Report to the Western Association of Fish and Wildlife Agencies
From the USGS National Wildlife Health Center

July 9, 2017

The USGS National Wildlife Health Center provides national leadership to safeguard wildlife and ecosystem health through dynamic partnerships and exceptional science.

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EMERGING WILDLIFE DISEASE SURVEILLANCE AND WILDLIFE DISEASE UPDATES

Surveillance for Invasive Pathogens to Protect our Nation's Amphibians

On-going national wildlife disease surveillance is essential for early detection and rapid response to diseases that threaten the lives of wildlife, humans, and livestock. *Batrachochytrium salamandrivorans* (*Bsal*) is an emerging fungal pathogen that has decimated populations of some salamander species in Europe. Salamanders contribute to forest health through invertebrate predation that results in increased litter retention and carbon capture in the soil. The U.S. has the highest biodiversity of salamanders in the world; the translocation of *Bsal* to the U.S. could result in ecosystem disruption in the many regions where salamanders reside.

In 2016, the USGS National Wildlife Health Center (NWHC) and the USGS Amphibian Research and Monitoring Initiative conducted a spatial risk analysis to determine where *Bsal* would most likely be introduced to the U.S. and which regions of the country would be the most impacted. The risk assessment was used to direct a coordinated collection and analysis of more than 8,000 samples from over 30 amphibian species in 20 states in 2016-2017 to determine whether the pathogen had already been introduced. All samples were negative for *Bsal*. The NWHC is collaborating with multiple federal and state partners, including the multi-agency *Bsal* Task Force to contain and mitigate the impacts of this pathogen, should it be introduced. The NWHC is also developing methods to test the environment for *Bsal* and other chytrid fungi to provide an additional tool for early detection of these emerging pathogens. For additional information on *Bsal*, please see this Wildlife Health Bulletin from April 2016 and a USGS fact sheet titled "Early action to address an emerging wildlife disease". For questions regarding *Bsal* surveillance, please contact Daniel Grear, 608-270-2478, dgrear@usgs.gov.

National Surveillance Continues to Detect Spread of White-Nose Syndrome in Bats

The USGS National Wildlife Health Center (NWHC) continues to assist state and federal wildlife agencies nationwide with early detection of *Pseudogymnoascus destructans* (*Pd*), and to address specific research priorities identified by partners in conjunction with the White-Nose Syndrome National Plan. During annual bat population surveys, participating state agencies collect swabs of bat skin, guano, hibernaculum sediment, and environmental substrate. If clinical signs of white-nose syndrome (WNS) are observed in the population, carcasses or wing biopsies from affected bats are collected for diagnostic testing.

Since winter 2013/2014, 281 unique hibernacula have been surveyed nationwide. These samples have resulted in the detection of *Pd* at 118 hibernacula of previously unknown *Pd* status from 16 states, including 42 sites where there was no physical or behavioral evidence of WNS observed in the bat populations. Nearly 95 percent of all detections of *Pd* originated from samples collected from bats rather than from environmental substrates collected inside of hibernacula. Data analysis and modeling of risk factors associated with *Pd* movement from data collected during the past three years of the project are currently underway.

This past winter (2016/2017), WNS was confirmed for the first time in Nebraska (Cass County) and Oklahoma (Delaware County) where *Pd* was first detected in 2015. These findings increase the number of states with confirmed cases of WNS to 31, while the number of affected Canadian provinces remains at five. Alabama reported the first confirmation of WNS in a southeastern myotis (*Myotis austroriparius*)

and Washington reported the first confirmation of WNS in a Yuma myotis (*M. yumanensis*) collected from the same county (King) where a little brown bat (*M. lucifugus*) with WNS and a silver-haired bat (*Lasionycteris noctivagans*) with *Pd* were detected in spring 2016. The search for environmental reservoirs of the fungus in the area is on-going. Finally, Texas announced detection of *Pd* in six counties (Childress, Collingsworth, Cottle, Hardeman, King, and Scurry) and on two new bat species: cave myotis (*M. velifer*) and the western sub-species of Townsend's big-eared bat (*Corynhinus townsendii townsendii*). No clinical signs or mortality have been reported in Texas (as of July 2017). Mississippi is the only other state where *Pd* has been detected in hibernacula in the absence of confirmed WNS to date. Northern long-eared bats (*M. septentrionalis),* little brown bats (*M. lucifugus),* and tricolored bats (*Perimyotis subflavus)* remain the species that most often test positive for *Pd.*

