As you are all undoubtedly aware, federal agencies are increasingly being directed to improve the efficiency in which we conduct programs in an effort to support our leader’s efforts in reducing the Federal budget deficit. The NWDP is working with other programs in Wildlife Services and APHIS to examine ways in which we can more efficiently provide the critical services necessary to protect and secure our Nation’s agriculture, natural resources, and public health.

Recently Wildlife Services worked with Veterinary Services, International Services, and Animal Care within APHIS to develop a plan on how we can more effectively provide support on health issues that involve wildlife. Additionally, over the last 18 months, the NWDP has reduced its workforce by over 50% in our program office and 25% in our field program. While we realize these actions will affect the scope and depth of the services we provide our cooperators and the public, the NWDP, Wildlife Services, and APHIS as a whole, remain committed to our mission of protecting the health and value of American agriculture and natural resources.

Although we have eliminated some disease projects in FY12, such as the national highly pathogenic avian influenza early detection system, we will continue our collaborations to conduct morbidity and mortality surveillance in wild birds, comprehensive feral swine disease surveillance, and plague and tularemia monitoring. Additionally, we have initiated some smaller projects such as vector surveillance for blue tongue and epizootic hemorrhagic disease, *Baylisascaris procyonis*, diseases in mute swans, and avian Borna virus. You can find information on these projects in this issue of The Carrier, or in one of the Program Activity Reports posted on our website. We will also continue to provide emergency response support to state and federal agencies.

Clearly, these are difficult financial times for our country. The need for fiscal frugality by government agencies will affect all our programs. Such constraints will require us to increase our collaborations with traditional and non-traditional partners, to effectively reach our common goal of protecting wildlife, agricultural, and human health. We have made great strides on this common endeavor in recent years, and the NWDP looks forward to being a part of future progress.
Baylisascaris Surveillance in Wildlife Populations
By Emily Blizzard

The disease producing capability of nematodes in the genus Baylisascaris has been a rising concern in recent years. Infections by these parasites have important health implications for individuals and populations of domestic animals, captive and free ranging wildlife, zoo animals, and humans. Within North America, there are four significant species of Baylisascaris, each utilizing a separate definitive host (a species in which the parasite does not cause disease but is capable of sexually reproducing). Baylisascaris procyonis is the most pathogenic species and uses raccoons (Procyon lotor) as its definitive host. Baylisascari columnaris, B. melis, and B. transfuga are progressively less pathogenic and use skunks, badgers, and bears as their definitive hosts, respectively.

The NWDP has recently initiated sampling procedures for B. procyonis and B. columnaris. Baylisascaris procyonis is a large intestinal nematode commonly found in raccoons throughout the United States and is recognized as a cause of fatal or severe neurological disease in both animals and humans. Over 90 species of birds and mammals have been documented with clinical signs of disease caused by B. procyonis in North America. When poultry become infected producers may experience mass mortality events. Brood or chicken houses located in areas where B. procyonis exists can easily become contaminated. Infected raccoons shed an estimated 115,000 - 179,000 B. procyonis eggs/worm/day in their feces. Thus, restricting access of susceptible wildlife species to pens and feeds, along with removing potentially infectious feces is essential to protecting poultry.

A review of the life cycle of B. procyonis can help to fully appreciate the potential implications of infections. An adult raccoon infected by adult worms can produce and shed eggs into the environment within 50-76 days. Shed eggs (non-infective) then embryonate for 11 to 14 or more days, depending on temperature and humidity, before they become infective. These eggs can potentially remain viable in the environment for several years allowing billions of eggs to accumulate at latrine sites. Infective eggs may then be either ingested by juvenile raccoons or by an intermediate host (e.g., rodents, lagomorphs, humans). An intermediate host is a suitable species in which the disease agent develops and may cause disease but cannot sexually reproduce. Infective eggs ingested by a raccoon hatch inside the small intestine then travel to the intestinal lumen reaching maturity in 32-38 days, perpetuating the cycle. When an intermediate host ingests an infective egg, though, the larvae hatch and migrate throughout the host (organ systems, spinal cord, brain, etc.). These migrating larvae can result in severe, organ specific disease. When an adult raccoon consumes an infected intermediate host, or other definitive host, the life cycle is also completed.

