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The Committee met on October 4, 2011 at the Adam's Mark Hotel in Buffalo, New York, from 8 Am – 12 noon. There were 33 members and 38 guests present.

### **Pneumonia in Bighorn Sheep**

#### **Peregrine Wolff, Nevada Department of Wildlife**

This review will address what is new in 2011 for the following topics concerning bighorn sheep pneumonia and bighorn sheep / domestic sheep interactions; collaboration with the domestic sheep industry, policy, research, and publications.

Collaborative efforts with the domestic sheep industry:

American Sheep Industry (ASI) task force on bighorn / domestic sheep invited representatives from the state sheep producers, livestock veterinarians, state departments of Agriculture, state and federal land management agencies (USFS and BLM), and state wildlife managers for a meeting , to discuss Strategies For The Coexistence Of Domestic Livestock And Bighorn Sheep On Public And Private Lands. The meeting was held during the national sheep industry convention on January, 20, 2011 in Reno, Nevada. Dr Jim Logan was instrumental in organizing the meeting. The meeting was intended to gather interested individuals together with the goal of taking "... a fresh look at the issue of possible conflict that can arise when domestic and bighorn sheep come in close proximity to one another. The discussion will concentrate on strategies that have proven to be helpful and beneficial in dealing with this conflict, which will hopefully lead to strategies for the coexistence of domestic livestock and wild sheep on public and private lands."

The ASI proposed a coalition that would be formed to develop a working framework" to support the sustainability of domestic sheep grazing operations on public lands across the Western United States while maintaining the viability of bighorn sheep populations where appropriate." This coalition would be made up of representatives from the participating states, sheep industry, and departments of agriculture, wildlife management, and natural resources or public lands management. Representatives of Federal land management agencies and researchers would contribute in an advisory role.

The goal of the coalition would be to develop a framework to be used by state and federal land management agencies to minimize or eliminate conflict between domestic sheep and bighorn sheep.

The January meeting Agenda included presentations on

- Open range, its viability and importance to both species
- Economics of sheep grazing in the west
- Economics and importance of sheep grazing in WY
- Presentation of the WY model for management of domestic sheep and bighorn sheep on public lands
- Western Association of Fish and Wildlife Agencies (WAFWA) and Wild Sheep Foundation perspective
- Research updates

Discussion followed on how to develop a path forward.

A day and one-half follow up meeting was held in June in Denver, CO and included the same mix of participants. The first day included presentations on the following:

- An overview of disease issues
- Updates on research with a focus on vaccination strategies for Pasteurellaceae sps. in bighorn sheep
- Updates from the USFS

Breakout sessions followed where all participants addressed the major critical needs within three categories: research, management and policy.

The groups were fairly consistent in their responses. Summary points within these categories are as follows:

#### Research

- “Managed Separation” allows flexibility (specific habitats, landscapes and situations)
- No new BMPs - synthesis of existing lists
- Evaluate BMP’s “on the landscape,” and under-controlled conditions
- Vaccine for both BHS and DS - emphasis on DS
- Genetic selection of DS that do not shed *M. haemolytica* with high leukotoxin levels. Make a safer domestic sheep
- Genetic selection of BHS for disease resistance survival
- Examine populations of DS and BHS that co-exist w/out die-offs
- The issue must be looked at as a health issue only, not as an issue of public grazing
- Evaluate available data - details and statistics

#### Management:

- All work must be done with trust, honesty and communication
- “Effective Separation” best strategy
- Identify and analyze alternative AUMs or allotments for DS, including “dual use” – (identify currently open allotments for displaced bands of domestic sheep)
- Evaluate BMPs, and quantify what works to stop sheep from wandering into each other’s territory
- What is “acceptable risk” in BHS populations

#### Policy:

- Use state models (WY) for overall management model for the co-existence of domestic and bighorn sheep.
- Collaborative group needed, to create accountability for finding a solution
- Industry (ASI) and advocacy (WSF) collaborate (research / accountability)
- Clarify federal and state policies for BHS management
- Implement policy from D.C. down to state USFS and BLM managers
- Collaboration between USFS, BLM and State Wildlife Managers
- Develop local working groups that include input from all stake holders