Despite active national surveillance efforts to detect the spread of WNS, the 2016 detection of WNS in Washington State illustrates the ongoing importance of investigating wildlife mortality events as part of a comprehensive wildlife disease surveillance strategy, and we encourage wildlife managers to report unusual bat mortality or bats displaying clinical signs suggestive of WNS to the NWHC for further investigation. We can also answer questions about designing WNS surveillance and response plans relevant to your state and help with testing samples collected as part of opportunistic or targeted surveillance efforts in accordance with the national *Pd* surveillance strategy. Tribal, state, and federal agencies with questions about ongoing surveillance efforts, or who may wish to participate, should contact Dr. Anne Ballmann (608-270-2445, aballmann@usgs.gov).

Please visit www.whitenosesyndrome.org for more information about the national multi-agency WNS response effort. A recently completed fact sheet titled "White-Nose Syndrome in North American Bats – USGS updates" is available online. For paper copies, please contact Gail Moede Rogall, gmrogall@usgs.gov. Also, a WNS poster and handout are available at https://www.whitenosesyndrome.org/resource/white-nose-syndrome-poster-available-your-use.

Avian Influenza 2016/2017 Update

The U.S. interagency surveillance program for the detection of highly pathogenic avian influenza (HPAI) virus in wild birds continued in the 2016-2017 surveillance year. Agencies that comprise the *Interagency Steering Committee for Surveillance for HPAI in Wild Birds* include USDA Animal and Plant Health Inspection Service, U.S. Geological Survey, U.S. Fish and Wildlife Service, Centers for Disease Control and Prevention, the National Flyway Council, and numerous state agencies. Between July 1, 2016 and February 1, 2017 a total of 33,695 birds were sampled, with 96 percent of those samples coming from dabbling ducks. Pursuant to this surveillance effort, HPAI H5N2 was detected in two mallards (*Anas platyrhynchos*) including one from Fairbanks-Northstar Borough, AK, in August 2016, and one from Fergus County, MT, in December 2016. In each case, the HPAI virus was the Eurasian-American lineage H5N2 (clade 2.3.4.4) that was first detected in North America in December 2014.

Globally, HPAI H5 subtype detections have continued in wild and domestic birds in Europe, Asia, and Africa during the fall and winter of 2016-2017 with more than 40 countries reporting outbreaks to the World Organisation for Animal Health (OIE). As of March 13, 2017, there have been 576 reported outbreaks in poultry, with nearly seven million poultry destroyed worldwide. Additionally, during the same timeframe there were 638 reported outbreaks involving more than 75 species of free-ranging or captive wild birds (618 of these were HPAI H5N8 viruses). In January 2017, a mortality event involving more than 1,200 white-winged terns (*Chlidonias leucopterus*) and other wild bird species was reported in Uganda; HPAI H5N8 was isolated from numerous birds from this outbreak. At least five different HPAI H5 subtypes have been detected during these outbreaks worldwide. For additional information on the current global HPAI situation, please reference the following OIE Situation Report. **Contact**: Hon Ip, 608-270-2464, hip@usgs.gov.

