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United States National Animal Health Surveillance System: 2016 Surveillance Activity Report



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This report was prepared by USDA-APHIS-VS Center for Epidemiology and Animal Health (CEAH) Surveillance Design and Analysis (SDA). For more information, please contact Dr. Celia Antognoli at celia.antognoli@aphis.usda.gov or Dr. Stanley Bruntz at Stanley.d.bruntz@aphis.usda.gov

USDA-APHIS-VS-CEAH NRRC Building B, MS 2E6 2150 Centre Avenue Fort Collins, CO 80526-8117 970.494.7200

E-mail: NLRAD.NAHRS@aphis.usda.gov

Web site: http://www.aphis.usda.gov/animal-

health/nahrs

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Overview of the U.S. National Animal Health Surveillance System

This is the annual report of the United States Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) Veterinary Services (VS) National Animal Health Surveillance System (NAHSS) for calendar year 2016. The NAHSS is a system created to detect events and trends related to animal health for all stakeholders involved in public, animal, and environmental health. VS is implementing a comprehensive and integrated surveillance (CIS) approach within the NAHSS to provide a dynamic knowledge base for actions designed to improve animal health, productivity, marketability, and product safety in an efficient and integrated way. The NAHSS is an interdisciplinary network of partners working together to protect animal health and promote free trade through surveillance, control, and prevention of foreign, emerging, zoonotic, and endemic diseases. The NAHSS infrastructure also provides the tools necessary to detect chemical or environmental agents that could affect animal health.

The NAHSS has multiple functioning elements that include field operational resources; a veterinary diagnostic laboratory network, including the National Animal Health Laboratory Network (NAHLN); well-developed data and sample collection resources; a data storage and management system; and analytic and reporting tools with the expertise to convert raw data into information for decision-making. NAHSS includes passive and active surveillance for reportable diseases, including those reported to the World Organization for Animal Health (OIE) as well as those diseases covered by federally funded surveillance programs. In addition, the surveillance system includes monitoring for diseases that States are not mandated to report.

The National Animal Health Reporting System (NAHRS) is an important component of the NAHSS. The NAHRS program is designed to provide summary-level data on the presence of diseases on the National List of Reportable Animal Diseases (NLRAD) in the United States. NAHRS gathers monthly data from participating State animal health officials (SAHOs) on the presence of NLRAD-listed diseases, identified with a high level of certainty (See Appendix 1.) NAHRS plays an important role in U.S. reporting of notifiable diseases to the OIE. For more than 30 years, VS has reported occurrences of OIE-notifiable diseases to the OIE. The United States meets its OIE reporting obligations using a variety of sources including NAHRS reporting, foreign animal disease (FAD) reports, national program disease surveillance reports, and others.

This annual report includes a summary of selected federally supported active and passive surveillance activities in calendar year 2016, as well as a summary of NAHRS reporting by participating States. This document also includes an overview of the OIE and U.S. reporting to the OIE in 2016. In addition, we include the 2016 NLRAD-NAHRS Reportable Disease List (Appendix 1) as well as the U.S. status of OIE-listed diseases for CY 2016 (Appendix 2.)

Selected Active and Passive Surveillance Activities in CY 2016

The following selected reports are summarized from various surveillance programs and activities conducted by APHIS and partners during 2016. This is not a complete list of the surveillance activities conducted. In most cases, we indicate whether the surveillance data reflects fiscal year 2016 (Oct. 1, 2015, through Sept. 30, 2016) or calendar year 2016 (Jan. 1 through Dec. 31, 2016) activities.

The CIS approach is a natural progression from historical disease eradication programs to a flexible, responsive, and cost-efficient surveillance system. This approach is not based on specific diseases, but rather is designed around the fundamental components of surveillance. CIS can be adapted to all species as well as the evolving animal health issues that APHIS-VS, States, and animal industries face. These include diseases not currently present in the United States, zoonotic diseases of public health concern, emerging diseases that threaten our industries and economy, diseases that are introduced with malicious intent, and selected endemic disease conditions of high economic impact.

Avian Influenza (AI) Surveillance

APHIS' AI surveillance program addresses the following poultry populations:

- Large-volume commercial poultry industry
- Small-volume, high-value commercial poultry industry
- Live-bird marketing system (LBMS)
- Backyard flocks

The program also includes non-poultry avian populations, including wild, migratory birds, and zoo or exhibition birds.

Commercial Poultry – Surveillance for AI in commercial poultry is described under provisions of the National H5 and H7 Low Pathogenicity Avian Influenza (LPAI) Control Program of the National Poultry Improvement Plan (NPIP), which was implemented in September 2006. Forty-nine States, one U.S. Territory, and 112,119 flocks participated in NPIP AI surveillance in FY 2016, conducting a total of 3,051,068 tests for AI. Testing is conducted by approved laboratories at the State level and non-negative samples are forwarded to VS' National Veterinary Services Laboratories (NVSL) for confirmation. For 2016, NVSL received 1,670 specimens from 19 States (Alabama, Arkansas, California, Delaware, Iowa, Illinois, Indiana, Kentucky, Maryland, Michigan, Minnesota, Missouri, North Carolina, Nebraska, New Hampshire, Pennsylvania, South Dakota, Virginia, and Wisconsin.) There were two H5/H7 events in commercial poultry during 2016 caused by North American lineage viruses infecting turkeys: January 2016 H7N8 LPAI (eight premises) and HPAI (one premises) in Indiana turkeys – molecular and epidemiologic data suggest a single introduction with limited lateral spread, and mutation to HPAI in a single flock likely affected during lateral spread; and April 2016 H5N1 LPAI in Missouri turkeys representing a single introduction with no further spread. Swine lineage IAV H1/H3 was isolated from in turkeys in seven States (Illinois, Indiana, Michigan, Minnesota, Missouri, North Carolina, and South Dakota); H1N1pdm09 was detected in four States (Indiana, Michigan, Minnesota, and Missouri.)

Live Bird Marketing System (LBMS), Upland Game, Backyard Birds and Exhibition Birds – The uniform standards for testing in the live bird marketing system were implemented as a State-Federal-industry cooperative program in 2004 for the prevention and control of H5 and H7. Nearly 100,000 tests for avian influenza were performed from birds in 37 States during FY 2016. Testing is conducted by approved laboratories at the State level and non-negative samples are forwarded to NVSL for confirmation. For 2016, NVSL received 1,664 specimens from 22 States (California, Connecticut, Florida, Georgia, Idaho, Indiana, Kansas, Kentucky, Massachusetts, Maryland, Maine, Minnesota, Missouri, North Carolina, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island, Tennessee, Texas, and Virginia.) For H5/H7 events, H5N2 LPAI of North American lineage (based upon sequence)

was detected in live bird markets in New Jersey, New York, and Pennsylvania; the event was traced to a source flock that supplied a single distributor in New York. An H2N2 virus first detected in late 2014 continues to circulate in northeastern LBMs and at least one market was positive for the H5N2 LPAI and H2N2 concurrently. While the H5N2 LPAI was predominantly isolated from the source Muscovy duck flock, the potential impact of a reassortment event is greater where a more poultry-adapted virus, such as this H2N2, is circulating at the same time. Also, H1N1 (avian lineage) was detected from ducks in New Jersey and Pennsylvania. For antibody detections in 2016, H7N3 antibody was detected in a Massachusetts backyard flock and H9N2 antibody in Iowa game pheasants; both premises tested negative for virus.

Wild Birds – In July 2015, State and Federal agencies initiated a national wild bird surveillance effort to provide information to guide management actions addressing some of the issues associated with HPAI virus in birds. This includes risks to commercial poultry, backyard poultry, game bird farms, wild birds, wild bird rehabilitation facilities, falconry birds, and captive bird collections in zoos/aviaries. Specific objectives of the plan were to: 1) determine the distribution of influenza viruses of interest in the U.S.; 2) detect spread of influenzas of interest to new areas of concern; and 3) provide a flexible surveillance framework that can be modified to monitor wild waterfowl populations for avian influenza, detect reassortant avian influenza viruses, and estimate apparent prevalence of important influenzas once detected in an area of concern. In FY 2016, a total of 45,088 wild bird samples were collected and tested for avian influenza. Of these, there was one Eurasian origin H5 PCR-only detection (no viable virus, sequencing unsuccessful) from a hunter-harvested mallard in Oregon in November 2015, and one confirmed HPAI Eurasian-North American reassorted H5N2 positive mallard sampled in August 2016 in Fairbanks, AK.

For more information on avian influenza testing in poultry and wild birds, see the proceedings of the 2016 USAHA Annual Meeting http://www.usaha.org/upload/Proceedings/2016 Proceedings FINAL.pdf

Bovine and Farmed Cervid Surveillance

Bluetongue and Epizootic Hemorrhagic Disease (EHD) Surveillance

Bluetongue virus (BTV) and epizootic hemorrhagic disease virus (EHDV) are members of the *Reoviridae* family and are transmitted by biting *Culicoides* midges. Worldwide, 24 bluetongue serotypes have been identified and in the United States, bluetongue virus types 2, 10, 11, 13, and 17 are considered endemic. Of the endemic types, BTV-2 is restricted primarily to Florida and the other types are more widespread. In recent years, NVSL has identified 10 previously unrecognized bluetongue serotypes from U.S. ruminant species (BTV types 1, 3, 5, 6, 9, 12, 14, 19, 22, 24). None of the non-endemic bluetongue types has caused widespread disease outbreaks. The types of *Culicoides spp.* vectors responsible for transmission of the non-endemic types are unknown.

In the United States, EHD is one of the most significant infectious diseases of white-tailed deer, whereas infection in cattle has been primarily subclinical or rarely resulting in mild disease. In recent years, though, there have been multiple cases of EHDV causing severe disease in cattle herds and other species.

Summary of BTV isolates identified in 2016 – Bluetongue virus serotypes 1, 2, 3, 17, and 22 were identified in CY 2016. BTV-1 was identified in sheep; BTV-2 was identified in deer; BTV-3 was identified in deer and sheep; BTV-17 was identified in cattle and sheep; and BTV-22 was identified in sheep.

Summary of EHDV isolates identified in 2016 – EHDV-1, EHDV-2, and EHDV-6 viruses were isolated. EHDV-2 was the predominate isolate identified.