The group also agreed on the following Consensus Statement:

*There should be efforts to consolidate existing BMPs, validate (through research) select BMPs and provide BMP recommendations to areas of concern. Recognizing that unique situations require unique solutions, area-specific BMPs should be identified, implemented and monitored. We already have the BMPs identified; they just need to be consolidated into one document that would allow for uniformity, site-specific selection, implementation and necessary monitoring.*

Policy:

H.R. 2584 Appropriations Bill for Department of Interior, Environment and related agencies.

Representative Michael Simpson, Chair of the House Interior and Environment Appropriations Subcommittee added Section 442 to the Appropriations bill.

Domestic livestock grazing sec. 442

None of the funds made available by this Act or any other Act through fiscal year 2016 may be used to plan or carry out any action or any subsequent agency regulation for managing bighorn sheep (whether native or nonnative) populations on any parcel of Federal land (as defined in section 3 of the Healthy Forests Restoration Act of 2003 (16 U.S.C. 6502) if the action may or will result in a reduction in the number of domestic livestock permitted to graze on the parcel or in the distribution of livestock on the parcel.

Both WAFWA and WSF submitted letters to Representative Simpson urging removal of Section 442 from the Bill. The inflammatory nature of the section's language was felt to potentially undermine the major efforts of domestic sheep and bighorn sheep managers to work collaboratively towards insuring that both species have a place on public range lands.

United States Forest Service /Bureau of Land Management

In August a directive from USFS Associate Deputy Chief, Jim Pena directed the forest managers that when making decisions that required National Environmental Policy Act (NEPA) analysis to utilize methodologies used in the Payette analysis (established as the "best available science") to evaluate risk assessment and directive guidelines for developing a bighorn sheep population viability analysis.

The goal of the risk analysis is to current data and science to assess risk of contact (low, moderate, high) based on spatial and temporal overlap between allotments and bighorn sheep herds. The goal of these risk analysis continues to be to provide for separation on forest land if persistence of bighorn sheep populations is a management priority.

Both USFS and BLM are working with states to map wild sheep distribution and vacant/active domestic sheep and goat grazing allotments. In addition to maps habitat modeled by the source habitat models or state specific models will be incorporated where available these maps are critical for conducting and standardizing a qualitative risk assessment for bighorn sheep across the western states.

Research:

Vaccination

Dr. S. Srikumarin, Washington State University, has been working on developing an inactivated vaccine against *M. haemolytica* for use in bighorn sheep populations at risk of encountering domestic sheep. In preliminary trials the vaccine has been shown to be safe and effective when animals are challenged with *M. haemolytica*. Currently the vaccine regimen would require booster every six mos. and delivery of the vaccine into free-ranging populations would be challenging. Dr. Srikumarin is investigating the use of a live vaccine delivered in a pelleted food source.

Sinus tumors of rocky mountain bighorn sheep in Colorado

Dr. Karen Fox, Colorado State University, has been investigating the incidence of sinus tumors recognized in a number of herds of RMBHS in Colorado. Tumors have been found within maxillary, frontal and corneal sinuses in up to 25% of examined heads from select herds. The condition appears somewhat similar to enzootic nasal tumor virus a disease of domestic sheep and goats. Further studies are needed to determine the causative agent and the prevalence in herds within and outside of Colorado. Dr. Fox is currently seeking samples from both affected and unaffected animals.

A number of publications have been published in 2010 / 2011, which addresses bighorn sheep pneumonia. These publications are available on the University of California (Davis) Wildlife Health Center website dedicated to Wild and Domestic Sheep Disease.

<http://www.mwvcrc.org/content/view/122/102>

Cassaigne, I.G., R.A. Medellin and J.A. Guasco. 2010. Mortality during epizootics in bighorn sheep: effects of initial populations size and cause. *Journal of Wildlife Diseases*, 46(3), pp. 763-771.

