Report to the Fish and Wildlife Health Committee
of the Association of Fish and Wildlife Agencies
from USGS Science Centers
September 24, 2014

Wildlife Health Information Sharing Partnership – Event Reporting System (WHISPers)
The USGS National Wildlife Health Center (NWHC) is introducing a new online database for reporting wildlife health events that will be an easy and efficient way for wildlife professionals across North America to share disease event information, such as outbreak onset and ending date, general location, species involved, numbers involved, diagnoses, and laboratory and contact names. It is a partner-driven, web-based system for tracking basic information about historic and ongoing wildlife mortality and morbidity events. The primary goal of the system is to provide natural resource partners and the public with timely, accurate situational awareness regarding these events. The system also serves as a searchable archive of historic mortality and morbidity event data. Initially, the NWHC will populate this database with the wildlife mortality data the NWHC has maintained for several years (see http://www.nwhc.usgs.gov/publications/quarterly_reports/index.jsp); after the initial rollout, other wildlife professionals will be able to enter data that can be viewed by others. A Frequently Asked Questions handout is available. **Contact:** Jonathan Sleeman, National Wildlife Health Center, 608-270-2401, jsleeman@usgs.gov

NWHC Reorganization
The National Wildlife Health Center recently reorganized the structure of its branches for the purpose of aligning the Center structure with its strategic science goals and objectives outlined in the NWHC Strategic Science Plan. The reorganization will also streamline and improve the technical services provided by the NWHC; foster collaborative interactions among scientists internal and external to the Center; and will ensure our work meets the needs of our partners and stakeholders. The organizational structure and functions of our cross-disciplinary branches are described in detail in a Functional Statements document. A July 2014 Wildlife Health Bulletin gives an overview of the three science branches: Applied Wildlife Health Research; Wildlife Epidemiology and Emerging Diseases; and Wildlife Disease Diagnostic Laboratories. **Contact:** Jonathan Sleeman, National Wildlife Health Center, 608-270-2401, jsleeman@usgs.gov

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Wildlife Highlights

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 black-footed ferret. Field trials completed by Colorado Parks and Wildlife and NWHC in 2012 confirmed the safety of the vaccine in wild prairie dogs and non-target animals. Field studies to assess vaccine efficacy in free-ranging prairie dogs began in the summer of 2013. Vaccine and placebo baits are being distributed in select prairie dog colonies in seven western states: Arizona, Colorado, Montana, South Dakota, Texas, Utah, and Wyoming. Prairie dogs are trapped and sampled to determine bait uptake. The field study will continue into 2015. During the 2014 field season, some sites are hosting a media field day where reporters and others are invited to learn more about the SPV field trials at selected prairie dog colonies. **Contact:** Tonie Rocke, National Wildlife Health Center, 608-270-2451, trocke@usgs.gov

Persistence of plague in enzootic form problematic to keystone or foundation species

Plague, the disease caused by the primarily flea-borne bacterium *Yersinia pestis*, was introduced to the Americas circa 1900. Invasion of the disease that caused such widespread human suffering in Eurasia generated significant attention among medical practitioners, but an understanding of the ecological consequences has progressed slowly. In some mammals, plague erupts in epizootics that result in large scale mortality. Whether such outbreaks are important to maintain *Y. pestis* populations or are simply paroxysms that amplify the bacterium locally remains unclear. Although epizootics of plague are clearly disruptive, continuous disease transmission during enzootic periods might characterize *Y. pestis* maintenance. Persistence of plague in enzootic form can cause chronic problems as exemplified by several controlled experiments during non-epizootic periods. Ecosystem disruptions due to plague can be especially dramatic when the disease influences keystone or foundation species such as prairie dogs, ground squirrels, and voles. Preliminary evidence suggests that enzootic plague substantially influences populations of a variety of species in the western U.S. Manipulative field studies of plague ecology are ongoing in Colorado, South Dakota, New Mexico, and Idaho. **Contact:** Dean Biggins, Fort Collins Science Center, 970-226-9467, bigginsd@usgs.gov

Creating a North American Bat Population Monitoring Program

Bats in North America are facing unprecedented threats including white-nose syndrome (WNS), wind energy development, habitat loss and fragmentation, and climate change. Until now, there has been no coordinated monitoring program to track bat population responses to such threats. The North American Bat Monitoring Program (NABat) is a multi-agency effort spearheaded by U.S. Fish and Wildlife Service, U.S. Geological Survey, U.S. Forest Service and the National Park Service and has been under development since 2012. NABat integrates several new and ongoing sampling schemes including maternity and hibernacula counts, acoustic surveys along driving transects, and stationary acoustic surveys joined in a common sampling framework. Data will be managed by the USGS Bat Population Data (BPD) Project and web-based applications are being developed this winter. The BPD will also integrate WNS diagnostic, monitoring, and surveillance data by establishing data partnerships with the National Wildlife Health Center, the National WNS Coordination team, and the WNS Diagnostic Laboratory Network. A centralized database system for WNS data is a priority outlined in the WNS National Response Plan. **Contact:** Laura Ellison, Fort Collins Science Center, 970-226-9499, ellisonl@usgs.gov