Bovine Spongiform Encephalopathy (BSE) Surveillance

In FY 2016, APHIS tested 26,564 samples for BSE under the ongoing surveillance program. Figure 1 summarizes the U.S. BSE OIE points summary from 2010-2016. The primary purposes of the program are to continue monitoring and

assessing changes to the BSE status of U.S. cattle and to provide mechanisms for early detection of BSE. The program enables USDA to detect BSE at a rate of one infected animal per 1 million adult cattle with a high degree of confidence. It also maintains surveillance at levels that exceed international standards, emphasizes sample collection from cattle subpopulations where BSE is most likely to be detected, and retains sample collections from all important surveillance sources. Currently, the OIE categorizes countries as either negligible risk, controlled risk, or undetermined risk for BSE. For live cattle and for many products derived from cattle, the trade conditions recommended by the OIE guidelines are based on the BSE risk classification of the exporting country. In May 2013, the OIE upgraded the BSE status of the United States from BSE controlled-risk status to BSE negligible-risk status. This upgrade provides the U.S. cattle industry a major economic benefit via greater access to international markets. The BSE status upgrade also decreased the level of surveillance required by the OIE from Type A to Type B surveillance.

Other notable changes to the BSE program occurred in 2015 and 2016. Beginning in FY 2015, USDA discontinued testing of any animals under 12 months of age. In FY 2016, the BSE surveillance program reduced the targeted number of samples collected from approximately 40,000 to 25,000. Even with the large sample reduction, the OIE point goals of the surveillance program were still easily met.

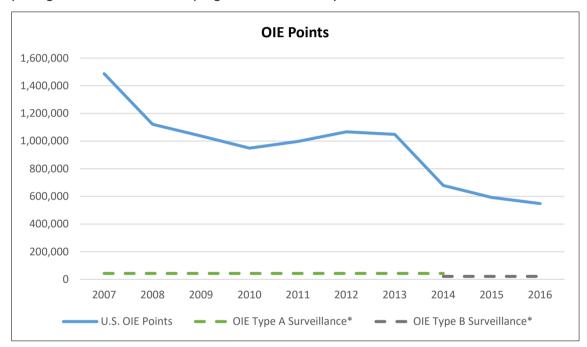


Figure 1. Comparison of the number of BSE OIE points accumulated by the U.S. to the number of OIE points required for OIE Type A and Type B surveillance, 2010-2016

* OIE Type A Surveillance requires 300,000 points over a 7-year period (42,857 points/yr.) with surveillance designed to detect prevalence of 1 infected animal per 100,000 adult cattle at a 95 percent confidence level. OIE Type B Surveillance requires 150,000 points over a 7-year period (21,429 points/yr.) with surveillance designed to detect prevalence of 1 infected animal per 50,000 adult cattle at a 95 percent confidence level. As Figure 2 shows, U.S. surveillance – designed to detect BSE at a rate of 1 infected animal per 1 million adult cattle with a high degree of confidence – far exceeds international standards. See OIE Terrestrial Animal Health Code, Article 11.4.22 for more information.

Brucellosis Surveillance in Cattle and Bison

The U.S. Cooperative State-Federal Brucellosis program has been highly successful in eradicating bovine brucellosis from our domestic cattle and bison herds. All 50 States have been Class Free for bovine brucellosis since July 2009, despite recent detections in the Greater Yellowstone Area (GYA) States of Idaho, Montana, and Wyoming. The GYA remains our primary focus for brucellosis in livestock because the disease is endemic in GYA wild elk and bison.

In FY 2016, brucellosis was newly detected in two cattle herds, and one privately owned bison herd remained affected in the GYA States. All three of the herds are located within their respective State's designated surveillance

area (DSA). One of the cattle herds has successfully completed all required testing and was released from quarantine; the other two herds remain under quarantine with herd management plans, including movement controls and additional herd testing. APHIS-VS continues a national bovine brucellosis slaughter surveillance plan designed to detect brucellosis infection with 95 percent confidence that the prevalence level of brucellosis does not exceed 1 infected animal per 100,000 animals. This level is higher than required by OIE standards. In FY 2016, APHIS-VS tested approximately 1.9 million head of cattle under the Market Cattle Identification (MCI) slaughter surveillance program and an additional 97,000 head of cattle at livestock markets. Approximately 148 epidemiologic investigations were conducted on suspicious MCI surveillance tests. An additional 250,000 head of cattle and domestic bison were tested on farms or ranches. These tests were conducted primarily for movement and private sales, epidemiologic investigations, herd certification, or show or exhibition purposes. In FY 2016, approximately 1.9 million calves and approximately 262,296 adult cattle were vaccinated for brucellosis and approximately 276 herds were certified as brucellosis certified-free cattle herds.

Tuberculosis (TB) Surveillance in Cattle and Cervids

Five TB-affected beef herds were detected during FY 2016. Four herds were located in Michigan and one in Indiana. Two of the TB-affected herds were detected as a result of area surveillance, one herd was detected through epidemiological investigation, one herd was detected through slaughter surveillance, and one herd was detected through movement testing. An affected dairy complex detected in 2015 via slaughter surveillance continued a test-and-remove program for elimination of TB in the herd. In addition to cattle surveillance, 10,750 cervids were serologically tested and 2,095 were skin tested for TB in FY 2016. There were no positives confirmed for *Mycobacterium bovis* in those animals.

For FY 2016, a total of 6,389 granulomas were identified from 153 federally inspected establishments. The minimum standard for slaughter surveillance is one granuloma submitted per 2,000 adult cattle slaughtered annually. Of these, a total of 14 had histology compatible with mycobacteriosis, (0.023 percent). *M. bovis* was confirmed in ten (71.4 percent) of these cases. TB is confirmed by polymerase chain reaction (PCR) testing of formalin-fixed and direct PCR and culture of fresh tissue. Of the remaining four histology compatible cases, *M. avium* was identified in two and two were negative on PCR. One of the ten confirmed cases occurred in an adult cow over two years of age from Canada, and nine cases occurred in feeder cattle. Of the nine fed cattle cases, five occurred in Mexican-origin cattle and four were in domestic origin steers. Six infected steers came through a Pennsylvania slaughter plant in one lot and led to the identification of a new Indiana affected beef herd. Two Texas and one Arizona steers were found but USDA was not able to find an affected herd of origin for any of those traces.

Voluntary Chronic Wasting Disease (CWD) Herd Certification Program

The APHIS-VS National CWD Herd Certification Program (HCP) was implemented in 2014. It is a voluntary Federal-State-industry cooperative program administered by APHIS and implemented by participating States. The program provides uniform national herd certification standards that minimize the risk of spreading CWD in farmed cervid populations. Participating States and herd owners must comply with requirements for animal identification, fencing, recordkeeping, inspections/inventories, as well as animal mortality testing and response to any CWD-exposed, suspect, and positive herds. APHIS-VS monitors the approved State HCPs to ensure consistency with Federal standards through annual reporting by the States.

With each year of surveillance without disease detection, herds participating in the HCP will advance in status until reaching 5 years with no evidence of CWD, at which time herds are certified as being low-risk for CWD. Only captive cervids from enrolled herds certified as low-risk for CWD may move interstate. Currently, 29 States participate in the voluntary CWD Herd Certification Program and have approved HCPs. FY 2016 marks the fourth year that approved States have submitted their CWD HCP annual reports to APHIS-VS. In FY 2016, there were 2,704 enrolled cervidae herds: 2,129 deer, 447 elk, and 128 mixed-species herds. Of those, there were 2,331 certified cervidae

herds: 1,789 deer, 421 elk, and 121 mixed-species herds. A total of 9,556 captive cervids were tested for CWD as part of the voluntary HCP in FY 2016.

Cattle Fever Tick (CFT) Surveillance

The Cattle Fever Tick Eradication Program (CFTEP) was created in 1906 to eliminate bovine babesiosis—a severe and often fatal cattle disease—from the U.S. cattle population. The cattle tick (*Rhipicephalus annulatus*) and the tropical cattle tick (*R. microplus*) are carriers of the protozoan parasites (*Babesia bigemina* and *B. bovis*) that cause babesiosis. These ticks are well established in Mexico. A permanent, 500-mile quarantine zone along the Texas-Mexico border was created in 1938 to maintain the Nation's status as free from babesiosis and cattle fever ticks. The disease and the ticks were officially eradicated from the continental United States in 1943, with the exception of a narrow permanent quarantine "buffer" zone in south Texas that follows the Rio Grande River. This zone is also known as the "systematic quarantine zone" because cattle with ticks on quarantined premises must be systematically treated every 7 to 14 days for 6 to 9 months.

The CFTEP is a cooperative program between APHIS-VS and the Texas Animal Health Commission (TAHC). The TAHC provides support personnel and conducts surveillance in tick-free areas of Texas. APHIS-VS leads the program and maintains the permanent quarantine zone through surveillance and tick control activities. USDA's mounted patrol inspectors, known as "tick riders," patrol designated sections to intercept tick-carrying wildlife and stray and smuggled Mexican-origin livestock. Intercepted animals must be quarantined, inspected, and treated.

In FY 2016, APHIS-VS conducted 16,657 inspections of individual premises for ticks, including 5,142 river trail patrols. Also in FY 2016, APHIS-VS identified 42 newly infested premises inside the buffer zone, 13 more than in FY 2015. There were 44 newly affected premises at the end of FY 2016 outside the border – 16 more than in FY 2015. In addition, 33 of 60 stray cattle captured along the border were infested with CFT, and 8 of the 30 stray horses/mules were infested.

A defined quarantine area that includes affected premises is established when infected premises are identified. To release a quarantine area, every infested premises must have all cattle treated for at least 9 months, including inspections and treatments every 2 weeks. As a result, APHIS-VS conducted 124,112 individual animal inspections and 51,940 treatments throughout South Texas. In FY 2016, the quarantine buffer zone and the free area of Texas contained 86 newly guarantined premises, compared to 57 in FY 2015.

