildlife Health Research—to involve the best scientists and to include pre-existing regional expertise, the program will annually award grants through a competitive grants program to address both urgent and long term ecosystem health issues including evaluating “vital signs” and protocols. Proposals to the competitive grants program will be reviewed and selected by the advisory committee with the assistance of external reviewers;
- Graduate and Post-Doc Field Research Element—this program element will facilitate research by graduates and post-doctorate researchers to tackle priority wildlife health research projects in the Park.

Chronic Wasting Disease (CWD) Update from USDA-APHIS-Veterinary Services

Dr. Dean Goeldner, USDA-APHIS-Veterinary Services (VS), updated the Committee and began by reporting that in FY 2007 APHIS received approximately \$16.6 million in appropriated CWD funding. All earmarks were removed from the FY07 appropriation that was passed as a yearlong continuing resolution.

CWD Final Rule: In September 2006, APHIS delayed implementation of the final CWD rule that had been published in July 2006. This delay was precipitated by petitions to the rule received from three organizations representing state agencies and officials, including USAHA. On November 3, 2006, APHIS published these petitions for public comment. After reviewing these comments, APHIS requested additional information from the states in late June 2007 regarding their restrictions for the movement of cervids into their states. Based on all the information received, APHIS has begun drafting new proposed rule language and is circulating it internally for review. The primary focus of the changes to the CWD rule will be in the interstate movement restrictions.

CWD Testing: In FY 2007 more than 17,000 farmed and captive cervids were tested for CWD using immunohistochemistry. This is an increase over the recent three year average of approximately 15,000 samples tested. Rectal biopsy evaluation also continues.

Status: There were no additional CWD-positive herds identified nor any CWD positive herds depopulated in FY 2007. At this time, four positive elk herds remain in Colorado and one positive deer herd remains in Wisconsin. Funding from VS continues to offer indemnity and cover depopulation, disposal and testing costs for CWD-positive and exposed herds and trace animals.

Regarding free-ranging cervids, again in FY 2007, \$5 million in CWD cooperative agreement funding was made available to the state wildlife agencies. The tier system developed in consultation with AFWA remained unchanged from FY 2006. Forty-eight states requested funding. Unrequested funds were redistributed to tier one states that requested additional assistance.

APHIS-VS is now in the fifth year of CWD cooperative agreement assistance to state wildlife agencies and our regional epidemiologists report that the work plans for these agreements continue to improve. However, there appear to be increasing needs for alternative surveillance strategies and more effective management strategies.

APHIS-VS again provided \$750,000 to support tribal CWD activities in FY 2007. In addition to the ongoing cooperative agreement with the Native American Fish and Wildlife Society, 23 individual tribes will receive CWD assistance.

For fiscal year 2008, the agriculture appropriations bill has not yet been passed by Congress. However, current indications are that the APHIS line item for CWD will be somewhat decreased from the FY 2007 level, depending on the number of congressional earmarks that are included in the final bill and the amount of funding that is included to cover them. This may mean that there will be somewhat less cooperative agreement funding available to the states and tribes in 2008. APHIS-VS will continue to work with AFWA to assure an equitable distribution of this funding.

Hemorrhagic disease in 2007

Dr. David Stallknecht, Southeastern Cooperative Wildlife Disease Study (SCWDS) reported that SCWDS has received an unprecedented number of samples for virus isolation originating from both penned and wild white-tailed deer this year. As of October 16, 237 virus isolations have been made at SCWDS. This number also is unprecedented and SCWDS continues to receive large numbers of samples as well as telephone reports and inquires every day. Nearly all virus isolations have been epizootic hemorrhagic disease virus-serotype 2 (EHDV-2) from white-tailed deer, although very low numbers of EHDV-1 and Bluetongue Virus (BTV)-10, -11, and -17 viruses have been isolated. EHDV-1, BTV-10, 11 and 17 have been isolated from Missouri and BTV-17 was isolated from a mule deer in New Mexico and pronghorn in Wyoming. The current distribution of isolates is presented below (Figure 1). A distribution map that is updated weekly can be seen at the SCWDS website (www.scwds.org).