Avian Cholera Winter 2016/2017 National Summary

The USGS National Wildlife Health Center (NWHC) investigated eight wildlife mortality events between November 1, 2016 and March 1, 2017 in which avian cholera (caused by the bacterium *Pasteurella multocida*) was either suspected or confirmed as the causative etiologic agent. Five additional events were reported by state wildlife management agencies. The 13 events were spread over ten states (California with four events, and one each in Idaho, Illinois, Missouri, Montana, Nebraska, New Mexico, Oregon, Texas, and Washington) and three flyways (Mississippi, Central, and Pacific). The estimated mortality reported to date in these events ranges from less than ten to over 6,500 birds. The three largest events include Canyon County, Idaho (beginning February 2017) with an estimated mortality of 6,500 dabbling ducks as of March 6, 2017; Yolo County, California (January 2017) with an estimated mortality of 3,750 (primarily American coot [*Fulica americana*] and a small number of dabbling ducks); and McNary National Wildlife Refuge (NWR) and surrounding areas in Washington (February 2017), with an estimated mortality exceeding 2,000 birds. The McNary NWR event primarily involved mallard ducks (*Anas platyrhynchos*), but also included other dabbling ducks, herons, owls (barn owl [*Tyto alba*] and great horned owl [*Bubo virginianus*]), and raptors (northern harrier [*Circus cyaneus*], red-tailed hawk [*Buteo jamaicensis*], and bald eagle [*Haliaeetus leucocephalus*]). More information about avian cholera can be found on the NWHC website. **Contact**: NWHC Field Epidemiology Team, 608-270-2480, NWHC-epi@usgs.gov.

Canine Distemper in Wisconsin

Beginning mid-March 2017, the Wisconsin Department of Natural Resources (WI DNR) received reports of unusual mortality involving raccoon (*Procyon lotor*), gray fox (*Urocyon cinereoargenteus*), and striped skunk (*Mephitis mephitis*) occurring in two counties in southeastern Wisconsin. Two raccoons, a gray fox, and a striped skunk were submitted to the NWHC, with subsequent samples tested at the Wisconsin Veterinary Diagnostic Laboratory and the Wisconsin State Laboratory of Hygiene. NWHC scientists determined that canine distemper virus was the cause of death (with rabies ruled out). The WI DNR continued to receive reports of unusual small mammal mortality through early June, including cases in central and northern Wisconsin counties. Similar suspected distemper outbreaks in the spring of 2017 involving raccoons have been reported and investigated by the Minnesota Department of Natural Resources (six counties) and Virginia Department of Game and Inland Fisheries (two counties).

Distemper is a highly contagious, systemic, viral disease that infects a wide variety of mammalian species with domestic dogs considered to be the natural reservoir species. The disease is common and can cause significant outbreaks in susceptible wildlife species. Vaccination is essential for the prevention of disease and outbreaks in domestic dogs. Because the clinical signs of distemper can mimic rabies, contact with sick animals should be avoided. People and their domestic pets/livestock should avoid contact with sick or dead wildlife and contact the appropriate wildlife officials in their area for further guidance. **Contact**: NWHC Field Epidemiology Team, 608-270-2480, NWHC-epi@usgs.gov

Bisgaard Taxon 40-Associated Mortality

Between August and October 2016, NWHC received a number of avian cases in which death was associated with a *Pasteurella*-like bacterium called *Bisgaard* taxon 40. The most significant of these was a mortality event involving rhinoceros auklets (*Cerorhinca monocerata*) that occurred in the Salish Sea area of Washington State. At this location, approximately 420 dead adult and juvenile auklets washed ashore and were observed by volunteer beach survey teams. Ten adult auklet carcasses were submitted to the NWHC for diagnostic evaluation. In seven of these birds, bacterial septicemia associated with *Bisgaard* taxon 40 was determined to be the cause of death. Following this event, NWHC continued to isolate this bacterium from dead birds collected from various locations in the Great Lakes region and the

mid and north Atlantic coast of the U.S. (including Wisconsin, Maryland, Massachusetts, and Maine). These mortalities involved birds of the order Charadriiformes and included common tern (*Sterna hirundo*), roseate tern (*S. dougallii*), laughing gull (*Leucophaeus atricilla*), herring gull (*Larus smithsonianus*), and great black-backed gull (*L. marinus*). NWHC also received similar reports and diagnostic results on 44 birds examined by the Canadian Wildlife Health Cooperative in British Columbia. *Bisgaard* taxon 40 was first recognized in 2003 in gulls, but has not previously been associated with mortality in wildlife. NWHC is currently reviewing historical diagnostic cases where *Bisgaard* taxon 40 was identified, as well as trying to determine the extent of this bacterium's occurrence among apparently healthy gulls. **Contact**: NWHC Field Epidemiology Team, 608-270-2480, NWHC-epi@usgs.gov