The NWDP’s objectives for monitoring Baylisascaris species in wildlife are to determine the apparent prevalence and distribution of B. procyonis in raccoons and B. columnaris in skunk populations on a national scale; to identify and document factors associated with B. procyonis expansion; correlate human cases with infection rates in wildlife and domestic animals; and compile risk assessment maps for humans living in endemic areas. Wildlife Disease Biologists in twenty-three states have agreed to participate in this activity, and several have already submitted samples. Thus far, 506 samples have been received in Fort Collins where they are morphologically identified through PCR or via microscopy when possible. Sample collection for the current surveillance project will continue until September 30, 2012.

Tularemia Bioassay
By Dennis Kohler

Tularemia is a bacterial disease caused by Francisella tularensis. The organism infects and induces disease in a broad range of mammalian hosts, including humans. Tularemia also is considered a biodefense threat and therefore work with the agent is highly regulated. A national surveillance program has been established to test blood samples collected from wildlife for antibodies to F. tularensis. Surveillance results will serve as an index for tracking changes in distribution across the country and potentially enable prediction of outbreaks. The microagglutination assay is a widely used technique for detecting antibodies to F. tularensis and is based on the ability of antibodies to induce clumping of the bacteria. Recently, the Centers for Disease Control have limited the number of samples they will analyze for the Wildlife Services national surveillance system. Consequently, Colorado State University in cooperation with the NWDP, is working to develop an in-house assay for detecting antibodies for F. tularensis. The diagnostic test uses a formalin-killed F. tularensis that is stained with crystal violet. This antigen preparation was initially evaluated with control mouse serum and sera from mice that had been vaccinated and challenged with virulent Schu4 strain organisms. Antibodies were readily detected in mice experimentally-infected with F. tularensis but not in control mice. The next step was developing the ability to use this approach to test Nobuto strips collected in the field. Initial results revealed 87.5% sensitivity to samples of coyote blood eluted from Nobuto strips were judged to be positive and 100% specificity to all negative samples.

http://www.aphis.usda.gov/wildlife_damage/nwdp/
**PLAGUE AND TULAREMIA PROJECT**

By Sarah Bevins

Tularemia is a zoonotic disease caused by the bacterium *Francisella tularensis*. It is considered to be one of the most virulent pathogens ever studied based on its infectious nature and ability to readily aerosolize. Naturally occurring tularemia infections have been documented in hundreds of mammal species and numerous vectors. This extremely broad host range has complicated efforts to understand its ecology. In addition, while many human infections in the United States are linked to tick or deer fly exposure, tularemia transmission has also been linked to contaminated water or direct contact with infected mammals. The NWDP is part of a collaborative group that collects long-term data on tularemia exposure in wildlife from across the United States. The goal of this group is to develop a better understanding of tularemia presence in the environment.

Plague is caused by *Yersinia pestis*, a flea-borne bacterium most often associated with rodents, but can infect a wide range of mammal species. Although plague appears to exist at very low levels, human infections and wildlife mortality events occur every year. While the number of human cases is low, undiagnosed infections can be fatal and there is the risk that a pneumonic plague infection could spread rapidly from person to person in the absence of disease recognition. Despite the relatively limited occurrence of human plague cases in the United States, evidence of plague exposure in non-domestic rodents and carnivores is substantial in the West, and is a motivating reason to continue active plague surveillance.

From 1 Oct 2010 to 30 Sept 2011, the NWDP, in collaboration with the Centers for Disease Control and Prevention, the Texas Department of State Health Services, the Washington State Department of Health, along with other state programs, assisted 43 states and 1 territory with plague and tularemia surveillance. Over 7,000 wildlife samples were submitted to the Plague and Tularemia Nobuto Archive and a subset of those were tested for exposure to plague and tularemia. Of that subset, 88 tested positive for plague exposure and 10 samples tested positive for tularemia exposure. A majority of plague positive wildlife originated in New Mexico (n=55), followed by positive exposures in Nevada (n=9) and Wyoming (n=6). All positive exposures, except for one, came from coyotes. Although overall seroprevalence is still very low for Tularemia, exposure was detected in wild canids (n=7) and feral swine (n=3) in multiple states. A large-scale analysis is underway to compile plague and tularemia data collected by the NWDP during the previous 5 years and use that data to quantify disease patterns across the United States.