Results of *Mycoplasma ovipneumoniae* ring test

Numerous microorganisms have been associated with pneumonia in bighorn sheep, but *Mycoplasma*

ovipneumoniae is considered to be one of the key pathogens. This bacterium presents considerable diagnostic challenges due to its slow or inconsistent growth on solid agar media and its lack of readily detectable phenotypic characteristics for speciation of the bacterium when it does grow. Over the past several years, inconsistencies among different diagnostic and research laboratories in detecting *M. ovipneumoniae* from diagnostic samples collected from bighorn sheep have come to light. Consistency among laboratories is key to developing effective disease management strategies; however, little formal evaluation of the extent of variation in results among labs (also known as proficiency testing or a ring test) has accompanied testing procedures. For the wildlife management community to make informed management decisions, development of a proficiency testing program for *M. ovipneumoniae* in wild bighorn sheep is needed. In conjunction with our partners, NWHC scientists examined the consistency of testing results for *M. ovipneumoniae* from the five diagnostic laboratories that voluntarily participated in the study. The partners and participating laboratories considered the ring test a success, and some laboratories made changes to their protocols based on the results of this test. Thus, this ring test served to provide new insights on current methods and the consistency of inter-laboratory results for the benefit of bighorn sheep disease management efforts. For more information about the ring test and the report, please contact Dan Walsh. **Contact:** Daniel Walsh, National Wildlife Health Center, 608-270-2481, dwalsh@usgs.gov

Effects of land use on prevalence of avian malaria in the National Park of American Samoa

Introduced avian malaria (*Plasmodium relictum*) has contributed significantly to the decline of native Hawaiian forest birds but we know less about the identity, distribution, and ecology of this disease on other Pacific islands. We investigated parasite diversity, host range, and the effects of land use on the prevalence of avian malaria in the National Park of American Samoa where the indigenous avifauna is relatively intact. *Plasmodium relictum* was not detected, but we found two unique malarial lineages (ORW1, SCEDEN01) that are distinct from *P. relictum* and most likely represent two unrelated species of *Plasmodium* based on partial sequence data from parasite mitochondrial genes. Both lineages have been described from passerines in Australasia and their geographic distribution suggests that they are indigenous throughout the SW Pacific. Overall prevalence of both lineages was higher on Ta'u (22%, 75/341) than Tutuila (9.2%, 27/294) Islands, with most infections occurring in Polynesian Starlings, Samoan Starlings, and Wattled Honeyeaters. Prevalence was relatively constant from year to year and between seasons on both islands, but the highest rates of infection (9.7% - 37.4%) were in agricultural clearings within or adjacent to more densely forested park lands. Prevalence in more remote, undisturbed areas of the National Park of American Samoa was lower, ranging from 1.4% - 7.7%. Differences in prevalence may be related to agricultural activity that increases available mosquito habitat. While the abundance, diversity, and widespread distribution of Samoan forest birds suggests that they have a long co-evolutionary relationship with their malarial parasites and few population level impacts from infection, environmental change associated with global warming and shifting land use practices may upset this balance. **Contact**: Carter Atkinson, Pacific Island Ecosystems Research Center, 808-985-6401, catkinson@usgs.gov

New publication investigates genetic exchange of influenza A viruses between the Americas by wild birds

USGS Alaska Science Center scientist Andy Ramey, in collaboration with scientists from throughout the

southern United States, recently published a paper in *Transboundary and Emerging Diseases* that examines the evidence for the redistribution of influenza A viruses between South America and North America by blue-winged teal. Through the genomic characterization of viruses isolated from birds sampled during northward spring migration, the authors found evidence for restricted viral gene flow between southern South America and the United States, most likely the result of geographical barriers within the Neotropics such as the Amazon Basin. Thus, blue-winged teal may facilitate viral redistribution among the northern Neotropics, Canada, and the United States, but not areas further south. The abstract for this article is available online at: http://onlinelibrary.wiley.com/doi/10.1111/tbed.12244/abstract. More information on avian influenza research at the Alaska Science Center can be found at: http://alaska.usgs.gov/science/biology/avian_influenza/index.php. **Contact:** Andrew Ramey, Alaska Science Center, 907-786-7174, aramey@usgs.gov

New USGS publication investigates parasitic infections in tundra-nesting geese

Protozoon blood parasite infections, such as malaria, can have negative health impacts on vertebrate hosts including wild birds. In a new publication authored by nine USGS Alaska Science Center scientists, the prevalence, transmission, and diversity of blood parasites is described in five species of tundra-nesting geese in Alaska. The authors describe parasitic infections in geese sampled at both the Yukon-Kuskokwim Delta and Arctic Coastal Plain and provide evidence for parasite transmission in Alaska since at least the early 1990s. Modeling results suggest that the transmission of blood parasites may have increased through time on the Arctic Coastal Plain. This study provides important baseline information for assessing the potential impacts of climate change on avian health and disease. The abstract for this article is available online at: http://www.nrcresearchpress.com/doi/abs/10.1139/cjz-2014-0041. More information about the Wildlife Disease Program at the Alaska Science Center can be found at: http://alaska.usgs.gov/science/biology/wildlife_disease/index.php. **Contact:** Andrew Ramey, Alaska Science Center, 907-786-7174, aramey@usgs.gov

New USGS publication identifies seasonal patterns for influenza A virus subtypes in wild birds

Seasonal patterns of influenza A prevalence in wild birds have been previously described; however the relative abundance of different viral subtypes in wild birds is not well-understood. In a new publication authored by USGS Alaska Science Center scientist Andy Ramey and USGS National Wildlife Health Center scientist Jeff Hall, in collaboration with scientists from throughout the southern United States and Central America, seasonal specific patterns of influenza A viruses are described in blue-winged teal sampled throughout Canada, Guatemala, and the United States. The authors found that H7 subtype viruses, the same viral subtype responsible for outbreaks of disease in poultry and humans, are seasonally abundant in the southern United States and Central America during spring. Thus, surveillance and biosecurity measures may be seasonally adjusted to better protect against the spillover of viruses of this subtype from wild birds into poultry production systems. The article is available online at: http://www.jwildlifedis.org/doi/abs/10.7589/2013-09-232. **Contact:** Andrew Ramey, Alaska Science Center, 907-786-7174, aramey@usgs.gov