Miller, M.W. and L.L. Wolfe. 2011. Pasteurellaceae from Colorado Bighorn Sheep Herds. *Journal of Wildlife Diseases*, 47(3), 2011, pp. 800–804.

Wehausen, J.D., T. Scott, T. Kelley, and R.R. Ramey, II. 2011. Domestic sheep, bighorn sheep, and respiratory disease: a review of the experimental evidence. *California Fish and Game* 97(1):7-24.

### **Management of Brucellosis in Elk and Bison in Wyoming**

Terry Kreeger, Wyoming Game and Fish Department

In compliance with the newly-developed Designated Surveillance Area, the Wyoming Game and Fish Department, in coordination with the Wyoming Livestock Board, will conduct enhanced surveillance for brucellosis in elk. The surveillance will be concentrated around the periphery of the DSA and will be comprised of three tiers of decreasing priority. Tier One, the highest priority, will focus on the southern boundary of the DSA where there is currently little data on elk seroprevalence. Surveillance will be conducted through a combination of hunter blood kits and additional personnel to sample elk in the field.

### **Update on Chronic Wasting Disease in the United States**

Tom Gidlewski, USDA, APHIS, National Wildlife Research Center

It has been roughly a decade since we learned that chronic wasting disease (CWD) is not confined to Colorado and Wyoming. During this time funds were made available for extensive wildlife surveillance for CWD and numerous infected areas were discovered. This 2011 update on chronic wasting disease in the United States reviews the current status of infected states including the rate of disease spread as well as the success of management efforts. CWD current and applied research is reviewed. It appears that elimination of CWD in established populations is very unlikely and future efforts need to be directed toward minimizing the spread of the disease into unaffected areas. Hunters are apparently unwilling to participate in the drastic efforts necessary to severely reduce a cervid population to the level necessary to affect CWD transmission. We now know that the CWD agent is readily excreted in clinical animals and persists in the environment markedly facilitating transmission. Hopefully, technological advances such as vaccination will provide the necessary tools for intervention.

### **How can we do more with less? Techniques to increase efficiency of chronic wasting disease surveillance**

Dr. Daniel P. Walsh, National Wildlife Health Center, United States Geological Survey

With drastic reductions in resource allocations for chronic wasting disease (CWD) surveillance, pressure has been placed upon wildlife management agencies to continue to conduct necessary and oft times mandated disease surveillance efforts with minimal budgets. Under these constraints, there is an increasing demand for efficient and economical surveillance systems for disease detection among wildlife managers. In an effort to meet these needs, we developed a weighted surveillance system for use in detection of CWD in regions where it presently is not known to occur. Our weighted surveillance approach exploits inherent differences in prevalence among demographic groups arising from the CWD disease processes and dynamics to increase efficiency in disease detection. We employ a Bayesian statistical estimation procedure that allows us to account for the uncertainty in estimates of these inherent differences within a rigorous framework. The overall structure of our weighted surveillance technique is constructed using a “points” system, which allows for samples to enter the CWD surveillance stream from multiple sources, while being intuitive and easily applied by wildlife managers. We believe that our weighted surveillance approach provides a viable alternative to traditional surveillance approaches, and because of its potential to increase efficiency and thereby produce economic benefits; it represents the next step in the evolution of CWD surveillance.

### **Enteric Pathogens, Wildlife, and Public Health: an emerging issue for wildlife, agriculture and public health agencies**

Colin Gillin<sup>1</sup>, Anne Justice-Allen<sup>2</sup>, Julia Burco<sup>1</sup>, Sarah Smolley<sup>3</sup>, Oregon Department of Fish and Wildlife<sup>1</sup>, Arizona Game and Fish Department<sup>2</sup>, University of California, Davis School of Veterinary Medicine<sup>3</sup>

According to the Centers for Disease Control and Prevention, food-borne intestinal disease in the U.S. affects 1 in 6 US citizens annually (48 million), with 128,000 people hospitalized, and 3,000 deaths. Enteric disease from food-borne pathogens is often widespread due to the extensive and well-structured food distribution system within the US. Overall, rates have been declining for the past 10 years for disease due to the 4 of 5 (*Campylobacter*, *E. coli* O157, *Listeria*, *Salmonella*) major pathogens with food-borne disease due to *Vibrio* increasing.