**DEVELOPMENT OF GUIDELINES FOR THE SURVEILLANCE OF BOVINE TB IN WILDLIFE**

By Kerri Pedersen

Bovine Tuberculosis is a chronic bacterial disease caused by *Mycobacterium bovis*. The disease primarily affects cattle, but also can affect other species, including humans and several wildlife species. It is usually transmitted to humans by ingestion of unpasteurized milk, inoculation by contaminated instruments, or inhalation of aerosolized respiratory tract bacteria. The disease can be spread among livestock and wildlife by the fecal-oral route, ingestion of contaminated food, or through the respiratory tract. Occurrence of bovine tuberculosis has been greatly reduced in cattle over the last few years. However, there is concern that spillover into wildlife may maintain the organism in the environment and function as a source of re-infection for livestock.

Concern about possible spillover of the disease into wildlife led the NWDP to collaborate with Veterinary Services’ National Tuberculosis Eradication Program on the development of a manual to assist state and federal agencies in detecting *M. bovis* infections in wildlife. Agencies with expertise in addressing bovine tuberculosis in wildlife, including the Michigan and Minnesota Departments of Natural Resources, were consulted, and the most current literature on the disease was reviewed and incorporated into the manual. Although the manual provides general guidelines for implementing surveillance, interagency cooperation is highly encouraged when developing a state-specific plan.

The overall goal for creating the manual was to provide a resource regarding *M. bovis* in wildlife for states with new detections of the disease in domestic animals. Guidelines provided in the manual were developed specifically to determine presence or absence of *M. bovis*, not to determine prevalence. Instructions for determining which wildlife species to target, selecting geographic areas for sampling, supplies necessary for sampling, personal protective equipment, and specific sample collection procedures are included in the manual. Pictures of tissue specimens and other pertinent information for sampling a variety of wildlife species are included as appendices. The manual even includes information on shipping, testing, and reporting processes. A supplemental MSExcel® spreadsheet to calculate appropriate sample sizes based on case-specific parameters was even developed.

The manual was finalized in June and can be found on the NWDP and Veterinary Services websites, and should serve as a valuable tool for agencies. The completion of this manual is a direct result of a successful collaborative effort among many federal and state agencies.
Feral swine (Sus scrofa) are considered an invasive exotic species in the United States. Their populations continue to expand and an estimated 5 million individuals occur in at least 38 states. Feral swine are able to tolerate and exploit a wide variety of environmental conditions, grow and reproduce rapidly, are aggressive competitors for local resources, and lack natural predators throughout the majority of their geographic distribution.

Feral swine are competent hosts for a number of endemic and exotic diseases that pose a threat to agriculture and human health. Although diseases such as Classical swine fever, Foot-and-mouth disease, and African swine fever are not currently found in the United States, feral swine have been identified as a high-risk pathway for their transmission into other susceptible populations. Surveillance for endemic and foreign animal diseases in wildlife requires heightened vigilance and a proactive approach given their intractable nature. Obtaining an adequate number and appropriate distribution of samples from wildlife, including feral swine, is difficult and often requires extensive resources.

The NWDP collected over 3,000 samples from 32 states from 1 October 2010 to 30 September 2011 as part of its comprehensive feral swine disease surveillance project. The majority of samples were collected from feral swine populations considered to be at high risk of a foreign animal disease introduction or living in close proximity to domestic swine facilities.

Classical swine fever is a highly contagious viral septicemia affecting only swine. Also known as hog cholera, it has been eradicated from many developed nations with extensive swine production, including the United States, but is still endemic in much of the world. Outbreaks in countries previously considered disease-free can have severe economic impacts through high swine mortality, the curtailment of exportation of swine and pork products, and from costs incurred to control and eradicate the disease. The NWDP plays an important role in the Animal and Plant Health Inspection Service’s swine health surveillance program by collecting sera from feral swine populations to determine if classical swine fever has been introduced. During fiscal year 2011, 1,866 nasal swabs and 2,360 serum samples have been submitted for diagnostic testing. Thirteen out of the 1,849 nasal swabs tested by the National Animal Health Laboratory Network and Veterinary Services on a negative cohort project to detect an introduction of these diseases into the United States. From 1 October 2010 to 30 September 2011, the NWDP collected oral swabs from 463 feral swine in 11 states for validation of the foot-and-mouth disease real time, reverse transcriptase polymerase chain reaction test, and 291 whole blood samples from 7 states were provided for African swine fever test validation. This project also served to assess procedures and processes related to sample collection, testing, and communication, which ultimately improves capacity for future cooperative surveillance projects.