Hemorrhagic disease (HD) occurs annually in the United States and as is occurring in 2007, most outbreaks in white-tailed deer are caused by EHDV-2. There is no reason to assume that this outbreak is associated with a particularly virulent strain; EHDV-2 can cause high mortality rates, especially when deer are infected in the northern United States. There are two aspects of this

outbreak that have sparked speculation and discussion. The first involves a potential expansion of the traditional HD range due to climate change and the second involves clinical disease in cattle.

The historic distribution of reported HD, as shown below, includes much of the United States. It is important to note that this distribution map is compiled from reports of clinical disease from 1980-2003 (Figure 2). The map does not represent the entire distribution of HD viruses because infections in white-tailed deer in some areas, such as portions of Texas and Florida, often are subclinical. Based on the historic distribution, it appears that the current outbreak falls primarily within the historic range of HD, although some expansion may be occurring.

Although it is premature to suggest that the 2007 activity is a product of global climate change, we cannot ignore the fact that the Southeastern United States is in an unprecedented drought and that our initial cases in the eastern United States were spatially associated with areas of especially severe drought in Kentucky and Tennessee. But whether the current drought is a result of climate change is an issue yet to be determined. The drought/HD relationship is not new and has been suggested since the 1980's. SCWDS currently is analyzing its historic data to better understand this potential relationship.

Epizootic hemorrhagic disease is not a recognized disease of cattle, but it is well established that they can be infected. There are two contrasting observations that cause confusion related to the issue of clinical disease in cattle. First, as is occurring this year, suspected cattle disease associated with EHDV-2 infection is a common occurrence during large scale EHDV epizootics. Such reports occur routinely when the virus is causing deer mortality in the northern United States. In most cases, cattle show mild disease, but occasional reports of abortion and even death (both unconfirmed) do occur. Such reports are not obtained from HD-endemic areas. Unfortunately, "suspected" cattle cases are seldom confirmed and it needs to be clearly understood that the presence of antibodies in such animals does not confirm EHDV as a cause of either morbidity or mortality. On several occasions, including one this year, we have isolated EHDV-2 from a cow with bluetongue-like disease, but even this may not confirm that the virus was the cause of the disease.

In contrast, clinical disease never has been associated with experimental EHDV infections of cattle, including one SCWDS study (Abdy, M.J., E.W. Howerth, and D.E. Stallknecht. 1999. Experimental infection of calves with epizootic hemorrhagic disease virus. *American Journal of Veterinary Research* 60(5) 621-626). The truth likely lies somewhere between the field observations and the results of these experimental studies and the following hypothesis would fit with the limited data currently available: The reported disease in the field is bluetongue-like and it is not unreasonable to speculate that EHDV would cause similar signs and lesions. With BTV infections, clinical disease in cattle is not common but is mild when it occurs. However, even mild disease is the exception rather than the rule. If EHDV causes a generally mild disease in a very small proportion of those cattle infected, it may well be that the disease would not be detected in the small number of animals included in experimental studies and would only be detected in the field under exceptional challenge conditions as is occurring now. If this hypothesis is correct, EHDV would be of minor concern to cattle producers, but could be responsible for sporadic disease in certain areas of the United States. All reports received at SCWDS concerning suspected disease in cattle have been associated with the northern edge of the HD range (as defined by reported disease in white-tailed deer) and it is possible that such potential problem areas could be defined by vector distribution and herd immunity.

The reports of suspected EHD in cattle and confirmed HD in wild and penned deer can lead to one group of producers/managers blaming the other for their problems. Cattle, wild deer, and penned deer can all be infected with EHDV and can serve as a source of virus to vectors. It is not cattle, penned deer, or wild deer that represent the reservoir for these viruses. Rather, all ungulate species can be involved in viral amplification. In reality, the population dynamics of the biting midge vector, *Culicoides sonorensis*, may be the most important factor in these outbreak situations.