In October 2014, the TAHC and the USDA confirmed the presence of CFT on Cameron County, TX, premises located outside of the permanent quarantine zone. To protect the land, premises, and animals from exposure to CFT, the TAHC created a temporary preventative quarantine area (TPQA) in Cameron County. Surveillance efforts have been ongoing since the TPQA went into effect. The TPQA originally started with six new premises located outside the permanent quarantine zone. In FY 2016, there were 17 infested premises identified in the TPQA, consisting of approximately 223,000 acres. In addition, APHIS is working with the TAHC, the USDA Agricultural Research Service (ARS), and a major veterinary pharmaceutical company to evaluate an anti-tick vaccine for cattle within the permanent quarantine buffer zone in South Texas, with plans to expand to a larger population.

Swine Surveillance

Brucellosis Surveillance in Swine

In FY 2016, all 50 States and U.S. territories maintained their free status for swine brucellosis, as defined by the Swine Brucellosis Control and Eradication Program

(http://www.aphis.usda.gov/animal_health/animal_dis_spec/swine/downloads/sbruumr.pdf). The Kentucky Federal Brucellosis Laboratory tested 169,071 cull sow/boar slaughter samples and 2,981 feral swine samples for swine brucellosis surveillance. In FY 2016, no commercial production swine herds were found to be infected with swine brucellosis; however, feral swine remain a reservoir of brucellosis and brucellosis continues to be identified in non-

biosecure herds with exposure to feral swine. Biosecurity measures remain vital in preventing or minimizing contact with feral swine.

Classical Swine Fever (CSF) Surveillance

In FY 2016, 18 approved NAHLN laboratories and the NVSL Foreign Animal Disease Diagnostic Laboratory conducted CSF surveillance testing on a total of 12,705 specimens. All surveillance specimens were confirmed negative. VS conducted 30 swine FAD investigations for suspected CSF and all were confirmed as negative after testing. Table 1 lists the number of tested animals and surveillance streams for CSF testing in FY 2016. Additional information about the CSF surveillance program is available on the APHIS Web site at https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information/ct classical swine fever surveillance

Table 1. Number of animals tested under the national CSF surveillance plan for FY 2016

Surveillance Stream	Number of Tested Animals
Sick pig specimens submitted to veterinary diagnostic laboratories	3,284
Slaughter swine with high probability of CSF exposure	1,629
Feral swine	2,990
Swine with high probability of CSF exposure ¹	4,717
Swine with low probability of CSF exposure ²	
FAD submissions tested for CSF	30

¹Waste feeders and populations from States with high probability of CSF exposure

Influenza A Virus in Swine (IAV-S) Surveillance

USDA-APHIS-VS completed almost 8 years of cooperative IAV surveillance in 2016. The number of voluntary submissions to this program increased consistently from 2011 to 2016 as the industry gained confidence in the anonymous nature of the surveillance. The objectives of the surveillance program continue to be: (1) monitoring the genetic evolution of swine influenza viruses, (2) identifying and providing influenza virus isolates for research and to establish an objective database for genetic analysis of the isolates, and (3) the selection of isolates for development of relevant diagnostic reagents, updating diagnostic assays, and vaccine seed stock products. VS' swine IAV surveillance activities are providing valuable sequencing information. The sequencing results from program isolates are being submitted into GenBank, ® the National Institutes of Health genetic sequence database that is publically available. This data can yield information needed for vaccine and diagnostics decision-making and contributes to the analysis for possible zoonotic threats.

In FY 2016, APHIS-VS implemented four modifications to enhance the efficiency and cost-effectiveness of the surveillance. Because of the modifications listed below, the number of accessions decreased, but the number of viruses submitted to the program remained relatively constant. Modifications included:

- 1. Sample screening costs for the Matrix PCR flowed to the industry.
- 2. Matrix PCR test CT cutoff values lowered for samples to be accepted into USDA-funded further testing.
- 3. The M gene would be monitored through NVSL whole genome sequencing while payment to NAHLN labs for M gene sequencing was discontinued, and
- 4. One sample per accession, rather than two, would move forward for subtyping.

² Populations from States with low probability of CSF exposure

In FY 2016, VS tested a total of 123,434 samples from 36,856 accessions into the IAV-S surveillance activities. Circulating subtypes identified through swine IAV surveillance in FY 2016 included H1N1, H1N2, and H3N2. The predominant subtypes were H1N1 and H1N2. The dominant HA and NA constellations detected in FY16 were delta1 H1N2-2002, gamma H1N1-classical, Cluster IV-A H3N2-2002, and delta2 H1N2-1998 (Figure 2). Out of the M genes sequenced (n = 785), 781 were pandemic-lineage while four were trig-lineage. The emerging human-like H3N2 was detected with increased frequency (7.32 percent in FY 2016 compared with 2.11 percent in FY 2015).

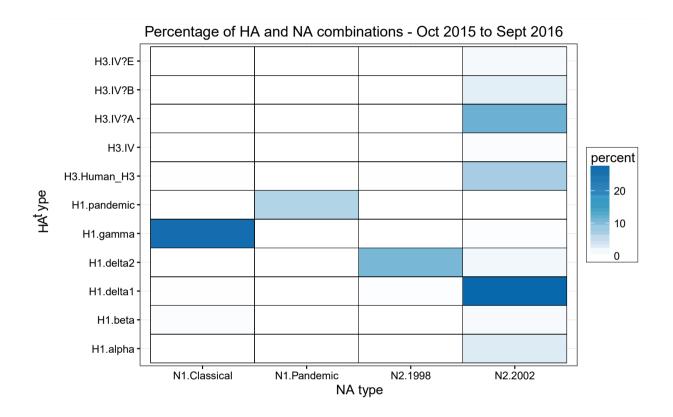


Figure 2. Percentage of HA and NA combinations, FY 2016

IAV-S surveillance reports are now posted on the APHIS web site at https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-diseaseinformation/ct swine health monitoring surveillance

Pseudorabies Virus (PRV) Surveillance

FY 2016 was the seventh full year of national PRV surveillance. Ten NAHLN laboratories, USDA's Federal laboratory in Kentucky, and NVSL conducted the PRV surveillance testing on a total of 200,383 samples. NVSL performed confirmatory testing on any non-negative test and positive assay results were reported to SAHOs for investigation. No commercial herds were found to be positive for PRV in FY 2016. Table 2 lists the number of swine tested for PRV from the various surveillance streams or populations from FY 2014 through 2016. Additional information about the PRV surveillance program is available on the APHIS Web site at

https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information

Table 2. Number of swine tested in each PRV targeted surveillance population in FY 2014, FY 2015, and FY 2016

Surveillance stream / Targeted population	Number of swine tested FY 2014	Number of swine tested FY 2015	Number of swine tested FY 2016
Diagnostic laboratory serologic submissions:			
Sick pig submissions	222	595	231
Routine serology/herd profiling	24,522	22,267	18,848
Swine with high probability of feral swine exposure	6,771	4,208	5,882
Swine with known feral swine exposure	904	591	620
Total – Diagnostic laboratory serologic submissions	16,958*	<mark>32,426a</mark>	<mark>27,679</mark> b
Cull sow-boars at slaughter	278,022	234,915	210,643
Market swine at slaughter	13,318	9,311	7,228
Feral swine	2,798	3,063	2,986
Swine cases highly suspicious for PRV	0	0	0
TOTAL	279,450*	248,613	200,383

^{*} Four samples were tested in FY 2014 as epidemiologic traceback samples.

Swine Enteric Coronavirus Disease (SECD)

SECD is a collection of coronaviruses first identified in the United States in 2013. Porcine epidemic diarrhea virus (PEDv) appeared in the United States in April 2013. Since that time, PEDv has spread widely within the U.S. swine industry. In early 2014, an additional related virus, porcine delta coronavirus (PDCoV), appeared in this country. Infections with these novel SECD viruses can cause significant morbidity and mortality, particularly in young piglets.

In response to the large number of SECD cases that were causing significant hardship for the U.S. swine industry, USDA issued a Federal Order in June 2014, making SECD a reportable disease. At the same time, USDA made funds available to cover specific costs associated with the disease. A revised Federal Order was issued on January 4, 2016, to more effectively use remaining emergency funding. In FY 2016, SECD remained a reportable disease, which means that producers, veterinarians, and diagnostic laboratories are required to report all cases of SECD to USDA or State animal health officials (SAHOs). The reporting criteria are unchanged in the revised Federal Order. Of the SECD laboratory accessions reported, 3,747 out of 32,344 were positive for PEDv and 476 out of 24,412 were positive for PDCoV during FY 2016. APHIS-VS has generated weekly situation reports since July 31, 2014. These weekly reports and additional information about SECD can be found at http://www.aphis.usda.gov/animal-health/secd

Feral Swine Surveillance

Feral swine (Sus scrofa) are a harmful and destructive invasive species. Their geographic range and population numbers are increasing in the United States. Though exotic to North America, feral swine have become widely distributed through accidental releases of domesticated pigs and Eurasian wild boars that escape from shooter operations or alleged illegal transport and release of feral swine between States for hunting.

Nationwide, feral swine cause an estimated \$1.5 billion in property and agricultural damage annually, and this number is growing. These wild pigs destroy crops and erode soils through their rooting, wallowing, and consumption activities. Feral swine also prey on native mammals, young domestic livestock, and birds. Feral swine compete with wildlife and livestock for food and contaminate fields and streams with *E. coli* and other bacteria.

They also carry more than 30 bacterial and viral pathogens in addition to numerous parasites that can affect people, pets, other farm animals, and wildlife. Because feral swine are susceptible to several foreign animal diseases, they could play a key role in spreading these diseases should they enter the United States.

Currently, feral swine have been reported or are believed to exist in at least 38 States as well as in parts of Canada and Mexico. The estimated feral pig population in the United States is more than 5 million and is rapidly expanding. Range expansion over the last few decades is due to a variety of factors including their adaptability to a variety of climates and conditions, translocation by humans, and a lack of natural predators. Additional information on the location of feral swine in the United States can be found at the Southeastern Cooperative Wildlife Disease Study (SCWDS) website: http://swine.vet.uga.edu/nfsms/information/map2016.htm

In 2014, in response to the increasing damage and disease threats posed by expanding feral swine populations in the United States, Congress appropriated money to USDA-APHIS for a collaborative, national feral swine damage management program. The overarching goal of the APHIS National Feral Swine Damage Management Program is to protect agricultural and natural resources, property, animal health, and human health and safety by managing damage caused by feral swine in the United States and its territories. Additional information about this program can be found here: https://www.aphis.usda.gov/aphis/ourfocus/wildlifedamage/operational-activities/feralswine/feral-swine-program

As part of the Feral Swine Damage Management Program, USDA-APHIS Wildlife Services, in collaboration with APHIS-VS, annually samples feral pigs in the United States for several diseases. In CY 2016, APHIS-Wildlife Services tested 2,990 feral swine samples from 33 States for CSF, 2,986 feral swine samples from 32 States for PRV, and 2,981 samples from 32 States for swine brucellosis. None of the sampled pigs were positive for CSF. However, 19.0 percent of the pigs tested positive for pseudorables exposure and 5.5 percent for swine brucellosis exposure.