DEVELOPING WILDLIFE HEALTH CAPACITY AND TOOLS

WHISPers: Building a National Wildlife Health Database

Emerging infectious diseases have increased globally in the past two decades with the majority of new pathogens originating in wildlife. On-going national wildlife disease surveillance is essential for early detection and rapid response to protect the lives of wildlife, humans, and livestock. Hundreds of wildlife disease events are investigated throughout the U.S. each year by state and federal natural resource agencies, but the results are stored in individual internal databases. Although managers have long recognized that wildlife do not respect jurisdictional boundaries, sharing disease information across agencies or with the public was difficult and inefficient. The Wildlife Health Information Sharing Partnership (WHISPers) is a centralized web-based repository for wildlife health surveillance data on thousands of events investigated by the NWHC and partners. In 2015, WHISPers went live to partner agencies and the public and has significantly increased the availability and accessibility to information on over 7,000 morbidity and mortality events collectively spanning over 40 years. Data are provided in map and table format that can be searched, sorted, and downloaded by anyone, anywhere. Since 2015, new data have been uploaded quarterly, increasing the utility of WHISPers as a mechanism for situational awareness of emerging pathogens and wildlife disease events. Soon, data will load in near-realtime from the internal NWHC wildlife morbidity and mortality event database to the public WHISPers interface. Future goals are to create a front-end feature and application to allow state and federal agencies to enter and analyze data on additional on-going or historic wildlife health events in WHISPers. These features will increase the acquisition, preservation, availability, and use of these data by the entire wildlife health field. As a result, we will also improve our ability to understand, predict, and manage the effects of disease on wildlife, humans, and agriculture. **Contact:** Neil Baertlein, 608-270-2460, nbaertlein@usgs.gov.

Power to the People: Developing Accessible Tools for Statistical Modeling

A wealth of new analytical techniques developed for analyzing ecological data exists, including analysis of fish and wildlife disease investigations. Unfortunately, these developments are often highly technical and require computer programming acumen, and often remain inaccessible to fish and wildlife managers. This inaccessibility prevents both scientists and managers from learning when and how to apply appropriate statistical tools, which slows the progress of science and the effectiveness of management programs. To address this problem, NWHC, in collaboration with the University of Montana, has begun development of web applications that make sophisticated statistical modeling techniques easily accessible. In 2016, an application was developed that focused on providing an efficient means of gathering and quantifying expert opinions. Expert elicitation is an important scientific technique for understanding problems which are not well studied or are novel (e.g., new emerging diseases). This application provided the ability to quickly gather and quantify a large number of experts' opinions for

further sophisticated statistical analyses. In 2017, a new application is being developed for designing and conducting weighted surveillance programs for Chronic Wasting Disease (CWD), which is a type of surveillance that focuses on detecting new disease foci in a cost-efficient and statistically rigorous manner. Weighted surveillance is gaining in popularity among wildlife agencies trying to manage the spread of CWD with limited resources, but tools for its application are not readily available. Additional applications will be developed for the modeling of population demography and disease processes. The fruits of these research efforts will be used by the scientific and wildlife management community at large. **Contact:** Dan Walsh, 608-270-2481, dwalsh@usgs.gov.

Peering Into the Crystal Ball: Forecasting Wildlife Diseases in the Face of Uncertainty