Pseudorabies is an economically important viral disease of swine throughout the world. In 2004, all 50 states in the United States attained pseudorabies-free status in commercial swine herds. However, the virus is known to exist in feral swine populations in 26 states. The spread of virus from feral swine back to domestic swine remains the primary potential source for reintroduction into commercial herds. During fiscal year 2011, NWDP collected 3,122 serum samples from feral swine; 573 (22.5%) were positive for pseudorabies exposure. Feral swine carry a number of endemic diseases that pose a risk to humans, domestic cattle and swine operations. One example is swine brucellosis caused by the bacterium Brucella suis. During fiscal year 2011, NWDP collected 3,128 serum samples to assess status of swine brucellosis in feral swine; 115 (3.8%) were positive for Brucella antibodies.

At the request of the National Pork Board, the NWDP has initiated surveillance activities to elucidate the geographic distribution and apparent prevalence of Trichinella and Toxoplasma in feral swine. During fiscal year 2011, 36 samples were collected for Toxoplasma testing and 2,786 to test for Trichinella. Diagnostic results are pending.

The NWDP initiated surveillance activities for swine influenza virus on 1 November 2010. As of 29 September 2011, Wildlife Disease Biologists have collected samples in 31 of the 38 states known to have feral swine. Nasal swabs were collected in targeted counties and serum samples continue to be collected nationally. Thus far, 1,866 nasal swabs and 2,360 serum samples have been submitted for diagnostic testing. Thirteen out of the 1,849 nasal swabs tested by the National Animal Health Laboratory Network and Veterinary Services on a negative cohort project to detect an introduction of these diseases into the United States. From 1 October 2010 to 30 September 2011, the NWDP collected oral swabs from 463 feral swine in 11 states for validation of the foot-and-mouth disease real time, reverse transcriptase polymerase chain reaction test, and 291 whole blood samples from 7 states were provided for African swine fever test validation. This project also served to assess procedures and processes related to sample collection, testing, and communication, which ultimately improves capacity for future cooperative surveillance projects.
Mute swans (Cygnus olor) are considered an invasive species in many parts of the United States, including the Great Lakes region and the Northeastern United States. They are prolific and are not typically afraid of humans, which explain their large population densities in many urban areas. They inflict significant ecological damage by eating submerged aquatic vegetation that serves as food for native waterfowl, and habitat for fish and crabs. Their aggressive nature can prevent other birds from nesting as well as threaten human safety.

Wildlife Services has received funding from the Great Lakes Restoration Initiative to lethally remove mute swans in an effort to minimize the ecological damage they cause. Wildlife disease biologists in the Great Lakes region and in the Northeast have been opportunistically collecting samples from these birds for disease surveillance. The goal of the mute swan disease surveillance project is to learn more about the various pathogens carried by swans, in particular, those that have the potential to impact agricultural or human health. The project has grown into a collaborative effort including Michigan State University, Agricultural Research Service, Southeastern Cooperative Wildlife Disease Study, and Texas A&M University.

One of the primary diseases of concern is Newcastle disease virus because of its negative impact on domestic and wild birds. Many die-offs that have occurred in the Great Lakes region and Northeastern United States have been attributed to Newcastle disease. If mute swans are infected, they may transmit the disease to other susceptible wild birds or poultry. Many of the mute swans are removed from areas where they may come into contact with humans (swimming, watersports). Consequently, Schistosomes (the parasite that causes swimmer’s itch) were also included as a target parasite for screening. Many other parasites with varying levels of virulence also have been detected in intestinal tracts of sampled swans. Salmonella species are ubiquitous in nature but in most cases the serotypes are species specific. However, there are a few serotypes capable of causing disease in multiple species, including humans. Toxoplasmosis is a parasitic disease caused by the protozoan, Toxoplasma gondii that infects most mammals. Samples were collected from swans to evaluate their exposure to T. gondii. Avian influenza is another disease of interest. In Europe, mute swans have been implicated in carrying H5N1. Serum samples were collected to evaluate exposure, and combined cloacal/oropharyngeal samples were collected to further identify the specific serotypes of avian influenza circulating in mute swans. Swan samples were submitted to test for Avian Borna Virus, a disease previously thought to be found only in parrots and other pet birds, but recently determined to be common in Canada geese (Branta canadensis) (see article below).