Equine Surveillance

Equine Arbovirus (West Nile Virus, Eastern and Western Equine Encephalitis) Surveillance and Web Reporting APHIS publishes biweekly updates on the number of equine cases of West Nile virus (WNV) and eastern and western equine encephalitis (EEE and WEE) during the arbovirus transmission season, which runs approximately from June through November. Equine arbovirus case reporting is carried out through collaboration with the Centers for Disease Control and Prevention (CDC) and State veterinary and public health officials. CDC provides arbovirus case information through its ArboNET reporting system, an electronic surveillance and reporting system used to track and report arboviral activity. Biweekly updates and veterinary case definitions for WNV and EEE/WEE are published online at http://www.aphis.usda.gov/animal-health/equine-health

West Nile Virus - In CY 2016, 33 U.S. States reported 380 equine cases of WNV. The 380 reported equine cases of WNV are the highest since 2012 (Figure 3). The most cases were reported by Texas (136), Washington (27), and California (21). Figure 4 shows the distribution of cases among the States.

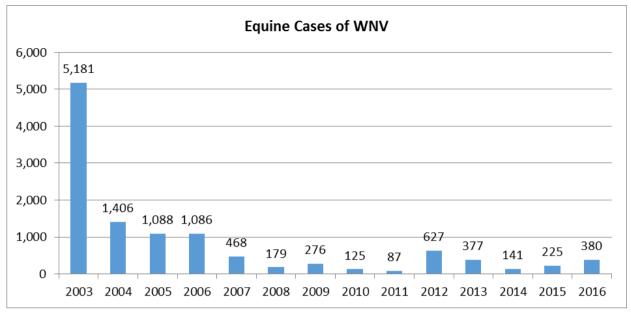


Figure 3. Reported U.S. equine cases of West Nile virus, 2003-2016

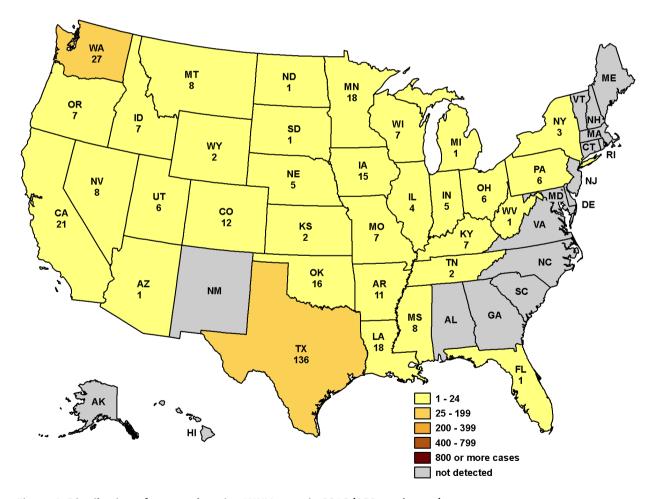


Figure 4. Distribution of reported equine WNV cases in 2016 (380 total cases)

Eastern Equine Encephalitis – In CY 2016, 15 U.S. States reported 118 equine cases of EEE. This was higher than 70 reported cases in 2015 (Figure 5). Florida reported the most cases with 24, followed by Wisconsin (19) and South Carolina (15). Figure 6 shows the distribution of cases among the States.

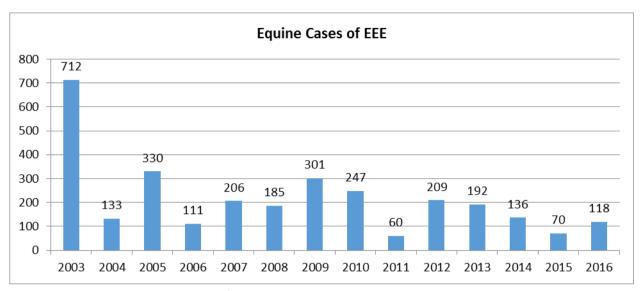


Figure 5. Reported U.S. equine cases of eastern equine encephalitis, 2003-2016

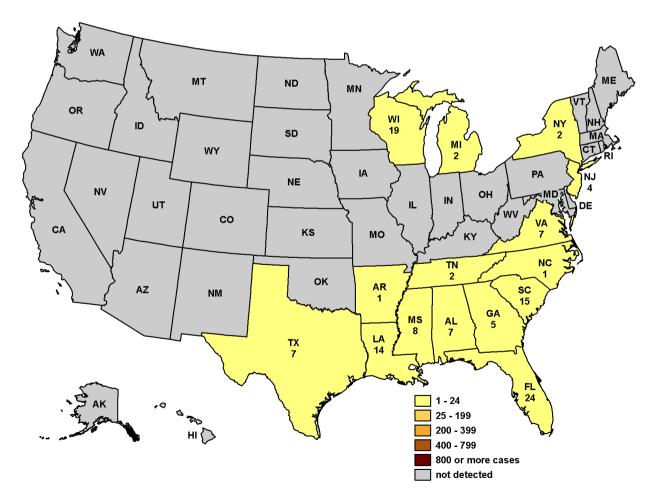


Figure 6. Distribution of reported equine EEE cases in 2016 (118 total cases)

Equine Piroplasmosis

Since November 2009, more than 320,000 domestic U.S. horses have been tested for equine piroplasmosis (EP) through active surveillance and movement testing. To date, 342 EP-positive horses (332 Theileria equi-positive, 10 Babesia caballi-positive) have been identified through this surveillance. These positive horses are unrelated to the 2009-2010 T.equi outbreak on a Texas ranch where 413 positive horses were identified in connection with the outbreak and natural tick-borne transmission on the ranch was documented to have occurred over at least 20 years and has since been eradicated. Of the 342 positive horses identified through active surveillance, 289 were Quarter Horse racehorses, 14 were Thoroughbred racehorses, and 33 were horses previously imported to the United States before August 2005 under the complement fixation test. The epidemiology investigations conducted in all of these cases have indicated no evidence of tick-borne transmission and the cases in racehorses specifically have involved iatrogenic transmission as the method of spread.

In FY 2016, a total of 22,192 domestic U.S. horses were tested for EP, with the identification of 76 horses positive for T. equi. Seventy-four were Quarter Horse racehorses, one was a Thoroughbred racehorse participating in unsanctioned racing, and one horse was an Azteca mare suspected to have been illegally moved from Mexico. The Quarter Horse racehorses were participating in sanctioned racing, unsanctioned racing, or both, and three of these horses were found to be dually infected with both T. equi and equine infectious anemia (EIA). The majority of these horses were found as clusters of positives associated with the same trainer and/or owner and epidemiology investigations conducted have implicated iatrogenic transmission (needle/syringe/IV equipment reuse, blood transfusions, contamination of multi-use drug vials, etc.) as the primary method of transmission in all racehorse cases identified in 2016.

Equine Infectious Anemia

Equine infectious anemia (EIA) regulations vary by State and may include requirements to test for interstate movement, upon change of ownership, for entry into events, or for commercially housed horses. In addition to State requirements, racing authorities, show venues, stables, and other organizations may also require EIA testing. Reporting of EIA testing is summarized on a calendar-year basis. During 2016, a total of 1,279,579 EIA tests were conducted, resulting in detection of 52 positive horses in 17 States. These results compared to 1,354,454 tests and 65 positives in 13 States in 2015. Figure 7 presents a summary of EIA testing from 2000-2016. Historical data and additional information on EIA are available online at http://www.aphis.usda.gov/animal-health/equine-health.

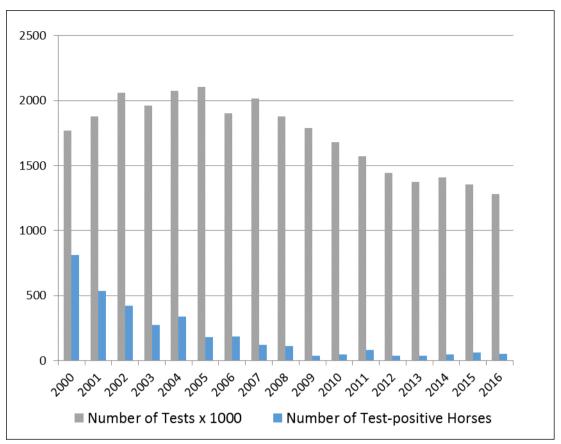


Figure 7. Equine infectious anemia test results, United States, 2000-2016

States are encouraged to provide EIA test data to VS through the NAHRS online reporting tool. VS requested EIA information by e-mail from States that did not use NAHRS and recorded the data in the NAHRS database.

Ovine and Caprine Surveillance

Scrapie Surveillance in Sheep and Goats

The United States accelerated its efforts to eradicate classical scrapie¹ in FY 2002 by adopting regulations requiring the official identification of sheep and goats and by implementing Regulatory Scrapie Slaughter Surveillance (RSSS) in FY 2003. During FY 2016, samples from 37,902 sheep and goats were collected at 179 sites in 39 States as part of the RSSS program. These samples were tested for scrapie using immunohistochemistry testing procedures on brain and/or lymph node specimens. These tests identified one case of classical scrapie in a sheep. As of the end of FY 2016, 520,504 animals have been tested for scrapie through RSSS. The percentage of mature sheep found positive at slaughter, adjusted for face color, decreased by 99.1 percent between FY 2003 and 2016 (Figure 8).