New publication examines the evolution and infectivity of rare influenza A virus in ducks

Prior to 2010, the H14 subtype avian influenza virus had only been detected on a single occasion in the former Soviet Union. However, from 2010 through 2013, viruses of this subtype were detected at numerous locations throughout the United States and Guatemala. In a new publication, USGS Alaska

Science Center scientist Andrew Ramey, with scientists from the University of Georgia and University of Maryland, describes the genetic diversity, evolution, and infectivity of H14 in New World ducks. Collectively, evidence suggests that recently detected H14 subtype viruses are adapted to ducks and do not cause clinical disease. The sampling that detected the H14 virus by the USGS and collaborators is part of a larger study along the Gulf Coast of the United States that examines the role of migratory birds in transporting potential pathogens such as avian influenza virus between North and South America. The article is available online in the journal PLoS ONE at: http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0095620. **Contact:** Andrew Ramey, Alaska Science Center, 907-786-7174, aramey@usgs.gov

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Disease Investigations

Request for wildlife mortality and morbidity event reporting (all states)
The USGS National Wildlife Health Center 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.

NWHC disease investigation services
To request diagnostic services or report wildlife mortality events in the lower 48 states, Alaska, or Puerto Rico, 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 request these services or report wildlife mortality events in Hawaii or Pacific Island territories, please contact the Honolulu Field Station (see below).

A field epidemiologist will be your primary point of contact for questions on disease epidemiology and management. A wildlife pathologist will be your primary point of contact on diagnostic findings and cause of morbidity or mortality. Field epidemiology and pathology team members are listed below. Further information can be found at our Website: http://www.nwhc.usgs.gov/services/.

Field Epidemiology Team Contacts:
Anne Ballmann, 608-270-2445, aballmann@usgs.gov
Barb Bodenstein, 608-270-2447, bbodenstein@usgs.gov
Robert Dusek, 608-270-2403, rdusek@usgs.gov
Hawaii and Pacific Islands: Thierry Work, 808-792-9520, thierry_work@usgs.gov

Wildlife Pathology Team Contacts:
David Green, 608-270-2482, degreen@usgs.gov
Susan Knowles, 608-270-2462, sknowles@usgs.gov
Julia Lankton, 608-270-2459, jlankton@usgs.gov

Valerie Shearn-Bochsler, 608-270-2457, vbochsler@usgs.gov

White-nose syndrome winter 2013/2014 summary

Wildlife officials in three states—Arkansas, Michigan, and Wisconsin—reported their first confirmed cases of white-nose syndrome (WNS) among clinically affected cave-hibernating bats this past winter season, increasing the total number of affected states to 25. Although no new Canadian provinces were added in winter 2013/2014 to the five that are affected, continued expansion of the disease was reported in Nova Scotia, New Brunswick, Quebec, and Ontario, as well as in Midwestern and Southeastern US states. Evidence of clinical WNS now extends as far west as Jackson County, Missouri, which is on the border with Kansas, as far south as Paulding County, Georgia, and as far north as the 49th parallel in Quebec. Non-lethal PCR-based swab surveillance for the causative fungus, *Pseudogymnoascus destructans (Pd)*, was expanded into Great Plains and Southern states last winter, and the fungus was detected for the first time in several central Mississippi counties. Despite the addition of several new states to the list of WNS confirmed states, there were not any large geographic jumps in the continued spread of white-nose syndrome during winter 2013/2014. Wide-spread detection of *Pd* and clinically ill bats in multiple counties throughout Missouri indicates that the disease is now endemic there.

Also of note, Woodward County, Oklahoma, classified in spring 2010 as "WNS suspect", was removed from the official list of areas suspected to be contaminated with *Pd* based on ongoing surveillance and subsequent reanalysis of archived samples at NWHC using an improved molecular test (PCR). As a result, cave myotis (*Myotis velifer*) has been removed from the list of species found to harbor *Pd*, although this species likely remains at risk for infection as WNS continues to spread westward. More information is available about these changes at https://www.whitenosesyndrome.org/news/ (posted May 7, 2014). *Pseudogymnoascus destructans* was also recently identified by molecular testing (PCR) in 3 additional species of bats including silver-haired (*Lasionycteris noctivagans*), Eastern red (*Lasiurus borealis*), and Rafinesque's big-eared (*Corynorhinus rafesquii*) at several locations already known to be contaminated with the fungus. The significance of these new detections (performed by an independent research group) is yet to be determined as none of the bats sampled had visible signs of white-nose syndrome. It is worth noting that Eastern red bats are considered migratory and are only known to occasionally swarm at entrances of hibernacula.View the current map of WNS Occurrence by County created by the Pennsylvania Game Commission at https://www.whitenosesyndrome.org/resources/map. Current NWHC bat submission guidelines are available at: http://www.nwhc.usgs.gov/disease_information/white-nose_syndrome/USGS_NWHC_Bat_WNS_submission_protocol.pdf. **Contact:** Anne Ballmann, National Wildlife Health Center, 608-270-2445, aballmann@usgs.gov

Occurrence of *Chlamydophila* sp. in apparently healthy birds associated with a mortality event caused by chlamydiosis