From 1 October 2010 to 30 September 2011, 461 mute swans were sampled for disease testing. Samples were collected from Michigan (56%), New Jersey (24%), New York (3%), Rhode Island (17%) and Wisconsin (0.4%). The results that have been completed to date are summarized in the table below.

<table>
<thead>
<tr>
<th>Disease</th>
<th>Negative</th>
<th>Positive</th>
<th>Pending</th>
</tr>
</thead>
<tbody>
<tr>
<td>Newcastle</td>
<td>87</td>
<td>113</td>
<td>260</td>
</tr>
<tr>
<td>Salmonella</td>
<td>455</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>Parasites</td>
<td>348</td>
<td>74</td>
<td>39</td>
</tr>
<tr>
<td>Avian Influenza</td>
<td>35</td>
<td>149</td>
<td>275</td>
</tr>
</tbody>
</table>

Sampling will continue through fiscal year 2012; however, the sampling protocol will change slightly. An additional 200 samples will be collected to allow further identification of Newcastle disease virus, eastern equine encephalitis, and intestinal parasites.

Avian Borna Virus

By John Baroch

Borna disease is a neurological disorder found in a variety of domestic and wild mammals, and humans. It can cause fatal movement and behavioral disorders in warm-blooded animals, and perhaps neuropsychiatric disorders in humans. The causative agent is Borna disease virus. The virus is a non-segmented negative strand RNA virus (Family Bornaviridae). Its name comes from the German city of Borna, where the disease was common during early 20th century, killing more than 16,600 horses between 1896 and 1940. The natural host is believed to be the bicolor white-toothed shrew (Crocidura leucodon). Virus is shed in the shrew’s urine. Other wildlife hosts have been proposed but not confirmed.

A second member of the family Bornaviridae was identified in 2008. Avian Borna virus causes proventricular dilatation disease in psittacine birds (e.g., parrots, macaws, conures). This disorder is characterized by damage to the nerves of the enteric system, resulting in accumulation of food in the paralyzed proventriculus, and eventually leading to death. There are reports of wild Canada geese (Branta canadensis) displaying borna disease symptoms, and scientists have previously detected the virus in brain tissue of trumpeter swans (Cygnus buccinator) that had exhibited signs of neurological disease prior to death.

In July 2010, researchers at Texas A & M University requested a loan of Canada goose samples from the NWDP Wild Bird Tissue
Borna virus and epizootic hemorrhagic disease are devastating diseases of ruminants, including deer, sheep, and other species. It is estimated that bluetongue costs the United States’ cattle and sheep industry $125 million annually and $3 billion worldwide. These viruses are transmitted by several species of Culicoides, also known as “no-see-ums”. Both viruses are found in the Orbivirus genus with numerous subtypes occurring throughout the world. In the United States, there are six serotypes of bluetongue (1, 2, 10, 11, 13, and 17) and 2 serotypes of hemorrhagic disease (1 and 2). Recent outbreaks of bluetongue virus-8 in Europe have prompted concerns that exotic strains could enter the United States and have severe impacts on livestock and wildlife.

Over the past two years, the NWDP has conducted surveillance for both viruses in seven states. From 1 October 2009 to 30 September 2010, wildlife disease biologists in Arizona, and Indiana began trapping Culicoides species in and around areas where livestock or wildlife had tested positive to either disease. In central Arizona, an entire herd of antelope tested positive to hemorrhagic disease during the fall of 2009, which prompted surveillance in that area the following summer. In Indiana, Culicoides were trapped near a farm where cattle had tested positive for bluetongue virus the previous fall. Trapping in both instances was conducted using Centers for Disease Control and Prevention light traps, and occurred for three consecutive nights, every other week from June through September. The samples were sent to the NWDP office in Fort Collins, CO for processing.