The most common food-borne disease pathogens tracked by the CDC are *Campylobacter*, *E. coli* O157, *Listeria*, *Salmonella*, and *Vibrio*. Of these, 11 % of the outbreak infections were caused by *Salmonella* spp. followed by *Campylobacter* spp.. Thirty-five percent of the cases resulted in hospitalizations and were caused by non-typhoidal *Salmonella* with 15 % caused by *Campylobacter* spp.. Cases of enteric infection that resulted in death involved 28 % from non-typhoidal *Salmonella* and 19 % from *Listeria monocytogenes*.

Recent efforts by produce growers and buyers and other stakeholders has led to agreements to improve food safety. In 2007, California and Arizona developed and enrolled producers in Leafy Green Marketing Agreements. These agreements describe Best Management Practices (BMP) and Good Agricultural Practices and Metrics that detail an audit procedure throughout the production and food distribution process. It requires actions in response to identified risks such as wildlife or domestic animal tracks or fecal material found in fields at audit, and flood events or the occurrence of increased risk land use practices (livestock, flood irrigation) on adjacent lands and field worker hygiene. Animals such as deer, swine, cattle, goats, and sheep are considered animals of significant risk and identification of animals or animal sign on crop land areas is analyzed by a trained auditor. Testing is required for many situations where food safety security has been compromised.

As part of this risk determination, Hazard Analysis Critical Control Point (HACCP) plans are used for determining risk assessments that quantify the level of risk and for implementing management practices that are proven to be effective at reducing risk of contamination. HACCP is a systematic preventive approach to food safety and pharmaceutical safety that addresses physical, chemical, and biological hazards as a means of prevention rather than finished product inspection - used at all stages of food production and preparation processes. The stages of HACCP include:

- Conduct a hazard analysis
- Identify critical control points
- Establish critical limits for each critical control point
- Establish critical control point monitoring requirements
- Establish corrective actions
- Establish procedures for ensuring the HACCP system is working as intended
- Establish record keeping procedures

Within this process wildlife management agencies should encourage management of wildlife resources in potential conflict areas that balances public health with management objectives. Stakeholder involvement is important throughout the process and should include growers, buyers, public health and other regulatory agencies including state agriculture animal health personnel. These approach will help in problem definition and identification of known contributors to disease occurrence.

Communication with and education of stakeholders in research based information concerning wildlife, livestock and human sources involved in crop contamination should include growers and buyers, regulatory and governmental agencies, and legislators. Wildlife management agencies should educate their staff concerning economics and production constraints for growers, liability of buyers and growers, and public health risks and impacts of food-borne disease. It should also be the responsibility of wildlife agency management and research personnel to educate and communicate the risks of wildlife pathogens to food-borne illness with the public health investigators.

As an example of a recent outbreak implicating wildlife, an Oregon case was presented that implicated deer droppings as a confirmed primary source of contamination at a strawberry farm. The deer fecal material contained the same strain of *E. coli* O157:H7 that sickened people in Multnomah, Washington, Clackamas, Yamhill and Clatsop counties. A newspaper article stated that lab testing confirmed deer as the source of the outbreak, according to the Oregon Public Health.