During 2013-2014 mortality events caused by *Chlamydophila* (formerly *Chlamydia*)*psittaci* occurred in free-ranging exotic rosy-faced lovebirds (*Agapornis roseicollis*) in Maricopa County, Arizona. Previous surveys for *C. psittaci* in wild birds have demonstrated high variability in the occurrence of this pathogen but it is has only been identified from a small number of mortality events involving wild birds (11 epizootics and 6 individual cases in the National Wildlife Health Center database since 1978). The introduction of psitticines such as the rosy-faced lovebird, as well as other exotic species (i.e. Eurasian

collared-doves (*Streptopelia decaocto))*, to avian communities, and the occurrence of two outbreaks less than 1 year apart in Maricopa County, Arizona, may suggest altered transmission dynamics of this disease. In this study we will investigate seroprevalence and shedding of *C. psittaci* in introduced species and native species associated with bird feeders in Maricopa County. **Contact:** Robert Dusek, National Wildlife Health Center, 608-270-2403, rdusek@usgs.gov

Wildlife and the distribution of Lyme spirochetes: minimal role of Eastern fence lizards

Scientists at the USGS Patuxent Wildlife Research Center have been involved with a multi-institution study of the ecological reasons why Lyme disease is common in the Northeastern and North-Central U.S. but rare in the south, even though the tick vector (*Ixodes scapularis*) is broadly distributed in both northern and the southern states. A large portion of that study involves relationships between ticks, Lyme spirochetes, and their vertebrate hosts. This year we produced two papers on the relationships between ticks, Lyme spirochetes, and Eastern fence lizards. The first paper showed that Eastern fence lizards are not competent reservoirs of Lyme spirochete, and that they play only a minimal role in the transmission dynamics of that spirochetes in central New Jersey pine barrens. The second paper (currently in press) showed that the feeding period of ticks on eastern fence lizards was shorter at higher ambient temperatures. **Contact**: Howard Ginsberg, Patuxent Wildlife Research Center, Coastal Field Station, 401-874-4537, hginsberg@usgs.gov

Snake fungal disease

In the last decade, there has been an increase in the number of reports of wild snakes from parts of the eastern United States with severe, and often fatal, skin infections. These infections, referred to as snake fungal disease (SFD), are consistently associated with the fungus *Ophidiomyces ophiodiicola*. Clinical signs are variable and range from thickened, crusty scales and nodules below the skin to skin ulcers and severe swelling of the head. The USGS National Wildlife Health Center (NWHC) has performed diagnostics on samples collected from over 70 snakes with clinical signs consistent SFD, and is also participating in a multi-state collaborative project aimed at better understanding the disease and its potential impacts on snake populations. Although the fungus is widely distributed in captive animals, *Ophidiomyces opiodiicola* has only been identified in wild snakes in the eastern United States. The NWHC would be interested in hearing about potential cases of SFD and testing samples from other parts of the United States (*i.e.*, west of the Mississippi River) to better determine the distribution of the fungus. Conservation agencies and natural resource managers in the eastern half of the U.S. are also encouraged to report suspected cases of SFD to the NWHC. More information about SFD, along with photographs of clinical signs, can be found at http://www.nwhc.usgs.gov/disease_information/other_diseases/snake_fungal_disease.jsp. **Contact:** National Wildlife Health Center, 608-270-2480, NWHC_epi@usgs.gov

Assessing brucellosis transmission in the Greater Yellowstone ecosystem using genomics

Brucellosis, caused by the bacterium *Brucella abortus*, has been expanding its distribution in the Greater Yellowstone Ecosystem (GYE), with increasing seroprevalence in elk and outbreaks in cattle over the past decade. Understanding transmission dynamics in the region is imperative for identifying source populations responsible for infections in wildlife and livestock, and for implementing effective disease control measures. The U.S. Geological Survey- Northern Rocky Mountain Science Center, together with collaborating partners (USDA, NPS, USFWS, MT Fish Wildlife and Parks, WY Game and Fish

Department, University of Montana, Northern Arizona University), have been working on a study with the goal to better understand brucellosis transmission dynamics in the GYE using whole genome sequence (WGS) data from *B. abortus* isolates collected over the past 30 years. So far, over 240 *B. abortus* WGS, derived from bison, elk and cattle isolates, have been obtained. Analyses are underway that apply a Bayesian phylogenetic diffusion modeling approach, incorporating data on time, host species and location, to estimate spatial and cross-species transmission rates. Preliminary results suggest multiple introductions of the pathogen into the GYE. Asymmetric cross-species transmission has been detected, with the highest rates between bison and elk, as well as elk and cattle. Spatial dispersion appears to be variable through time and the Jackson and Pinedale regions appear to be a source population for *B. abortus* diversity and linked to long distance transmission events. **Contact:** Pauline Kamath, Northern Rocky Mountain Science Center, 406-994-7456, pkamath@usgs.gov

Sea urchin mortality in the Hawaiian Islands

The NWHC Honolulu Field Station is collaborating with the University of Hawaii, the State of Hawaii Division of Aquatic Resources and The Nature Conservancy to investigate an unusual mortality of collector urchins (*Tripneustes gratilla*) ongoing since February 2014. Urchins play a critical role as grazers in tropical coral reefs by helping prevent overgrowth of algae on reefs. Awareness of this issue was made apparent in the early 1980s in the Caribbean when more than 90% of its urchin population declined over a 3.5 million square kilometer area over the span of about a year, resulting in an 80% decline of coral cover with attendant loss of biodiversity. Field investigations on Oahu have revealed at least two sites with mortalities, and a recent investigation on Maui confirmed presence of mortality on west Maui. Occasional reports have come from Hawaii and Kauai. A recent survey of urchins in south and southwest Maui revealed most to be healthy and the disease limited to a single area. The main species affected is collector urchins, but there have been occasional reports of other species of urchins dying in north Kauai. Efforts to identify the potential cause of the urchin die-off in the Hawaiian Islands are ongoing. **Contact:** Thierry Work, National Wildlife Health Center, Honolulu Field Station, 808-792-9520, thierry_work@usgs.gov