In addition to slaughter surveillance, field necropsies and live-animal biopsies are conducted for routine surveillance and as part of disease investigations or flock cleanup plans, including testing of potentially exposed, exposed, and suspect animals. In FY 2016, a total of 2,101 sheep and goats were tested as part of field investigations; 15 cases of classical scrapie in sheep were identified.

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¹ In 2009, the OIE recognized Nor98-like (atypical) scrapie as a separate disease from classical scrapie that does not meet the OIE criteria as a notifiable disease. This determination was made based on differences in epidemiology and laboratory findings (most notably, the lack of evidence to support transmission under natural conditions and its random widespread occurrence). In line with these findings and the 2009 revisions to the OIE scrapie chapter, the United States no longer depopulates.

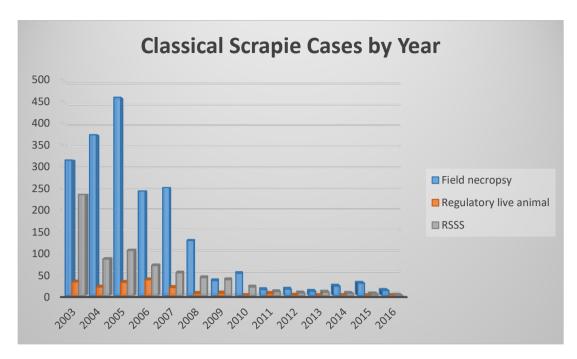


Figure 8. Classical scrapie cases by fiscal year, 2003 - 2016

Vesicular Stomatitis Virus Surveillance

In affected livestock, vesicular stomatitis virus causes blister-like lesions in the mouth, nostrils, hooves, and teats. While vesicular stomatitis can cause economic losses to livestock producers, it is a particularly important disease because its outward signs are similar to those of foot-and-mouth disease (FMD), an FAD of cloven-hoofed animals that was eradicated from the United States in 1929. Laboratory testing is required to distinguish these diseases in cloven-hoofed animals. Historically, outbreaks of vesicular stomatitis in domestic livestock occur in the Southwest United States during warm months and particularly along waterways. However, outbreaks are sporadic and relatively unpredictable. There have been eight vesicular stomatitis outbreaks since 2000 and the majority of the outbreaks began in May (five), followed by April (two), and August (one). The size of the past eight outbreaks varied from four infected animals in one State to over 2,000 infected animals in eight States (figures 9 and 10).

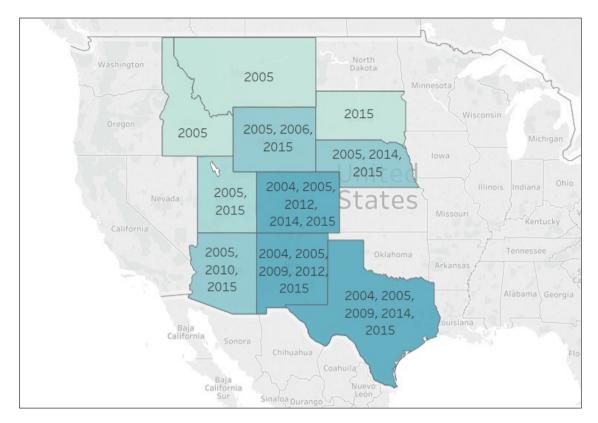


Figure 9. States with reported vesicular stomatitis detections since 2000

Vesicular stomatitis detections most commonly occur in equids and bovids with sporadic detections reported in sheep, goats, camelids, and swine. The numbers of equine and bovine vesicular stomatitis detections since 2000 are shown in Figure 10.

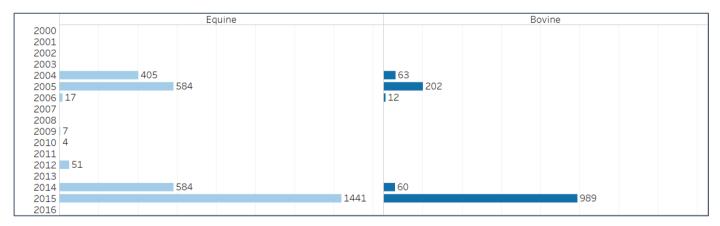


Figure 10. Equine and bovine vesicular stomatitis detections reported since 2000

Management and reporting of vesicular stomatitis cases changed in 2015 resulting in estimates only of the minimum number of positive animals. No cases of vesicular stomatitis were detected in 2016.

Animal Disease Traceability

On January 11, 2013, USDA published a final rule establishing general regulations for improving the traceability of U.S. livestock moving interstate (9 CFR Part 86). Under the final rule (*Traceability for Livestock Moving Interstate*), unless specifically exempted, livestock moved interstate must be officially identified and accompanied by an interstate certificate of veterinary inspection (ICVI) or other documentation, such as owner-shipper statements or

brand certificates. The proposed rule was issued on August 2011 for public comment. Several modifications were made to the final rule after USDA reviewed and considered the comments. These modifications include:

- Accepting the use of brands, tattoos, and brand registration as official identification when accepted by the shipping and receiving States or Tribes
- Permanently maintaining the use of back tags as an alternative to official ear tags for cattle and bison moved directly to slaughter
- Accepting movement documentation other than an ICVI for all ages and classes of cattle when accepted by the shipping and receiving States or Tribes
- Clarifying that all livestock moved interstate to a custom slaughter facility are exempt from the regulations
- Exempting chicks moved interstate from a hatchery from the official identification requirements
- Exempting beef cattle under 18 months of age from the official identification requirements in this rule, unless they are moved interstate for shows, exhibitions, rodeos, or recreational events. The specific traceability requirements for this group will be addressed in separate rulemaking, allowing APHIS-VS to work closely with industry to ensure the effective implementation of the identification requirements.

Animal disease traceability (ADT), or knowing where diseased and at-risk animals are, where they've been, and when, is very important to ensure a rapid response when animal disease events take place. An efficient and accurate animal disease traceability system helps reduce the number of animals involved in an investigation and the time needed to respond, and decreases the cost to producers and the government. The ADT framework was established to improve the ability to trace animals back from slaughter and forward from premises where animals are officially identified in addition to tracing animals' interstate movements. While APHIS-VS focuses on interstate movements of livestock, States and Tribal Nations are responsible for the traceability of livestock within their jurisdictions. This approach was designed to embrace the strengths and expertise of States, Tribes, and producers, while providing flexibility to use the most effective approaches to identify animals moving interstate nationally.

APHIS-VS established trace performance measures (TPM) to document progress in ADT, and by these measures the administration of the ADT program has been successful in the context of the framework of identification and movement documentation for covered livestock: specifically, the elapsed times to complete TPMs has decreased and percent of traces successfully completed for fiscal year has increased. This is largely attributed to the timely retrieval of official identification records (records of tags distributed and tags applied) and movement documents through databases for storing the associated information in an easily searchable format. However, while ADT has been successful in terms of the intended framework, significant gaps still exist within our tracing capabilities since the publication of 9 CFR Part 86. The most significant impediment resulting from the current framework is the restriction that the official identification requirement only applies to livestock that move interstate.

APHIS-VS is confident that the basic framework of ADT from the 2013 rule is being successfully implemented and believes discussions with industry to consider potential next steps are appropriate. During 2017, the agency conducted meetings with SAHOs, Federal officials, and the public to gather input on how ADT is working and identify gaps in the system and next steps. A State-Federal working group is compiling information from the outreach meetings to be presented at an animal traceability forum hosted collaboratively by the National Institute for Animal Agriculture, United States Animal Health Association, and APHIS in September 2017.

One Health Investigations

One Health is the concept that the health of animals, the health of people, and the viability of ecosystems are linked. This approach brings together the strengths of multiple health science professions including veterinarians, physicians, public health professionals, epidemiologists, ecologists, social scientists, toxicologists, and others —

working locally, nationally, and globally – to attain optimal health for people, domestic animals, wildlife, plants and our environment.

APHIS-VS' One Health Coordination Center (OHCC) coordinates and helps implement the One Health aspects of the VS mission. In this section, we describe some of the key One Health investigations that APHIS-VS was involved in during 2016.

Salmonella heidelberg. Since the beginning of 2016, CDC has reported human cases of Salmonella heidelberg in nine States. APHIS-VS has been participating in joint Federal and State calls with animal health and public health officials about the current outbreak of S.heidelberg associated with dairy bull calves sourced from Wisconsin. APHIS-VS partnered with CDC to review the ongoing collaboration between CDC, VS, and Wisconsin State agencies in response to this outbreak. Wisconsin Department of Agriculture, Trade, and Consumer Protection (WI DATCP) sampled the farms of concern and the livestock market linked to the calves associated with the outbreak. Investigation of the outbreak in calves continues. APHIS-VS has provided epidemiology assistance to WI DATCP. CDC considers the human outbreak closed; its final web update was posted March 20, 2017, at https://www.cdc.gov/salmonella/heidelberg-11-16/index.html

Variant influenza virus infections in humans. When an influenza virus that normally circulates in swine, but not people, is detected in a person, it is called a "variant influenza virus" and are designated with a lower-case "v" after the subtype (ex: H1N2v). As part of swine IAV surveillance activities, USDA personnel participate in routine monthly collaboration calls and joint public health-animal health investigations of CDC-laboratory confirmed human infections with variant influenza A viruses. These investigations result in close collaboration among local, State, and Federal public and animal health officials. NVSL provides diagnostic support for swine samples collected from outbreaks. Virus characterization data is shared with State and Federal animal and public health officials, and is also deposited in GenBank®, a public access database.

Between March and August 2016, 21 human infections with variant viruses were reported. Three of those infections were found to be an H1N2v virus and were primarily linked to exposure on family-owned farms. The remaining 18 cases were linked to swine exposure at seven different county fairs in Ohio (four) and Michigan (three). Swine were sampled at each fair and were found to be positive for an H3N2 virus. Human viruses were found to be genetically related to the swine viruses at the fair where the human exposure occurred.