Generally, wildlife does not constitute a significant source of EHEC O157 but sporadic isolation of the bacteria likely reflects environment-mediated transmission from humans and animal reservoirs (Ferens and Hovde, 2011). Collective studies looking at multiple wildlife species confirm this statement by either failing to document the presence of any *E. coli* O157:H7 (Adesiyun, 1999; Bardiau et al., 2010) or

showing very low prevalences (0.79% in white-tailed deer, 0.33% in pooled bird samples)(Rice et al., 2003). A current study screening numerous free-ranging wildlife species in the central coastal counties of California has demonstrated a 0% (0/445) prevalence of *E. coli* O157:H7 in coastal black-tailed deer (*Odocoileus hemionus columbianus*), 2.0 % (3/149) in Tule Elk (*Cervus Canadensis nannodes*), and 4.4% (9/206) of wild pig (*Sus scrofa*) (Gordus and Atwill, 2011). In independent studies in free-ranging deer across the United States, deer have generally been shown to infrequently shed *E. coli* O157:H7 in their feces, with prevalence ranging from 0.0 to 11% (Figure 1).

Figure 1. Studies evaluating deer as a source for *Escherichia coli* O157:H7 in North America.

Study	Animal source	Captive or	Fecal collection	Sample size	Prevalence (%)
		Wild			
Renter et al., 2001	white-tailed deer	<b>W</b>	rectum	1,426	0.25
Rice, et al., 2003	white-tailed deer	<b>W</b>	mixed	630	0.79
Sargeant, et al., 1999	white-tailed deer	<b>W</b>	ground (fresh)	212	2.4
Fischer et al., 2001	white-tailed deer	<b>W</b>	ground (fresh)	469 (1997), 120 (1998)	0.6 (1997), 0 (1998)
Gordus and Atwill, 2011	black-tailed deer	<b>W</b>	rectum	445	0
Dunn et al., 2004	white-tailed deer	<b>C</b>	ground (fresh)	55	1.8
		<b>W</b>	rectum	338	0.3
Cody et al., 1999	black-tailed deer	<b>W</b>	ground (unknown)	9	11.1
Keene et al., 1997	black-tailed deer	<b>W</b>	ground (unknown)	32	9.4

The two studies documenting the highest prevalences in deer include an investigation of *E. coli* infection traced to deer meat, where 3 of 32 fecal pellets (Keene et al, 1997) and an investigation into human *E. coli* O157:H7 infections linked to unpasteurized apple juice that demonstrated one of nine (11%) fecal samples to be positive (Cody et al., 1999). Both of these studies had extremely small sample sizes and were based on collection of fecal samples collected from the ground that were exposed to the environment, and potentially other contamination sources, for an unknown period of time. In the former deer meat case, prevalence in feces was not a factor in the outcome as the consumed meat could have been contaminated from a variety of other contact sources.

In the Oregon case, deer pellets, soil and strawberry plants were tested for the presence of the *E. coli* pathogen. However, many other factors associated with wildlife should have been considered including the period of time the deer feces was exposed to the environment and pathogens from external sources such as field run-off and flooding, the dry, pelletized nature of deer feces in late July, and other information about wildlife that could have been provided by wildlife agency staff. It is also possible both deer and the people infected with *E. coli* from contaminated strawberries may well have been the secondary recipients from an unidentified primary source.

Other information important to the investigation and some that was not available included information about the health of farm workers who were also present in the fields at the time of the outbreak, as well as samples from livestock and other animals, water, livestock manure sources, and potentially contaminated run-off from adjacent fields. Without a thorough investigation of all possible sources, it is often very difficult to identify a primary source but more accurately a list of possible sources. Due to the complexity of many food-borne illness investigations, there is an identified need for a multi-discipline approach with the inclusion of input from all subject matter experts and inclusion of all agencies involved (Fish and Wildlife, Agriculture, Public Health).

The implication of wildlife in cases of food poisoning and contamination of crops can result in consequences to the wildlife resource including reduced wildlife numbers through increased harvest, habitat access reduction through fencing and other physical barriers leading to loss of local migration corridors and reduced access to water sources, decrease in biodiversity, increased crop depredation on

adjacent properties (displacement, density issues, habitat degradation), and a fear of wildlife associated with disease by the public.