Winter deaths of eared grebes and bald eagles at Great Salt Lake attributed to West Nile virus

The Great Salt Lake (GSL) is a major water bird migration site, and in November and December 2013, the Utah Division of Wildlife Resources (UDWR) estimated that 10,000 - 20,000 of the 2 million eared grebes (*Podiceps nigricollis*) that were on the GSL during migration died and 85 of the 750 – 1,250 bald eagles (*Haliaeetus leucocephalus*) were found sick or dead. U.S. Geological Survey National Wildlife Health Center (NWHC) diagnosed West Nile virus (WNV) in dead eared grebes and bald eagles submitted from this GSL mortality event. Diagnoses were based on pathological findings, molecular detection of WNV genetic material in tissues, and isolation of virus from multiple tissues from each bird. There was no evidence of the presence of other infectious diseases. This is the first report of a WNV mortality event of this size and the first report of WNV in eared grebes. West Nile virus infection in bald eagles is also uncommon. The circumstances of this unusual WNV mortality in grebes and eagles may involve increased infectivity or pathogenicity of the virus or unusual environmental conditions. Further studies are ongoing. For more information, view the Wildlife Health Bulletin on this topic. **Contact:** National Wildlife Health Center, 608-270-2480, NWHC_epi@usgs.gov

Avian cholera in seabirds in Alaska

Large numbers of sick and dead seabirds were observed washing ashore along the northern coast of Saint Lawrence Island, Alaska in late November 2013. Citizens of Gambell and Savoonga, two tribal villages approximately 40 miles apart on this remote 100-mile long island in the Bering Sea, reported the event immediately to the University of Alaska's Marine Advisory Program stationed in Nome. Villagers were able to collect some specimens from the initial die-off, including a thick-billed murre (*Uria lomvia*), a Northern fulmar (*Fulmarus glacialis*), and a crested auklet (*Aethia cristatella*), which were sent to the National Wildlife Health Center for diagnostic evaluation. Avian cholera (*Pasteurella multocida*) was diagnosed based on bacterial cultures of liver and characteristic lesions in all bird specimens submitted. Prior to this event, avian cholera had not been reported in Alaska. The closest avian cholera outbreak reported in recent history involved snow geese (*Chen caerulescens*) on Banks Island, Northwest Territories, Canada. The closest avian cholera outbreak involving seabirds was reported in common eiders (*Somateria mollissima*) and occurred on East Bay Island, Nunavut, Canada.

Native communities on Saint Lawrence Island rely almost exclusively on the subsistence harvest of many marine species, including birds, for food. Many seabirds use this area of the Bering Sea as a staging area during migration and it is an overwintering area for eiders, including the world's remaining population of spectacled eider (*Somateria fischeri*). For more information, view the Wildlife Health Bulletin on this topic. **Contact:** Barbara Bodenstein, National Wildlife Health Center, 608-270-2447, bbodenstein@usgs.gov

Sea star mortality on the West Coast

Millions of sea stars on the west coast, from Alaska to Southern California, died during a mortality event that began in June 2013. The USGS National Wildlife Health Center collaborated with scientists from multiple entities to learn more about this mortality event, conduct necropsies, and assist to coordinate a response. Collaborators included the Monterey Bay, Seattle, and Vancouver, B.C. Aquaria; University of California–Santa Cruz and UC Davis/SeaDoc Society; Wildlife Conservation Society; Western Washington University; Cornell University; Roger Williams University; and a veterinary pathologist from Northwest ZooPath. The event affected various sea star species in wild and captive populations; the two species affected most are *Pisaster ochraceus* (purple sea star or ochre starfish) and *Pycnopodia helianthoides* (sunflower sea star). To date, no underlying cause(s) of these mass mortalities have been identified. In previous outbreaks, bacterial and viral agents as well as environmental toxins and contaminants were suggested as underlying causes, but they were not confirmed. The 2013 outbreak appears more severe than previous outbreaks, killing up to 95 percent of some populations and affecting a much larger geographic area along the west coast. For more information, please see the Wildlife Health Bulletin on this topic. **Contact:** Barbara Bodenstein, National Wildlife Health Center, 608-270-2447, bbodenstein@usgs.gov

Survey for malaria and other blood parasites in non-native reptiles of Florida

Malaria parasites in the genus Plasmodium have the potential to negatively impact the health of wildlife populations, and approximately half of the 200 currently known Plasmodium species are reported from reptile hosts. One malaria parasite species, *Plasmodium floridense*, is native to Florida. But, at least 50 non-native reptile species are established in Florida, and these species may have brought additional malaria parasite species with them. We are screening non-native reptile species in Florida for malaria and other blood parasites using both morphology (blood films) and DNA, and have two goals related to the

potential role of the non-native reptiles in disease of the native populations. First, we aim to learn whether the native species *P. floridense* is able to infect any non-native reptiles in Florida, where the non-native species may serve as reservoir for the parasite. Second, we seek to detect any potentially non-native malaria parasites that may be able to infect native reptile species, and potentially spill over from non-native to native reptile species. **Contact:** Bryan Falk, Fort Collins Science Center, South Florida Natural Resources Center, 305-242-7820, bfalk@usgs.gov