Disease in wildlife represents a growing threat to the well-being of wildlife populations, as well as human and domestic animal health. Understanding the processes that allow for their growth and spread is critical to permit development of effective management actions for protecting the health of humans, animals and the environment, and to forecast the risk and spread of these threats to new populations and regions. However, developing models to understand disease processes is challenging because of the scale and large uncertainty inherent in wildlife disease systems as well as the lack of suitable analytical tools. To overcome these obstacles, NWHC in collaboration with the Colorado Cooperative Fish and Wildlife Research Unit developed a novel analytical framework to model disease dynamics within wildlife populations while rigorously accounting for uncertainty in the system. They applied this statistical framework to model the spatial and temporal changes in CWD using surveillance data collected by the Wisconsin Department of Natural Resources. These efforts clearly demonstrated its usefulness in describing historic disease patterns as well as forecasting future growth and spread of CWD. Future work will use these new analytical techniques to evaluate the effectiveness of historic disease management actions, rigorously assess the origin of disease outbreaks, and link individual animal dynamics to system-wide outcomes. Ultimately, we believe these approaches will be used across a wide array of diseases to understand the critical drivers of disease and its spread, predict future disease states, and determine appropriate interventions for the protection and improvement of human, domestic animal and ecosystem health. Please see this USGS Technical Announcement for more information. Contact: Dan Walsh, 608-270-2481, dwalsh@usgs.gov.

WILDLIFE HEALTH RESEARCH UPDATES

Sylvatic Plague Vaccine for Prairie Dogs

Laboratory studies have demonstrated that oral vaccination of prairie dogs against plague using raccoon pox-vectored vaccine is feasible, resulting in significant protection against challenge with *Yersinia pestis*, the bacterium that causes sylvatic plague. The Sylvatic Plague Vaccine (SPV) Subcommittee, under the direction of the Executive Committee of the Black-footed Ferret Recovery Implementation Team, is continuing its work to complete development and delivery of the sylvatic plague vaccine as a management tool to combat plague in prairie dogs and promote the recovery of the endangered black-footed ferret. Field trials completed by Colorado Parks and Wildlife and the NWHC in 2012 confirmed the safety of the vaccine in wild prairie dogs and non-target animals. NWHC and numerous federal, state, and tribal partners have recently completed field trials in seven western states (Arizona, Colorado, Montana, South Dakota, Texas, Utah, and Wyoming) to assess vaccine efficacy in free-ranging prairie dogs. Analysis of data and samples demonstrated that relative abundance of prairie dogs in general was higher on SPV treated sites and survival was improved during plague outbreaks, suggesting SPV may be useful as a management tool to advance prairie dog conservation and possibly the recovery of the endangered black-footed ferret. Additional field trials to determine optimal use of SPV began in 2016 in western states and are continuing in 2017. Dr. Tonie Rocke and others recently published SPV field trial results in the journal EcoHealth, which was accompanied by this USGS media release. **Contact**: Tonie Rocke, 608-270-2451, trocke@usgs.gov.

Avian Influenza Virus Ecology in the North Atlantic: A Route for HPAI Introduction to North America

The NWHC in collaboration with National Institutes of Health, University of Iceland, and others continue their research on the ecology and movement of avian influenza viruses in the North Atlantic region. This research has demonstrated the importance of this region's migratory bird to the intercontinental movement of viruses between Europe and North America. Avian influenza viruses from both continents, as well as genetic hybrid viruses, were isolated in Iceland, even from within a single flock of birds, showing that this region is a hotspot of virus movement and reassortment. These studies also demonstrated the longer term persistence of these viruses within the North Atlantic avian community. Highly pathogenic avian influenza viruses (HPAIV) have been frequently found in wild and domestic European birds, especially during 2014, and most recently in the fall and winter of 2016/2017. This European epidemic increases the risk of HPAIV being transported from Europe to North America as bird populations migrate through the North Atlantic to breeding sites in Greenland and Canada. One of the significant findings from this research is the identification of gulls and marine birds as an integral component of AIV ecology in the North Atlantic region. Icelandic viruses were also discovered to have genetic relationships with viruses causing seal mortalities in Europe. Although no HPAIV has been identified in the North Atlantic region, viruses with genetic relationships to HPAIV H5N1 viruses have been detected in Iceland. **Contact:** Jeffrey Hall, 608-270-2458, jshall@usgs.gov