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## **SCWDS Hemorrhagic Disease Surveillance Update**

Mark Ruder, Daniel Mead, and David Stallknecht, Southeastern Cooperative Wildlife Disease Study, University of Georgia

An overview of epizootic hemorrhagic disease viruses (EHDV) and bluetongue viruses (BTV) isolated by SCWDS during the 2010 and 2011 transmission seasons was presented. During 2010, 14 viruses were isolated from the 85 virus isolation attempts made, representing 21 states and 7 species (59 white-tailed deer, 19 mule deer, 1 key deer, 3 elk, 1 unknown cervid, 1 cow, and 1 sheep). Table 1 lists virus isolates.

During the summer and early fall of 2011, SCWDS has received numerous reports of suspected hemorrhagic disease in free-ranging white-tailed deer populations. As of September 30, 2011, there have been 37 viruses isolated after 84 virus isolation attempts, representing 19 states and multiple species (76 white-tailed deer, 4 mule deer, 2 elk, and 2 unknown cervids). Table 2 lists the viruses isolated thus far in 2011.

**TABLE 1:** A list of the 14 viruses isolated from a total of 85 individual animal submissions made to SCWDS during 2011.

2010 Hemorrhagic Disease Diagnostics Virus Isolations Southeastern Cooperative Wildlife Disease Study				
STATE	COUNTY	MO NTH	SPECIES	VIRUS
ALABAMA	Geneva	Jul.	WTD <sup>c</sup>	EHDV-2
		Jul.	WTD <sup>c</sup>	EHDV-2
	Covington	Jul.	WTD <sup>c</sup>	EHDV-1
		Jul.	WTD <sup>c</sup>	EHDV-1
		Jul.	WTD <sup>c</sup>	EHDV-1
ARKANSAS	Jefferson	Nov.	WTD <sup>c</sup>	EHDV-2
		Aug.	WTD <sup>c</sup>	EHDV-6
FLORIDA	Lee	Jul.	WTD <sup>c</sup>	BTV-12
	Dixie	Sep.	WTD <sup>c</sup>	EHDV-2
MARYLAND	Anne	Aug.	WTD	EHDV-2
	Arundel			
NEW JERSEY	Salem	Sep.	WTD	EHDV-2
NEW MEXICO	Torrance	Oct.	elk <sup>c</sup>	EHDV-2
	Torrance	Sep.	elk <sup>c</sup>	EHDV-2
NORTH CAROLINA	Person	Sep.	WTD	EHDV-2

<sup>c</sup> captive animal

WTD = white-tailed deer

**TABLE 2:** A list of the 37 viruses isolated from a total of 84 individual animal submissions made to SCWDS during 2011 (current as of September 30, 2011).

2011 Hemorrhagic Disease Diagnostics Virus Isolations Southeastern Cooperative Wildlife Disease Study <i>thru September 30, 2011</i>				
STATE	COUNTY	MO NTH	SPECIES	VIRUS
ALABAMA	Marshall	Jul.	WTD <sup>c</sup>	EHDV-2
	Russell	Aug.	WTD <sup>c</sup>	EHDV-2
FLORIDA	Wakulla	Sep.	WTD	pending
ILLINOIS	Marion	Aug.	WTD <sup>c</sup>	EHDV-2
KANSAS	Anderson	Aug.	WTD	EHDV-2
	Butler	Aug.	WTD	EHDV-2
	Coffey	Sep.	WTD	pending
	Cowley	Aug.	WTD	EHDV-2
	Leavenworth	Sep.	WTD	EHDV-2
	h			
	Lyon	Aug.	WTD	EHDV-2
	Wilson	Aug.	WTD	EHDV-2
	KENTUCKY	Hopkins	Sep.	WTD
	Union	Jul.	WTD	EHDV-2
	LOUISIANA	Lafourche	Aug.	WTD
MARYLAND	Par.			
	Kent	Aug.	WTD	EHDV-2
MISSOURI	Holt	Sep.	WTD	pending