The National Assembly of State Animal Health Officials and the National Association of State Public Health Veterinarians continue to update a set of measures to minimize influenza virus transmission between swine, from people to swine, and from swine to people at swine exhibitions. This guidance was updated again in 2016. More information is available at http://nasphv.org/Documents/Influenza_Transmission_at_Swine_Exhibitions_2016.pdf and http://www.cdc.gov/flu/swineflu/index.htm

Human case of swine brucellosis identifies infected swine herds. In March 2016, an individual in New York State was diagnosed with *Brucella suis* infection. The individual was found to be part of a family farming operation that raised pasture pork. The pigs on the farm were tested and found to be the source of the infection for the individual. State and Federal animal health officials began an investigation and response that lasted for several months. The investigation resulted in discovering nine pasture pork farms in four Northeastern States that were infected with *B.suis*, with the strong indication that the infection had been circulating in those pasture pork operations for some time prior to its discovery. Tracing of swine movements into and out of the nine farms involved 52 other porkraising facilities in 13 States to ensure no other premises were infected. All swine from the nine infected premises were depopulated and the premises were cleaned, disinfected, and remained fallow for a period of 60-120 days before any pigs were permitted to be raised again in the same facility.

H7N2 LPAI in cats in New York City animal shelters. An outbreak of H7N2 LPAI virus among cats in an animal shelter in New York City was first reported on December 9, 2016. This is the first time this strain of influenza has been detected in and known to be transmitted among cats. Based on what is known at this time, the risk to humans is low. The strain of H7N2 detected is quite similar to the virus that was circulating in the LBMS in New York and New Jersey prior to 2006 and which caused an outbreak of LPAI in the Virginia poultry industry in 2002-2003. The source of the virus has not yet been determined. Enhanced surveillance in all NYC shelters has not yet been implemented. Increased passive surveillance will occur as the result of education of medical professionals and public health professionals.

The National Animal Health Reporting System (NAHRS)

The NAHRS program is designed to provide summary-level data on the presence of National List of Reportable Animal Diseases (NLRAD) reportable diseases in the United States. NAHRS gathers monthly data from participating SAHOs on the presence of diseases, identified with a high level of certainty, that are included on the NLRAD-NAHRS Reportable Disease List (Appendix 1). This list contains all of the OIE-listed diseases. In CY 2013, the NAHRS Reportable Disease List cooperatively incorporated all diseases identified on the proposed U.S. NLRAD. The U.S. NLRAD is based on OIE-listed reportable diseases and includes other significant diseases identified by commodity stakeholders.

NAHRS is a collaborative effort between participating States, the American Association of Veterinary Laboratory Diagnosticians (AAVLD), the United States Animal Health Association (USAHA), and the U.S. Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS). NAHRS functions under the guidance of the joint AAVLD-USAHA Animal Health Surveillance and Information Systems Committee—NLRAD-NAHRS subcommittee, which includes representatives from the AAVLD, USAHA, USDA-APHIS-Veterinary Services (VS), participating States, and experts representing the major commodity groups. NAHRS is managed by the VS Center for Epidemiology and Animal Health's (CEAH) Surveillance Design and Analysis (SDA) unit.

Objectives of the NAHRS are:

- > To demonstrate the integrated and transparent nature of disease surveillance and reporting in the United States and ultimately help protect the global market share of U.S. animals and animal products sold
- > To provide a primary source of information used in the completion of OIE reports by USDA-APHIS-VS
- To provide reporting that reflects the comprehensive summary-level animal disease status of the United States and individual State reporting that reflects the summary-level disease status in that State

NAHRS reporting system reflects a broad range of animal disease surveillance activities in the United States. Information on NAHRS, including the current NLRAD-NAHRS disease list, hard copy of the monthly State report form, NAHRS Operational Manual, and additional information for participants, can be found on the NAHRS Web site: http://www.aphis.usda.gov/animal-health/nahrs. The comprehensive NAHRS Operational Manual and Uniform Methods and Rules (UM&R) describe disease reporting criteria and participation requirements for member States and answers commonly asked questions on NAHRS.

U.S. NLRAD Update

A U.S. NLRAD framework document was completed and posted on the APHIS Web site (https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/program-overview/ct_national_list_reportable_animal_diseases) for stakeholder review and comment. The framework document describes specifics on NLRAD operations and management. The document was also presented at the 2016 AAVLD-USAHA meeting in Greensboro, NC. Comments received on the framework document are being used to guide the development of the proposed NLRAD rule.

NAHRS Reporting

Participating SAHOs collect, collate, and report on the occurrence of NAHRS reportable diseases identified with a high level of certainty using NAHRS reporting criteria. NAHRS reporting criteria include standards of laboratory testing and additional criteria outlined in the NAHRS Operational Manual and UM&R. The disease reporting criteria are considered minimum guidelines and SAHOs may use additional information to determine whether to report the presence of disease to the NAHRS (i.e., epidemiological link or other non-listed laboratory tests). The discretion of NAHRS reporting by SAHOs is considered essential for valid reporting of disease because disease testing technology

and other considerations may change rapidly. A designated State official approves the State monthly NAHRS report and submits it to CEAH through the secure NAHRS online reporting tool.

NAHRS collects data from reporting States on the presence or absence of diseases on the NLRAD-NAHRS Reportable Disease List (Appendix 3). A "yes" response from a State indicates that at least one new case of that particular disease met the level of certainty for reporting during the specific month; a "no" response indicates that, as far as SAHOs are aware, no new cases of disease met the level of certainty required to report the disease in the State that month. Reporting and notification of foreign animal diseases (FADs) and VS program diseases must follow specific requirements. As with all NAHRS reportable diseases, endemic diseases are reported only when there is a level of certainty of the disease in a State. A "no" response does not explicitly infer that the endemic disease does not occur in the State. CEAH validates NAHRS data against other national reporting systems, including VS program disease reports (i.e., brucellosis, pseudorabies, BSE, bovine tuberculosis, scrapie, EIA), ArboNET reporting, other State validated information, and OIE immediate reports. The data from these reports are included in the NAHRS annual reports for all States. In addition to submitting the monthly report, designated official personnel in participating States may use the secure NAHRS online reporting system to view their monthly reports, cumulative summary reports, national cumulative summary reports, and NAHRS annual reports.

Participation

In 2016, 35 States participated in NAHRS (Figure 11); each participating State contributes one report per month. Figure 12 shows the APHIS-VS districts used for reporting NAHRS summary data.

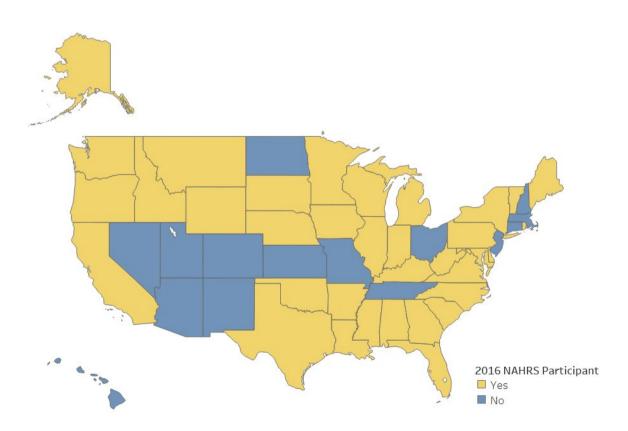


Figure 11. NAHRS 2016 State participants

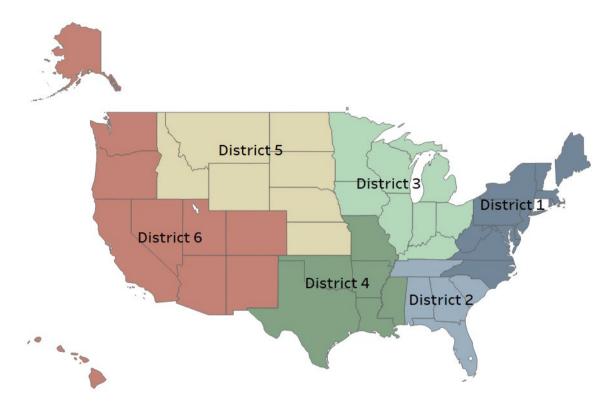


Figure 12. APHIS-VS districts used for reporting summary-level NAHRS data

Reporting Summary

The NAHRS Annual Report provides a summary-level overview of NAHRS reporting in 2016. The NAHRS report is published without identifying the State, owner, or premises where the disease occurred. The following tables and bullets were used to summarize data reported to NAHRS for each animal species or category:

- Table 1: CY 2016 Summary of Confirmed Positive Monthly State Reports by Species and VS District
- List of Reportable Diseases Not Reported to NAHRS in CY 2016

Bovine

Table 1. C Y 2016 Summary of Confirmed Positive Monthly State Reports for Bovine Diseases

	# of STATES that			# of REF	PORTS of th	e Disease			
Disease	reported the disease	District 1	District 2	District 3	District 4	District 5	District 6	Entire U.S.	
 Anaplasmosis (Anaplasma marginale, A. centrale) 	20	27	19	19	32	27	4	128	
Anthrax (Bacillus anthracis)	2			1	2			3	
Bluetongue	11	2	13	8	12	14	1	50	
Bovine brucellosis (B. abortus)	3		1			2	•••	3	
Bovine genital campylobacteriosis (Campylobacter fetus venerealis)	5			8		6	1	15	
Bovine tuberculosis (Mycobacterium bovis)	4			8	2	•••		10	
Bovine viral diarrhea (BVD)	20	24	14	49	24	30	19	160	
Brucellosis (<i>B. suis</i>) ¹	1		2					2	
Enzootic bovine leukosis (BLV)	22	51	23	57	30	32	24	217	
Epizootic hemorrhagic disease (EHD)	5			7		5	2	14	
Infectious bovine rhinotracheitis/infectious pustular vulvovaginitis (IBR/IPV)	17	4	12	38	24	2	15	95	
Malignant catarrhal fever (sheep form)	2	•••	•••	•••	•••	•••	2	2	
Paratuberculosis (Johne's disease Mycobacterium avium paratuberculosis)	27	70	6	80	34	47	27	264	
Q Fever (Coxiella burnetti)	1				1	2		2	
Rabies	11	14		5	3	3		25	
Trichomoniasis (<i>Tritrichomonas</i> [<i>Trichomonas</i>] foetus)	16		12	3	45	15	17	92	

¹Exposure to feral swine

Reportable bovine diseases not reported to NAHRS in 2016:

- Foot-and-mouth disease (FMD)
- Vesicular stomatitis (VS)
- Rinderpest
- Contagious bovine pleuropneumonia (Mycoplasma mycoides mycoides)
- Lumpy skin disease
- Rift Valley fever
- Aujesky's disease (Pseudorabies)
- Echinococcosis / hydatidosis
- Heartwater (Cowdria ruminantium)
- New World screwworm (*Chrysomyia hominivorax*)
- Old World screwworm (Chrysomyia bezziana)
- Babesiosis (Babesia bovis, B. bigemina)
- Hemorrhagic septicemia (*Pasteurella multocida*, serotypes B/Asian or E/African)
- Theileriasis (*Theileria annulata, T. parva*)
- Trypanosomiasis (*Trypanosoma congolense*, *T. vivax*, *T. brucei brucei*, *T. evansi*))
- Crimean Congo hemorrhagic fever
- Brucellosis (B. melitensis)
- Akabane
- Bovine spongiform encephalopathy
- Melioidosis (Burkholderia pseudomallei)

Ovine and Caprine

Table 1. CY 2016 Summary of Confirmed Positive Reports for Ovine and Caprine Diseases

	# of STATES			# of REF	ORTS of the	Disease		
Disease	that reported the disease	District 1	District 2	District 3	District 4	District 5	District 6	Entire U.S.
Bluetongue	5		3	2			5	10
 Caprine arthritis/encephalitis (CAE) 	16	33	6	45	1	21	8	114
 Enzootic abortion of ewes (Ovine psittacosis, Chlamydia psittaci) 	2	1					4	5
 Maedi-visna / ovine progressive pneumonia 	8	12		1		8	1	22

National Animal Health Reporting System Annual Report for 2016

 Ovine epididymitis (Brucella ovis) infection 	4	•••	•••	•••	•••	12	2	14
 Paratuberculosis (Johne's disease - Mycobacterium avium paratuberculosis) 	19	18	2	24		8	8	60
• Q fever (Coxiella burnetti)	6	2	•••	5	•••	1	5	13
• Rabies	3	8						8
• Scrapie	3			2	1		•••	3

Reportable Ovine and Caprine diseases <u>not</u> reported to NAHRS in CY 2016:

- Foot-and-mouth disease (FMD)
- Vesicular stomatitis (VS)
- Rinderpest
- Peste des petits ruminants
- Rift Valley fever
- Sheep pox and goat pox
- Anthrax
- Aujesky's disease (Pseudorabies)
- Echinococcosis / hydatidosis
- Heartwater (Cowdria ruminantium)
- New World screwworm (Chrysomyia hominivorax)
- Old World screwworm (*Chrysomyia bezziana*)
- Bovine tuberculosis (Mycobacterium bovis)
- Theileriasis (*Theileria annulata, T. parva*)
- Contagious caprine pleuropneumonia (Mycoplasma capricolum capripneumoniae)
- Nairobi sheep disease
- Salmonellosis (Salmonella abortus ovis)
- Tularemia (Francisella tularensis)
- Crimean Congo hemorrhagic fever
- Brucellosis (B. melitensis)
- Akabane
- Bovine brucellosis (B. abortus)
- Contagious agalactia
- West Nile fever
- Meliodosis (Burkholderia pseudomallei)
- Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psorergates ovis)

Equine

Table 1. C Y 2016 Summary of Confirmed Positive Reports for Equine Diseases

	# of STATES			# of REPO	ORTS of the	Disease		
Disease	that reported the disease	District 1	District 2	District 3	District 4	District 5	District 6	Entire U.S.
Equine encephalomyelitis (Eastern)	15	7	20	4	12			43
 Equine herpesvirus myeloencephalopathy (EHV1 - EHM) 	12	2	5	3	2	1	6	19
• Equine infectious anemia (EIA)	18	7	3	5	12	2	3	31
• Equine influenza (Virus Type A)	8	4		8	1	1	3	17
• Equine piroplasmosis (Babesiosis, Babesia [Piroplasma] equi, B. caballi)	6	···	1	1	5	1	2	10
• Equine rhinopneumonitis (EHV-1)	18	9	3	7	7	1	10	37
• Equine viral arteritis (EVA)	4		2	1	9	1		13
• Rabies	8	2	3	2	2		1	10
West Nile fever	33	7	3	18	20	10	12	70

Reportable equine diseases not reported to NAHRS in CY 2016:

- African horse sickness
- Anthrax (Bacillus anthracis)
- Echinococcosis / hydatidosis
- New World screwworm (Chrysomyia hominivorax)
- Old World screwworm (Chrysomyia bezziana)
- Trichinellosis (*Trichinella spiralis*)
- Contagious equine metritis (Taylorella equigenitalis)
- Dourine (*Trypanosoma equiperdum*)
- Glanders (*Pseudomonas mallei*)
- Japanese encephalitis
- Surra (Trypanosoma evansi)
- Venezuelan equine encephalomyelitis
- Vesicular stomatitis (VSV)

- Tularemia (Francisella tularensis)
- Equine encephalomyelitis (Western)
- Hendra
- Meliodosis (Burkholderia pseudomallei)

Porcine

Table 1. CY 2016 Summary of Confirmed Positive Reports for Porcine Diseases

·	# of STATES			# of RE	PORTS of Dis	ease		
Disease	that reported the disease	District 1	District 2	District 3	District 4	District 5	District 6	Entire U.S.
Aujesky's disease (Pseudorabies) ¹	1	•••			6			6
 New World screwworm (Cochliomyia hominivorax) 	1				1 ²			1
 Porcine reproductive and respiratory syndrome (PRRS) 	15	10		51	12	24	11	108
 Swine erysipelas (Erysipelothrix rhusiopathiae) 	1			1				1
 Swine Enteric Coronavirus Disease (SECD)(PEDV, PDCoV)³ 	10	1		39	12	17	2	71
• Transmissible gastroenteritis (TGE)	3			3				3

¹Only feral swine and transitional (high-risk) herds reported in 2016; no commercial production swine herds were positive.

Reportable porcine diseases not reported to NAHRS in CY 2016:

- Foot-and-mouth disease (FMD)
- Vesicular stomatitis (VS)
- Swine vesicular disease
- Rinderpest
- African swine fever
- Classical swine fever (hog cholera)

² Pet pig

³ Further information on SECD is included elsewhere in this report in the Swine Surveillance section of the Federally Supported Active and Passive Surveillance Activities in CY 2016 and at the following website: http://www.aphis.usda.gov/animal-health/secd

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- Anthrax (Bacillus anthracis)
- Echinococcosis/hydatidosis
- Rabies
- Brucella suis
- Old World screwworm (Chrysomyia bezziana)
- Trichinellosis (Trichinela spiralis)
- Japanese encephalitis
- Cysticercosis (Cysticercus cellulosae metacestode stage of Taenia solium)
- Tularemia (Francisella tularensis)
- Nipah virus encephalitis
- Meliodosis (Burkholderia pseudomallei)
- Vesicular exanthema

Poultry

Table 1. CY 2016 Summary of Confirmed Positive Reports for Poultry Diseases

	# of STATES that			# of REPC	ORTS of the	Disease		
Disease	reported the disease	District 1	District 2	District 3	District 4	District 5	District 6	Entire U.S.
Highly pathogenic avian influenza	2			1			1	2
 Avian chlamydiosis (psittacosis and ornithosis, Chlamydia psittaci)¹ 	1	2						2
 Avian infectious bronchitis 	12	25	21	2	12	•••	12	72
 Avian infectious laryngotracheitis² 	11	25	8	6	5		13	57
 Infectious bursal disease (Gumboro disease) 	3		9				12	19
 Low pathogenic avian influenza (H5 or H7) Poultry 	5	7		1	1	1		10
• Mycoplasmosis (<i>M. synoviae</i>)	13	27	23	7	17		21	95
 Mycoplasmosis (Mycoplasma gallisepticum) 	16	26	18	25	6	1	20	96
 Pullorum disease (Salmonella pullorum)³ 	2				2	2		3

¹ No commercial production flock detections in 2016

² Includes reports of vaccine-related cases and noncommercial production flocks

³ No commercial production flock detections in 2016

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Reportable poultry diseases not reported to NAHRS in CY 2016:

- Newcastle disease (Exotic)
- Duck viral hepatitis
- Fowl typhoid (Salmonella gallinarum)
- Turkey rhinotracheitis

¹ Backyard flocks

² Includes reports of vaccine-related cases and noncommercial production flocks

³ Backyard flocks

Aquaculture

FISH Diseases Reported:

- Viral hemorrhagic septicemia (VHS) was reported by one State in wild shiners
- Infectious salmon anemia (ISA HPR0). One State reported identification of HPR0 on routine testing in healthy fish. The United States reported this identification of the ISA HPR0 in healthy fish to the OIE on the July Dec 6-monthly report.
- Koi herpesvirus disease was reported once each by three States.
- Infectious hematopoietic necrosis (IHN) was reported in wild fish once each by two States.
- Bacterial kidney disease (Renibacterium salmoninarium) was reported one time by a State.

MOLLUSC Diseases Reported:

- Infection with Perkinsus marinus was reported one time by a State.
- Infection with Xenohaliotis californiensis was reported twice by one State.
- Infection with Haplosporidium nelson or costale (MSX) reported one time by a State.