Assistance with sorting and identifying the various Culicoides species was provided by two former Agricultural Research Services employees, Kristine Bennett and Ed Schmidtmann. Ed Schmidtmann has over 20 years of experience working with bluetongue and other arboviruses. His knowledge and identification skills were invaluable on the project. The trapping effort in Arizona produced over 2,500 Culicoides individuals from seven different species; majority of the samples consisted of C. sonorensis. Another 5,800 Culicoides individuals from nine species were collected in Indiana; majority of these insects being either C. biguttatus or C. stellifer. After identification, samples were shipped to the Agricultural Research Service Arthropod-Borne Animal Diseases Research Unit in Manhattan, KS, which has developed a multiplex real-time reverse transcription polymerase chain reaction that can simultaneously screen for 24 serotypes of bluetongue and 8 serotypes of hemorrhagic disease viruses. Initial testing has detected hemorrhagic disease positive Culicoides in Arizona, and a bluetongue virus positive Culicoides in Indiana.

Trapping was conducted in five additional states (Illinois, Maryland, Maine, Montana, New Jersey) from 1 October 2010 to 30 September 2011. Trapping occurred in August and September. Currently, samples are being sorted and identified in preparation for testing. Analysis of the data will continue through 2012. The results will provide insight on the ecology of bluetongue and epizootic hemorrhagic disease viruses in the United States.

Archive. The archive provided them with over 400 Canada goose samples from 12 states spread across all four migratory flyways. In addition, wildlife disease biologists in New Jersey and Kansas submitted heads of apparently healthy, hunter-harvested Canada geese and snow geese (Chen caerulescens). In the laboratory, all samples were screened by PCR. Samples found positive for avian Borna virus were cultured and sequenced.

Borna virus was isolated, and sequenced from a number of these samples. Researchers concluded that the virus is common and widespread in Canada goose. Surprisingly, the Canada goose Borna viruses aligned more closely with mammalian ones than with the psittacine clusters. These results indicate Canada goose can serve as asymptomatic hosts for Borna virus. There was however, a sample from a Canada goose recovered in Georgia that presented with encephalitis. This bird was infected with a Borna virus that shared 97% homology with the virus found in apparently healthy geese. When considering this case with earlier reports of proventricular dilatation disease-like symptoms in wild Canada geese, it appears that some individuals are susceptible to clinical infection.

It remains to be shown whether Canada goose serve as reservoirs for Borna virus. Previous work on several psittacine species and mallards indicate that fecal shedding is intermittent. The method of transmission remains unknown although the fecal-oral route seems likely, at least among geese.

(EhD and BTV, Continued from page 5)
STATE HIGHLIGHTS

Western Region

CALIFORNIA
Wildlife Disease Biologist Shannon Chandler is working with Wildlife Services specialists throughout the state to supply the California Department of Fish and Game with carcasses of deer that have symptoms of hair loss. Over the past 12 months mange mites of the exotic genus *Notoedres* have been discovered in 3 California counties. These mites cause Sarcoptic-type mange reactions and can lead to death in felines and squirrels. Currently feral cats, bobcats, and gray squirrels also have been documented to be affected. Wildlife Services has also provided California Department of Fish and Game with carcasses of bobcats without hair loss collected during depredation work to serve as control animals for their study.

HAWAII
Wildlife Disease Biologist Sam Goldstein is working on a project to determine the exposure of Japanese encephalitis virus and chikungunya virus in a variety of wildlife species found on islands in the Pacific. Goldstein is providing oversight to obtain samples for diagnostic work at Colorado State University. He is working with Wildlife Services specialists to obtain serum samples from brown tree snakes (*Boiga irregularis*) on Guam. WS has an ongoing program to reduce damage caused by brown tree snakes on Guam, including operational trapping and removing snakes to reduce their population. Goldstein also is working with cooperators in American Samoa to obtain serum samples from feral swine and several reptiles. The cooperators also will provide mosquitoes that will be included in the investigation.