VIRUS ISOLATION CONFIRMED HEMORRHAGIC DISEASE 2007
SOUTHEASTERN COOPERATIVE WILDLIFE DISEASE STUDY
COLLEGE OF VETERINARY MEDICINE
THE UNIVERSITY OF GEORGIA

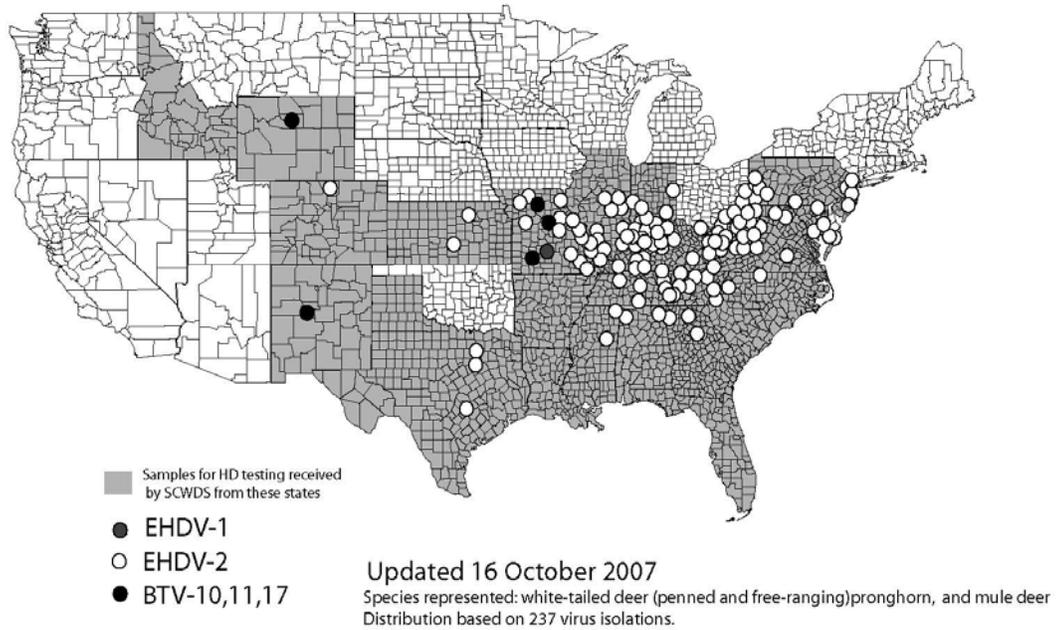


Figure 1. Virus Isolation Confirmed Hemorrhagic Disease, 2007

Hemorrhagic Disease in Deer during 1980-2003

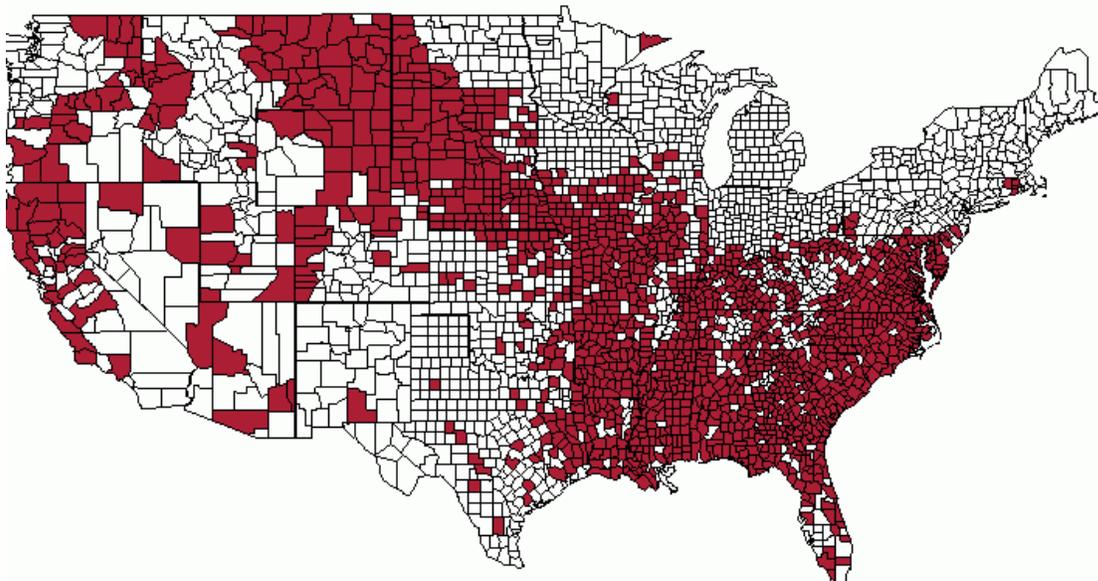


Figure 2. Hemorrhagic Disease in Deer during 1980-2003

Committee business

Six resolutions were approved by the Committee and forwarded to the Committee on Resolutions and Nominations.