USGS research on migration and avian influenza

USGS scientists continue working with United Nations Food and Agriculture Organization, the University of Oklahoma, and international partners in persistent zones of HPAI H5N1 infection in Asia. Swan geese were marked in August 2014 with GSM transmitters in Mongolia to identify migratory connectivity to breeding grounds in China (also with Alaska Science Center, Science and Conservation Center of Mongolia, Mongolia Academy of Sciences, and Mongolia State Central Veterinary Lab). In the March 2014 issue of *EcoHealth*, the multi-disciplinary team published research findings on avian influenza transmission within areas of highly intensive free-grazing duck and wild waterfowl in the Poyang Lake region of China, near the epicenter of H5N1. In 2014, a book chapter entitled, "Animal Migration and Risk of Spread of Viral Infections" was published in *Viral Infections and Global Change* (Blackwell Publishing), and in the August 2013 issue of *Frontiers in Public Health* the first avian influenza geospatial risk models focusing on the interface between wild and domestic birds were published. **Contact:** Diann Prosser, Patuxent Wildlife Research Center, 301-497-5914, diann_prosser@usgs.gov; and John Takekawa, Western Ecological Research Center, 707-562-2000, john_takekawa@usgs.gov

Recent publications of interest – Disease Investigations

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Johnson, J.A., L.H. DeCicco, D.R. Ruthrauff, S. Krauss, and J.S. Hall. 2014. Avian influenza antibody detections in Pacific coast Red Knots (*Calidris canutus roselaari*). Journal of Wildlife Diseases 50:671-675.

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Amphibians

Mathematical model to control the impact of Bd in amphibian population

Chytridiomycosis is a disease that poses a serious threat to anuran populations worldwide. Several studies confirmed that inoculation of *Janthinobacterium lividum* (Jl) could inhibit the disease. In this study, we developed a mathematical model of an amphibian juvenile-adult population in a single pond infected with chytridiomycosis caused by the fungal pathogen *Batrachochydrium dendrobatidis* (Bd) to investigate on how the inoculation of anti-Bd bacterial species Jl could reduce Bd infection on amphibians. Furthermore, we model how temperature plays an important role in the disease dynamics. We also showed how temperature variation influence the Bd disease on amphibians. Our findings confirm that chytrid fungus is limited by temperature and is less likely to occur in warmer ponds. Although our results predict various scenarios where it is possible for Jl to limit the impact of Bd, a better understanding of the Jl lifecycle is needed to fully understand such interaction. **Contact**: Jacoby Carter, National Wetlands Research Center, 337-266-8620, carterj@usgs.gov

Fisheries

Thiamine deficiency and immune dysfunction in lake trout
Although researchers have recognized the connection between thiamine and the death of the young salomonids for a decade, a new study provides additional insight into thiamine deficiency and the health of post age-0 fish. Early Mortality Syndrome, or EMS, results in embryonic mortality in salmon, steelhead trout, brown trout, lake trout, and Chinook salmon. Vitamin B1, or Thiamine, is an essential nutrient that animals must obtain through their diet. Alewives, an invasive species and one of the main diets of many Great Lakes fish, contain an enzyme called thiaminase that destroys the thiamine in fish that consume them. The lack of B1 leads to EMS as well as the newly reported immune dysfunctions which may be perpetuating infectious diseases in Great Lakes salmonid populations. In a study focused on lake trout, researchers at the USGS Leetown Science Center have demonstrated that fish who survive the initial impact of thiamine deficiency experience changes in immune function that resemble those occurring in humans with inflammatory diseases. **Contact**: Chris Ottinger, Leetown Science Center, 304-724-4453, cottinger@usgs.gov

Stream salmonids switch to terrestrial insect prey as stream metal concentrations increase
Aqueous metals can cause precipitous declines in stream invertebrate communities and can limit fish populations as well at relatively high concentrations. However, little is known about how fishes persist at moderate metal concentrations when their aquatic food source is greatly reduced. Researchers at the Fort Collins S.C., Crustal Geophysics & Geochemistry S.C., and Colorado State University used stream surveys of fish, their diets, and resource availability to determine how stressors that reduce aquatic prey could increase the need for and reliance of stream consumers on terrestrial insect prey. They found that fish (mainly Brook Trout and Brown Trout) consumed proportionately more terrestrial insect prey as stream metal concentrations increased. This finding indicates that aquatic food webs appear to become more "terrestrial" as the aquatic stressors impacting aquatic insect communities increased. These results suggest that intact riparian zones and aquatic-terrestrial linkages will be particularly important for maintaining economically important trout fisheries in moderately stressed aquatic systems. **Contact:** Johanna Kraus, Fort Collins Science Center, 970-226-9436, jkraus@usgs.gov

Postmortem analysis of ploidy of grass carp (*Ctenopharyngodon idella)*and black carp (*Mylopharyngodon piceus)*
Habitat impacts from Asian carps can be substantial regardless of their ploidy status. Generally, diploid carp are capable of reproducing, while triploids have limited or no ability to reproduce. However, successful natural reproduction and persistence of nuisance Asian carp species is occurring in some North American waters. Protocols have been implemented for fisheries biologists to send feral caught Asian carp (eyeballs) samples for ploidy analysis by flow cytometry. Postmortem analysis is now possible, whereby live tissue up to two weeks postmortem or tissue frozen with cryoprotectant is used. Correct ploidy identification is allowing states to determine if diploids are in their waters or crossing state lines in hauling trucks, and the results are informing predictions of spread in watersheds. The Mississippi Interstate Cooperative Resource Association (http://www.micrarivers.org/) has distributed SOPS

nationally, whereby relevant researchers, labs, and databases of feral captures are maintained and coordinated (e.g., http://nas.er.usgs.gov/; USGS Nuisance Aquatic Species database) and samples are being analyzed at Whitney Genetics Laboratory, Onalaska, Wisconsin (http://www.fws.gov/midwest/lacrossefishhealthcenter/) along with the eDNA surveillance program.
Contact: Jill A. Jenkins, National Wetlands Research Center, 337-266-8607, jenkinsj@usgs.gov