MONTANA	Musselshell	Aug.	WTD	EHDV-2
	Phillips	Aug.	WTD	EHDV-2
		Aug.	WTD	EHDV-2
	Powder River	Aug.	WTD	EHDV-2
	Valley	Aug.	WTD	EHDV-2
NEW JERSEY	Yellowstone	Aug.	WTD	EHDV-2
	Mercer	Aug.	WTD	EHDV-2
		Aug.	WTD	EHDV-2
	Middlesex	Sep.	WTD	EHDV-2
	Morris	Sep.	WTD	pending
NORTH CAROLINA	Gates	Aug.	WTD	EHDV-2
		Aug.	WTD	EHDV-2
PENNSYLVANIA	Yancey	Sep.	WTD	EHDV-2
	Erie	Aug.	WTD <sup>c</sup>	EHDV-2
		Aug.	WTD <sup>c</sup>	EHDV-2
	Northampton	Aug.	WTD <sup>c</sup>	EHDV-2
VIRGINIA		Aug.	WTD <sup>c</sup>	EHDV-2
	Chesterfield	Sep.	WTD	EHDV-2
	Frederick	Aug.	WTD	EHDV-2

<sup>c</sup> captive animal

WTD = white-tailed deer

### Update on Bat White Nose Syndrome in North America

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White-nose syndrome (WNS) in cave-hibernating bats was detected in five new U.S. states (Maine, North Carolina, Ohio, Indiana, Kentucky) and two new Canadian provinces (New Brunswick, Nova Scotia) during the Winter 2010/2011 season. This brings the total number of confirmed WNS-positive states and provinces to 16 and 4, respectively, since the disease was first detected in New York in February 2006. The genetic signature of *Geomyces destructans*, the causative agent of WNS, was also detected on bats in 3 additional states including Delaware, Missouri, and Oklahoma in the previous winter season, although the disease has yet to be detected in these states. No significant westward expansion of WNS was detected this winter beyond Trigg County, Kentucky. The disease continued to spread into new counties within WNS-confirmed states and provinces (Maryland, Virginia, West Virginia, Pennsylvania, Connecticut, Tennessee, Quebec, and Ontario). With the exception of one New Brunswick hibernaculum, where an estimated 4,980 bats died, all other new locations reported minimal to no bat mortality at the time of their surveys. Several surveys were conducted outside the entrances of the hibernacula only and may not reflect the true mortality counts. Also, because winter bat surveys are typically conducted once during the season to minimize disturbance to hibernating bats, total mortality estimates are not available until the following season when returning population counts are assessed. Thus far, WNS has not been confirmed in any new bat species this season. Six species, including Little Brown, Northern Long-eared, Tri-colored, Indiana, Eastern Small-footed, and Big Brown bats, are known to be susceptible to WNS. Genetic evidence of *Geomyces destructans* has been identified on three additional species (Southeastern myotis, Cave myotis, and Gray bats). For the latest WNS updates, consult the USGS-NWHC Wildlife Health Bulletins. [http://www.nwhc.usgs.gov/publications/wildlife\\_health\\_bulletins/index.jsp](http://www.nwhc.usgs.gov/publications/wildlife_health_bulletins/index.jsp).

Current bat submission guidelines to NWHC are available at:

[http://www.nwhc.usgs.gov/disease\\_information/white-nose\\_syndrome/USGS\\_NWHC\\_Bat\\_WNS\\_submission\\_protocol.pdf](http://www.nwhc.usgs.gov/disease_information/white-nose_syndrome/USGS_NWHC_Bat_WNS_submission_protocol.pdf)

White-nose syndrome research updates

The USGS National Wildlife Health Center (NWHC), along with many partners, continues to play a primary role in WNS research, including WNS transmission/pathogenesis/recovery studies, development

of improved tools for molecular detection of *G. destructans*, and investigation into the microbial ecology of *G. destructans* in bat hibernacula.