OKLAHOMA
The Colorado School of Mines/Department of Chemistry/Advanced Biodetection Laboratory in cooperation with the NWDP has been developing a field ready immuno-chromatography detection system for tularemia. The system utilizes small organisms called bacteriophages or simply phages which are essentially viruses for bacteria. The strategy behind the technology is that a serosample would be collected from an animal and mixed with a phage media and placed in the small plastic case with immuno-chromatography paper. If the bacteria is present in the sample the chromatography paper will remain colorless or blank. When the phages multiply they will migrate up the immuno-chromatography paper and show a colorimetric positive, supplying the biologists with results in minutes or hours rather than days or weeks. If the bacteria is not present in the sample the chromatography paper will remain colorless or blank. Wildlife Services Wildlife Disease Biologists are collecting horselflies and ticks in tularemia endemic areas and sending the specimens to Colorado School of Mines for analysis and detection of tularemia phages. This technology is in the final stages of development for plague and MRSA, and could prove to be a significant tool in future surveillance for Wildlife Services.

Eastern Region

MASSACHUSETTS/CONNECTICUT/ RHODE ISLAND
Wildlife Disease Biologist Randy Mickley collected mute swan (*Cygnus olor*) samples in conjunction with the Rhode Island Department of Environmental Management/Division of Forest Environments. The Department collected 79 birds from four locations around the state over a three day period. Mickley supervised the collection of over 700 samples from the 79 mute swans. Subsequently, he submitted serum and tissue samples to multiple researchers based at the Southern Cooperative Wildlife Disease Study, Michigan State University, Texas A & M University, USDA-APHIS-Agricultural Research Services, and USDA/APHIS/Wildlife Services, NWDP in Colorado for multiple disease projects.

MICHIGAN
Wildlife Disease Biologist David Marks has been working with the Wildlife Services, National Wildlife Research Center on a project investigating movement patterns of Virginia opossums (*Didelphis virginiana*) in northern Lower Michigan. This project is an effort to determine the role these animals may have in the epidemiology of bovine tuberculosis. Marks spent one week during July of this year trapping and radio-collaring opossums with Wildlife Services specialist Schanck. They also removed 11 deer under disease control permits from two farms to reduce risk of bovine tuberculosis spreading to cattle.

MISSOURI
The NWDP is collaborating with Dr. Dolores Hill with the Agricultural Research Service in Beltsville, MD on genotyping *Toxoplasma* and *Trichinella* found in feral swine from selected counties in Missouri. The project is being conducted to isolate and identify *Trichinella* species infecting feral swine by extracting larvae from tongue tissue. Wildlife Disease Biologist Tom Hutton submitted 51 feral swine tongues collected from Iron, Reynolds and Washington Counties for testing. Trichiniae larvae have been identified in three feral swine tongues collected in Reynolds County. While *Toxoplasma* results from these tongues are pending, 44 out of 216 (16%) of Missouri feral swine samples collected in 2007-08 (see map below) were reported seropositive for *Toxoplasma*, with most of those positive animals being from Iron, Reynolds and St. Clair counties. A summary of the project and the results to date were shared with members of Missouri’s Feral Hog Task Force.
For more information on the Wildlife Services Wildlife Disease Program in your state, please call 866-4 USDA WS, or contact the following staff:

Tom DeLiberto 970.266.6088
National Coordinator
Editor

Dale Nolte 970.266.6049
Assistant Coordinator

Tom Gidlewski 970.266.6350
Assistant Coordinator

Brandon Schmit 970.266.6079
Wildlife Disease Biologist

Kerri Pedersen 970.266.6272
Wildlife Disease Biologist

John Baroch 970.266.6308
Wildlife Disease Biologist

Mark Lutman 970.266.6077
Wildlife Disease Biologist

Dennis Kohler 970.266.6072
Wildlife Disease Biologist

Sarah Bevins 970.266.6211
Wildlife Disease Biologist

Emily Blizzard 970.266.6008
Biological Science Technician

Mary Kimball 970.980.1546
Budget Analyst

Amelia Lavelle 970.266.6011
Administrative Assistant
Associate Editor

**Photo of the Quarter**

Wildlife Disease Biologist Randy Mickley (MA) conducts mortality surveillance on Cape Cod National Seashore’s Jeremy Point, in Wellfleet, MA.

**Recent NWDP Publications**