Methylmercury impacts to reproduction in the eastern mosquitofish; implications for effects to fish populations with elevated methylmercury (MeHg) concentrations
This project is an effort to develop a MeHg guideline level for fish. With the assistance of collaborators at the University of Florida, we have developed a DNA library for the mosquitofish that will allow us to detect molecular queues indicating MeHg, as well as other contaminants, toxicity to mosquitofish. We are initiating dose response studies in which mosquitofish will be fed a MeHg contaminated diet over multiple generations with the intent to monitor effects upon reproduction (time to sexual maturity, sex ratio, brood size, vitellogenin, etc). In addition, those responses will be compared to results of microarray analyses to evaluate the utility of microarrays in field assessments of MeHg impacts to fish populations.
Contact: Tim Bargar, Southeast Ecological Science Center, 352-264-3520, tbargar@usgs.gov

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Contaminants

Development of an ecosystem-scale selenium accumulation model for the Lower Gunnison River Basin: determining remedy effectiveness in limiting selenium accumulation into native fishes, 2014-2017

The Fort Collins Science Center and Colorado Water Science Center is working with the Colorado River Water Board and the Selenium Management Task Force to determine if the 4.6 ug/L standard at the Whitewater gage is protective of endangered and managed fish species in the Critical Habitat Reach of the Lower Gunnison River Basin. Many tributaries in the Lower Gunnison River Basin are underlain by the Cretaceous Mancos Shale, a natural source of selenium, and are on the Colorado 303(d) list for dissolved selenium concentrations that consistently exceed the aquatic-life standard. Conversion of the natural landscape to irrigated agriculture exasperates selenium weathering and transport to the Gunnison River. The U.S. Fish and Wildlife Service in 2009 issued a Gunnison Basin Programmatic Biological Opinion requiring that users of the Gunnison and Colorado Rivers develop a Selenium Management Program (SMP) to "reduce adverse effects of selenium on endangered fish species in the Gunnison and Colorado rivers". In support of the SMP, USGS is working to develop an Ecosystem-scale selenium accumulation model (ESAM) for the critical habitats of the Gunnison River. The need for the model is because aqueous selenium is not readily accumulated by aquatic organisms; rather it is accumulated via the diet. By developing qualitative food webs and using the Ecosystem-scale selenium accumulation model we can determine if the standard set at the Whitewater gage is protective of these endangered and managed species (i.e., Colorado Pikeminnow, Razorback Suckers). **Contact**: Travis S. Schmidt, Fort Collins Science Center and Colorado Water Science Center, 970-226-9470, tschmidt@usgs.gov

Estimating risk to aquatic communities from common contaminants found in urban drainage in the United States: Polyaromatic Hydrocarbons and Pyrethroids

Bifenthrin and Polyaromatic Hydrocarbons are two of the most common contaminants found in urban rivers in the United States. However, there is little data on the effects of these compounds on aquatic insects or in mixture. Although standard toxicity test organisms have provided valuable data used to develop benchmarks and standards for aquatic life, these organisms share very little in common with the epi-benthic aquatic insects that are the most diverse and abundant organisms found in rivers. Further, standard toxicity tests are criticized for being environmentally unrealistic. To support the National Ambient Water Quality Assessment team, we are using a mesocosm facility known as the Aquatic Experimental Laboratory housed at the Fort Collins Science Center to evaluate responses by epi-benthic aquatic insect communities to these common urban contaminants. The investigation will give valuable insight into the unique responses by these taxa to the contaminants alone and in mixture so that signature community responses could be identified to help determine the stressor affecting aquatic insect communities in streams of the United States. **Contact**: Travis S. Schmidt, Fort Collins Science Center and Colorado Water Science Center, 970-226-9470, tschmidt@usgs.gov

Satellite tracking of birds from Alaska points to distant sources of lead and mercury exposure (Alaska)

U.S. Geological Survey scientists measured lead in blood from tundra swans that nest in Alaska and then followed the migration of these birds using satellite telemetry. Levels of lead in blood were higher in adults than young swans, suggesting exposure to lead occurs on wintering areas and/or during migration, rather than on the summer breeding grounds in Alaska. The lowest blood levels were found in swans that rarely migrate from their nesting grounds in southern Alaska. The highest levels of lead were in swans that nest on the North Slope of Alaska and these swans spend their winters along the Atlantic coast, primarily in North Carolina and Maryland. However, the overall blood lead concentrations in swans sampled in Alaska were below levels known to cause harm to birds or humans.

In another study by U.S. Geological Survey scientists and collaborators, historic and current levels of mercury were measured in yellow-billed loons that nest in Alaska. Yellow-billed loons are one of the rarest breeding birds in North America, the rarest of all loons world-wide, and are under consideration for listing under the endangered species act. Mercury in samples of blood and/or feathers from 115 yellow-billed loons captured between 2002-2012 and feather samples from 25 museum specimens from the 1845 to present were, on average, below levels thought to be harmful based on comparative data in common loons. However, some of the individual yellow-billed loons had mercury elevated enough to potentially decrease reproduction. In addition, mercury concentrations in museum specimens showed that exposure has doubled over time. Satellite telemetry data provides evidence that most of the yellow-billed loons that nest in Alaska winter in Asia. Mercury levels in blood, which indicates recent exposure, was lower than the levels in feathers, which are grown after molting on wintering grounds in Asia, indicating that the majority of mercury in the yellow-billed loons was acquired on their wintering grounds in Asia. These data, and the potential for further release of mercury from melting permafrost into the environment, point to mercury as a current and potentially increasing stressor of yellow-billed loons. **Contact:** Craig Ely, Alaska Science Center, 907-786-7182, cely@usgs.gov; and Joel Schmutz, Alaska Science Center, 907-786-7186, jschmutz@usgs.gov