- 1) Studies to determine the role of *G. destructans* as the cause of WNS and modes of fungal transmission have been completed, and a manuscript describing study results is in review. As a continuation of this work, NWHC scientists are collaborating with others to complete laboratory experiments to determine how/why fungal skin infection kills bats. The leading hypothesis is that fungal damage to bat wing skin catastrophically disrupts physiological homeostasis during hibernation. Additionally, NWHC scientists recently published findings demonstrating that bats with WNS can readily recover from the disease with provision of supportive care (food, water, and warm temperature). These results confirm that hibernation predisposes bats to infection by *G. destructans* and further indicate that management actions to reduce infection severity may allow bats to survive and naturally recover from WNS following spring emergence.
- 2) Scientists at the NWHC recently developed and published a rapid PCR test for detecting DNA from *G. destructans* on bat wing skin and have shared this new test with multiple laboratories as a much needed diagnostic tool. Additionally, work at the NWHC is ongoing to standardize non-invasive techniques (i.e. swabbing) to collect fungal samples from bat skin, and efforts are underway to develop/qualify a new quantitative PCR method for detecting *G. destructans* with enhanced specificity necessary to analyze environmental samples.
- 3) An environmental survey of caves was conducted by USGS scientists in collaboration with several states to characterize the distribution of *G. destructans* in cave soil. This study demonstrated that DNA from *G. destructans* was present in soil collected only from hibernation sites within the WNS-infested region of the United States. Follow-up analyses further confirmed that the viable fungus was also present in these samples indicating that the environment likely plays a role in the WNS disease/transmission cycle. Bat ecologists from the USGS Fort Collins Science Center have developed and deployed infrared video surveillance systems for use inside bat hibernation sites to investigate potential behavioral links between skin infection by *G. destructans* and WNS mortality. Through a collaborative study with Northern Arizona University, genomic analyses of multiple isolates of *G. destructans* from both Europe and North America suggest that *G. destructans* is an exotic species in North America of European origin. Additionally, a detailed analysis of the role of temperature on the proliferation and persistence of *G. destructans* is underway.

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### **Newcastle Disease Virus in Wild Double Crested Cormorants**

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Newcastle Disease (NDv) is a well known and serious disease of poultry. It does occur in wildlife as well, specifically Double Crested Cormorants (DCCO). DCCO are widely distributed over the United States as they can exist in freshwater, estuarine and marine habitats. They are also colonial nesting birds often sharing nesting sites with pelicans, gulls and shore birds. This species is apparently especially susceptible to the virus. Even though virus has been isolated in some other wild species it only develops into disease in DCCO. Investigators at the National Wildlife Health Center (NWHC) and others have noted that since the first detected outbreak of NDv in DCCO in 1992, there has been a rough two-three year cycle of outbreaks. Further, while not exclusively there, most outbreaks are clustered in the upper Midwestern United States (the Dakotas, Minnesota, Wisconsin, and Michigan). Adult birds develop an immune resistance to infection with NDv and this can be passed to younger birds protecting them, however, adults do not sustain protection and may become infected themselves again later in life. The virus affects the younger age classes the most as protected young birds have a lasting protection for only about their first 6 weeks. In order to better understand disease periodicity as well as other aspects of the biology of this disease in DCCO, the NWHC launched into a study with cooperators such as the USDA WS, and state wildlife management agencies. Biological samples (cloacal swabs and heart blood) were collected from agency harvested birds from three known positive sites in Minnesota during the summer of 2011. This year was selected because it was immediately after an active outbreak year (2010) in the same area. Birds of all four age classes were collected from all three sites, three times during the season

for a total of 540 samples. These samples will be tested in the laboratory at the NWHC by RT-PCR and virus culture and serum will be tested via serum neutralization and ELISA. Testing of this year's samples is being conducted this fall, as the last collection of samples was just completed in August. Information collected from these birds including age data and test results will be used in the development of force of infection models to help better understand disease dynamics of NDv in wild DCCO.

**Committee Business**

There were no resolutions or business items presented to the Committee.