Another Emerging Fungal Disease: This Time It's Affecting Snakes

In the last decade, reports of wild snakes from parts of the eastern U.S. with severe and often fatal skin infections have increased. These infections, referred to as snake fungal disease (SFD), are caused by the fungus *Ophidiomyces ophiodiicola*. Clinical signs of SFD are variable and include thickened dying scales, nodules below the skin, skin ulcers, and severe swelling of the head. NWHC recently reviewed cases of infection by *O. ophiodiicola* and reported the pathogen in wild snakes throughout the eastern half of the U.S. Many snake species are susceptible to *O. ophiodiicola* infection, including members from at least four of the five snake families that occur in North America. Snake populations have varying responses to *O. ophiodiicola*. While some populations have experienced severe infections and declines in association with the disease, other populations exhibit predominantly mild infections without obvious detriment. Changing environmental conditions, such as climate change and habitat fragmentation may exacerbate the disease and be responsible for its recent emergence in some areas. In 2017, NWHC continued collaborations on a project lead by researchers in the United Kingdom to better understand the epidemiology of SFD in different snake populations in Europe. A recent USGS news release highlights this collaboration and the discovery of SFD in Europe. **Contact**: Jeff Lorch, 608-270-2367, jlorch@usgs.gov.

Will Zika Virus Impact Poultry or Wild Birds?

Zika virus emerged as a major threat to human health, causing abnormally high birth defects in infants born to infected mothers in South America, and has infected people in at least 38 countries, including the U.S. While much progress has been made in understanding the human medical implications of this virus, very little is known about the impacts of Zika virus to U.S. agricultural industries or wildlife species. In particular, Zika virus belongs to the flavivirus group, which includes many viruses that are vector borne and infect birds, including West Nile virus. Zika virus is transmitted through the bite of infected *Aedes* sp. of mosquitoes. In 2016, the USGS developed diagnostic capability to detect Zika virus and anti-Zika virus antibodies in exposed wildlife. In collaboration with the USGS Alaska Science Center, NWHC will test sera from North American birds that overwinter in Central and South America and are sampled either on their overwintering grounds or on their northern migration to North America. Serological testing is on-going for 250 blue winged teal samples collected by the Alaska Science Center and the University of Georgia. NWHC also tested the ability of Zika virus to infect embryonated chicken eggs, young chickens, and passerines. This will experimentally determine whether poultry or wild birds may serve as reservoirs for the virus. Results from these exposure studies will likely be published in 2017. Additionally, NWHC

is collaborating with the USGS Upper Midwest Environmental Sciences Center to develop a rapid field deployable assay to detect Zika virus in samples obtained from mosquitoes, wildlife, and the environment. This assay will be a significant asset in monitoring the geographic spread of Zika virus and the potential for wildlife to serve as reservoirs for the virus. These activities will enable field technicians to rapidly detect Zika virus or, through testing serum, animals previously exposed to the virus. **Contact:** Erik Hofmeister, 608-270-2476, ehofmeister@usgs.gov

Chronic Wasting Disease in Deer, Elk, and Moose: An Epidemic in Slow Motion
Since its initial identification in Colorado in captive mule deer (*Odocoileus heminous*) in the late 1960s and free-ranging elk (*Cervus canadensis*) in the 1980s, chronic wasting disease (CWD) has affected captive and free-ranging cervids (members of the deer family) in about half the states in the U.S., as well as Canada, South Korea, and Norway, and continues to spread across North America through new and recurring outbreaks. The only prion disease known to affect free-ranging wildlife, CWD is increasing in prevalence in areas where the disease is already established; in heavily affected areas of Wyoming and Colorado, more than 40 percent of free-ranging cervids are infected and wildlife managers and researchers have documented CWD-associated population declines in white-tailed deer (*O. virginianus*), mule deer, and elk.

Currently, effective treatment for CWD does not exist, and management practices to prevent disease transmission in cervids are limited. Scientists at the NWHC work collaboratively with various federal and state natural resources agencies, academic institutions, nongovernmental organizations and industry partners to: 1) understand the biology, ecology, and epidemiology of CWD; 2) assess and predict the spread and persistence of CWD in wildlife and the environment; and 3) develop tools for early detection, diagnosis, surveillance, and control of CWD. NWHC research has been instrumental in developing surveillance strategies for early detection of CWD in Montana (Montana Fish, Wildlife and Parks Department) and Shenandoah National Park (National Park Service), identifying potential disease risks posed by CWD to noncervid species such as bighorn sheep (*Ovis canadensis*), and identifying environmental factors, like soil and plants, that may facilitate CWD transmission on the landscape.