PCB concentrations decline in waterbirds nesting in Green Bay, Wisconsin

The USGS Upper Midwest Environmental Sciences Center in collaboration with the USGS National Wildlife Health Center collected double-crested cormorant (*Phalacrocorax auritus*), black-crowned night-heron (*Nycticorax nycticorax*), and tree swallow (*Tachycineta bicolor*) eggs in 2010 from PCB-contaminated Green Bay, Wisconsin. Egg collections of the same species from the same locations were made in the early- to mid-1990s. Over this 15-year time period, concentrations of PCBs declined 70%, 88%, and 35% among cormorants, night-herons, and swallows, respectively. DDE concentrations in eggs declined 51%, 80%, and 47%, respectively, for the three species. These declines are consistent with regional contaminant trends in other species. A publication, which includes these results, is now available (Custer, T.W., P.M. Dummer, J.C. Franson, C.M. Custer, and M. Jones. 2014. Contaminant exposure of birds nesting in Green Bay, Wisconsin, USA. Environmental Toxicology and Chemistry 33:1832-1839). **Contact:** Tom Custer, Upper Midwest Environmental Sciences Center, 608-781-6375, tcuster@usgs.gov

Methyl-mercury a potent neuroendocrine disruptor

Methyl-mercury (MeHg) is a potent neuroendocrine disruptor that impairs reproductive processes in fish. The objectives of this study were to (1) characterize transcriptomic changes induced by MeHg exposure in the female largemouth bass (LMB) hypothalamus under controlled laboratory conditions, (2) investigate the health and reproductive impacts of MeHg exposure on male and female largemouth bass

(LMB) in the natural environment, and (3) identify MeHg-associated gene expression patterns in whole brain of female LMB from MeHg-contaminated habitats. The laboratory experiment was a single injection of 2.5 µg MeHg/g body weight for 96 h exposure. The field survey compared river systems in Florida, USA with comparably lower concentrations of MeHg (Wekiva, Santa Fe, and St. Johns Rivers) in fish and one river system with LMB that contained elevated concentrations of MeHg (St. Marys River). Microarray analysis was used to quantify transcriptomic responses to MeHg exposure. Although fish at the high-MeHg site did not show overt health or reproductive impairment, there were MeHg-responsive genes and pathways identified in the laboratory study that were also altered in fish from the high-MeHg site relative to fish at the low-MeHg sites. Gene network analysis suggested that MeHg regulated the expression targets of neuropeptide receptor and steroid signaling, as well as structural components of the cell. Disease-associated gene networks related to MeHg exposure, based upon expression data, included cerebellum ataxia, movement disorders, and hypercalcemia. Gene responses in the CNS are consistent with the documented neurotoxicological and neuroendocrine disrupting effects of MeHg in vertebrates. **Contact:** Cathy Richter, Columbia Environmental Research Center, 573-876-1841, crichter@usgs.gov

Spatial and temporal trends in occurrence of emerging and legacy contaminants in the Lower Columbia River 2008-2010
The Lower Columbia River in Oregon and Washington, USA, is an important resource for aquatic and terrestrial organisms, agriculture, and commerce. An 86-mile stretch of the river was sampled over a 3 year period in order to determine the spatial and temporal trends in the occurrence and concentration of water-borne organic contaminants. Sampling occurred at 10 sites along this stretch and at 1 site on the Willamette River using the semipermeable membrane device (SPMD) and the polar organic chemical integrative sampler (POCIS) passive samplers. Contaminant profiles followed the predicted trends of lower numbers of detections and associated concentrations in the rural areas to higher numbers and concentrations at the more urbanized sites. Industrial chemicals, plasticizers, and PAHs were present at the highest concentrations. Differences in concentrations between sampling periods were related to the amount of rainfall during the sampling period. In general, water concentrations of wastewater-related contaminants decreased and concentrations of legacy contaminants slightly increased with increasing rainfall amounts. USGS Press Release: Potentially Harmful Levels of Contaminants Found in Fish in the Columbia River (http://www.usgs.gov/newsroom/article.asp?ID=3878). **Contact:** David Alvarez, Columbia Environmental Research Center, 573-441-2970, dalvarez@usgs.gov

Acute and chronic sensitivity of white sturgeon (*Acipenser transmontanus*) and rainbow trout (*Oncorhynchus mykiss*) to cadmium, copper, lead, or zinc in laboratory water-only exposures: U.S. Geological Survey Scientific Investigations Report 2013–5204. White sturgeon (*Acipenser transmontanus*) are experiencing poor recruitment in the trans boundary reach of the upper Columbia River (UCR) in eastern Washington State. Limited toxicity data indicated that early life stages of white sturgeon were sensitive to metals; however, insufficient information is available to define acute or chronic toxicity thresholds for metals for this species. The objectives of this study were to (1) evaluate comparative sensitivity of white sturgeon and commonly tested rainbow trout (*Oncorhynchus mykiss*) to cadmium, copper, lead, or zinc in chronic water-only exposures; and (2) determine if U.S Environmental Protection Agency national recommended chronic water-quality criteria (WQC) or Washington State chronic water-quality standards (WQS) are protective of white sturgeon to the metal exposures. **Contact:** Chris Ingersoll, Columbia Environmental Research Center, 573-876-1819, cingersoll@usgs.gov

Publications of interest – Contaminants

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