The benefits of USGS research on CWD extend beyond wildlife management; for example, USGS scientists identified a novel enzyme from lichens with the ability to break down infectious prion protein that is being studied for its use in decontaminating human hospital environments in collaboration with an industry partner. Current and future efforts will focus on improving diagnostic testing platforms in collaboration with the U.S. Food and Drug Administration; providing surveillance and modeling technical assistance to a long-term CWD study carried out the Wisconsin Department of Natural Resources; developing modeling techniques for predicting CWD growth within free-ranging cervid populations and forecasting disease spread in regions of interest; and continued identification and development of novel anti-prion compounds and processes to disrupt disease transmission cycles. **Contact:** Bryan Richards, 608-270-2485, brichards@usgs.gov, or Christina Carlson, 608-270-2442, cmcarlson@usgs.gov.

SERVICES TO PARTNERS AND OTHER INFORMATION

Disease Investigation Services

To request diagnostic services or report wildlife mortality, please contact the NWHC at 608-270-2480 or by email at NWHC-epi@usgs.gov, and a field epidemiologist will be available to discuss the case. To report wildlife mortality events in Hawaii or Pacific Island territories, please contact the Honolulu Field Station at 808-792-9520 or email Thierry Work at thierry_work@usgs.gov. Further information can be found at http://www.nwhc.usgs.gov/services/.

Wildlife Mortality Reporting and Diagnostic Services Request Worksheet

To view, search, and download historic and ongoing wildlife morbidity and mortality event records nationwide visit the Wildlife Health Information Sharing Partnership event reporting system (WHISPers) online database at http://www.nwhc.usgs.gov/whispers/

Disease Webinar Series Sponsored by USGS Ecosystems Mission Area and AFWA

USGS and the Association for Fish and Wildlife Agencies co-host a monthly webinar series on fish and wildlife diseases. The purpose of this series is to keep partners informed about our current disease research and discuss how USGS science can support disease management efforts. Past Webinar topics include CWD, Avian Influenza, *Bsal*, WNS, Plague, Fish Diseases, and Online Tools. USGS Ecosystems Mission Area Web site: https://www2.usgs.gov/ecosystems/disease/disease.html#webinars

New Fact Sheet about the USGS National Wildlife Health Center

The USGS National Wildlife Health Center: Advancing Wildlife and Ecosystem Health is the title of this fact sheet that gives readers an overview of the NWHC, including a brief history of its formation, current capabilities, science branches, disease surveillance and science highlights. It is available online and in paper copies. **Contact:** Gail Moede Rogall, 608-270-2438, gmrogall@usgs.gov

To be added to the NWHC list to receive Wildlife Health Bulletins, please contact Gail Moede Rogall at gmrogall@usgs.gov

USGS Wildlife Health Information on Twitter and images on Instagram

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Request for Wildlife Mortality and Morbidity Event Reporting

The NWHC Quarterly Wildlife Mortality Report, published in the Wildlife Disease Association's newsletter and on the NWHC Web site, is intended to inform wildlife professionals of wildlife events of interest. We kindly request the help of wildlife professionals in submitting investigations of recent die-offs of mammals, birds, amphibians, and reptiles for inclusion in this report. Credit will be given to appropriate diagnostic laboratories and wildlife management agencies. The report can be found online at http://www.nwhc.usgs.gov/mortality_events/ongoing.jsp.

To view NWHC Quarterly Wildlife Mortality Reports, please visit:

http://www.nwhc.usgs.gov/publications/quarterly_reports/index.jsp

THANK YOU

The NWHC thanks all the state, federal and tribal agencies who worked with us. We are at your service to provide technical support, field investigation assistance, diagnostic capabilities, and collaborative research projects.