Reportable aquaculture diseases <u>not</u> reported to NAHRS in CY 2016:

- Fish: Spring viremia of carp
- Fish: Infectious pancreatic necrosis
- Fish: Epizootic hematopoietic necrosis
- Fish: Infectious salmon anemia
- Fish: Epizootic ulcerative syndrome
- Fish: Gyrodactylosis (Gyrodactylus salaris)
- Fish: Red sea bream iridoviral disease
- Fish: Viral encephalopathy and retinopathy (Viral nervous necrosis)
- Fish: Oncorhynchus masou virus disease
- Fish: Gyrodactylosis (Gyrodactylus salaries)
- Fish: Piscirickettsiosis (Piscirickettsia salmonis)
- Fish: Whirling disease (Myxobolus cerbralis)
- Fish: White sturgeon iridoviral disease
- Fish: Infection with salmonid alphavirus
- Mollusc: Infection with Bonamia ostreae
- Mollusc: Infecton with Bonamia exitiosa
- Mollusc: Infection with Marteilia refringens
- Mollusc: Infection with Perkinsus marinus
- Mollusc: Infection with Perkinsus olseni
- Mollusc: Infection with Xenohaliotis californiensis
- Mollusc: Infection with abalone herpes-like virus
- Crustacean: Taura syndrome
- Crustacean: Yellowhead disease
- Crustacean: Infectious hypodermal and haematopoietic necrosis
- Crustacean: Crayfish plague (Aphanomyces astaci)
- Crustacean: Infectious myonecrosis

Amphibian Diseases

No domestic-commercial reports through NAHRS reporting for:

• Infection with Batrachochytrium dendrobatidis

Infection with ranavirus

Crustacean: White tail disease

• Crustacean: Necrotizing hepatopancreatitis

Farmed Cervids

Table 1. CY 2016 Summary of Confirmed Positive Reports for Farmed Cervids Diseases

# of STAT that		# of REPORTS of the disease							
Disease	reported the disease	District 1	District 2	District 3	District 4	District 5	District 6	Entire U.S.	
Anthrax (Bacillus anthracis)	1				1			1	
 Bluetongue 	3		3	•••	4	•••		7	
 Chronic wasting disease 	4			8	5			13	
 Epizootic hemorrhagic disease (EHD) 	4		10	2	5	4		21	
• Rabies	1	1					•••	1	

Reportable Farmed Cervid diseases not reported to NAHRS in 2016:

- Foot-and-mouth disease (FMD)
- Vesicular stomatitis (VS)
- Rinderpest
- Akabane
- Rift Valley fever
- Aujesky's disease (pseudorabies)
- Echinococcosis / hydatidosis
- Heartwater (Cowdria ruminantium)
- New World screwworm (Chrysomyia hominivorax)
- Old World screwworm (Chrysomyia bezziana)
- Paratuberculosis (Johne's disease)
- Bovine tuberculosis

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- · Malignant catarrhal fever
- Crimean Congo hemorrhagic fever
- Brucellosis
- Akabane
- Q Fever (Coxiella burnettii)
- Q Fever
- Melioidosis (Burkholderia pseudomallei)

Lagomorph

- Myxomatosis: One State had two reports of disease
- Tularemia (Francissella tularensis): Three States had four reports of disease

Reportable lagomorph diseases <u>not</u> reported to NAHRS in CY 2016:

· Rabbit hemorrhagic disease

Other OIE Diseases

• Leishmaniosis: Two States had one report each of disease in canines (One imported)

Reportable other diseases not reported to NAHRS in CY 2016:

Camelpox

Bee Diseases (OIE-Listed) - Optional Reporting

Bee disease reported through NAHRS is optional, as other agencies have primary responsibility for bee diseases. The following bee disease occurrences were reported through NAHRS.

- American foulbrood of honey bees
- European foulbrood of honey bees
- Varrosis of honey bees
- Small hive beetle infestation

FAD Surveillance and Investigations

APHIS-VS conducted 853 FAD investigations in 2016 (Figure 13), resulting in the following detections:

- · Highly pathogenic avian influenza (HPAI)
- New World screwworm
- Foreign ectoparasites (ticks)

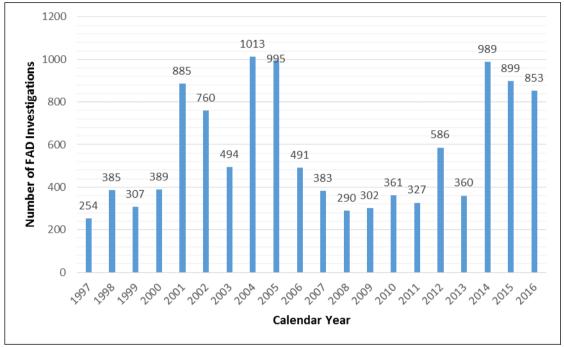


Figure 13. Number of FAD investigations by year, 1997-2016

In CY 2016, as in most proceeding years, the majority of FAD investigations were primarily due to vesicular complaints (blister-like lesions). Concern about vesicular lesions in ruminants, camelids, captive cervids, and swine is due to foot-and-mouth disease (FMD), which primarily affects cloven-hoofed domestic and wild animals. None of the 696 vesicular condition investigations identified in 2016 were positive for FMD. Swine had the most vesicular complaints in 2016, primarily due to Senecavirus A. A summary of investigated vesicular complaints is included in Table 3 and additional information is available online at

https://www.aphis.usda.gov/animal_health/emergency_management/downloads/summary_fad_investigations.pdf

Table 3. Vesicular conditions in 2016

Species/animal	Number of vesicular complaints
Equids (horses, donkeys, and mules)	153
Bovids (cattle, bison)	73
Swine	438
Sheep	9
Goats	19
Cervids	3
Camelids (Bactrian camel)	1
Total	696

OIE Reportable Disease Events

The need to fight animal diseases at the global level led to the creation of the Office International des Epizooties (OIE) established in Paris, France, in 1924 by an international agreement signed by 28 countries. In May 2003, the Office became the World Organisation for Animal Health but kept its historical acronym, OIE.

The OIE is the intergovernmental organization responsible for improving animal health worldwide. The OIE is a reference organization of the World Trade Organization (WTO). The United States is a member country of the OIE and a signatory country of the WTO. Member countries are obligated to comply with the WTO's Agreement on the Application of Sanitary and Phytosanitary Measures. The WTO assigned standards-setting authority for international trade-related animal health issues to the OIE. The United States meets its OIE reporting obligations using a variety of sources including NAHRS, FAD reports, national program disease surveillance reports, and others.

OIE member countries are required to comply with OIE notification requirements by reporting on the status of OIE reportable diseases through the secure, Web-based OIE World Animal Health Information System (WAHIS). Notification requirements include:

- A twice-yearly report on the absence or presence and evolution of diseases listed by the OIE and information of epidemiological significance to other countries;
- An annual OIE-Food and Agriculture Organization (FAO)-WHO report on any other information of significance to other countries, including information from twice-yearly reports, other animal diseases, zoonoses in humans, animal populations, veterinary services infrastructure, and laboratory tests and vaccines;
- Immediate notification and follow-up reports for the following events:
 - First occurrence of a listed disease and/or infection in a country;
 - Reoccurrence of a listed disease and/or infection in a country;
 - o First occurrence of a new strain of a pathogen of an OIE-listed disease in a country;
 - A sudden and unexpected increase in the distribution, incidence, morbidity, or mortality of a listed disease prevalent within a country;
 - o An emerging disease with significant morbidity, mortality, or zoonotic potential;
 - Evidence of change in epidemiology of a listed disease, including host range, pathogenicity, and strain, particularly if there is a zoonotic impact.

Additional information on the OIE, as well as the OIE List of Diseases Reportable, can be found at the OIE website: http://www.oie.int/

U.S. Reporting to the OIE in 2016

In the spirit of transparency, the U.S. submitted all required reporting to the OIE in 2016. Reporting included:

- U.S. Terrestrial and Aquatic January June 2016 Six-Monthly Report on the Notification of the Presence of OIE-Listed Diseases;
- U.S. Terrestrial and Aquatic July-December 2016 Six-Monthly Report on the Notification of the Presence of OIE-Listed Diseases;
- U.S. 2016 Annual OIE-FAO-WHO Animal Health Report;
- U.S. Annual Reconfirmation of Freedom Documentation (Official Recognition Disease Status) for:
 - foot and mouth disease (FMD),
 - African horse sickness (AHS),
 - classical swine fever (CSF),
 - contagious bovine pleuropneumonia (CBPP),
 - pestes des petits ruminants (PPR),

- o bovine spongiform encephalopathy (BSE) risk status; and
- o required immediate and follow-up U.S. OIE Reports (listed below).

Current and past submitted U.S. OIE report information, including routine and immediate reports, is available on the OIE World Animal Health Information (WAHIS) Interface

http://www.oie.int/wahis 2/public/wahid.php/Wahidhome/Home.

U.S. OIE Immediate Notification Disease Events in 2016

Summary of Reports: In 2016, the United States submitted five OIE immediate reports for animal disease events. These included two low pathogenic notifiable avian influenza reports; two HPAI reports; and one report on New World Screwworm (*Cochliomyia hominivorax*). Event summaries can be found on the OIE Web site: http://web.oie.int/wahis/public.php. Summaries on the Web site are organized by the year of their occurrence.

2016 Immediate OIE reports

Avian Influenza (Infection with Avian Influenza Viruses)

Al is caused by influenza type A viruses that can infect poultry (such as chickens, turkeys, pheasants, quail, domestic ducks, geese, and guinea fowl) and are carried by free-flying waterfowl such as ducks, geese, and shorebirds. Influenza A viruses are classified by a combination of two groups of proteins: hemagglutinin or "H" proteins, of which there are 16 (H1-H16), and neuraminidase or "N" proteins, of which there are nine (N1-N9). Many different combinations of "H" and "N" proteins are possible. Each combination is considered a different subtype, and each subtype can be further sub-classified as different strains. Al viruses are identified by their pathogenicity (low or high)—the ability of a particular virus strain to produce disease in domestic chickens. Any influenza A virus (including H5 and H7 avian influenza viruses) in its highly pathogenic form is reportable in birds, but only H5 and H7 LPAI viral infections in poultry are notifiable as per Chapter 10.4 on avian influenza of the OIE Terrestrial Animal Health Code (2016):

http://www.oie.int/index.php?id=169&L=0&htmfile=chapitre avian influenza viruses.htm

H7N8 HPAI—Indiana

OIE Immediate Report January 15, 2016—Resolved April 22, 2016

A turkey flock in Indiana was identified as having high mortality and subsequent testing identified H7N8 HPAI. USDA-APHIS, in conjunction with the Indiana State Board of Animal Health, responded to the event. A comprehensive epidemiological investigation and enhanced surveillance and testing activities were implemented.

The only positive detection of H7N8 HPAI in poultry was made on January 15, 2016. In addition to having no further HPAI detections, the State of Indiana met the following in resolution of the event:

- Mandatory surveillance in the State and control areas was completed with negative results for HPAI.
- Depopulation of all infected premises was completed and appropriate disposal completed.
- Cleaning and disinfection of the infected premises (including, but not limited to, outside areas, equipment, trucks, and other fomites).
- No HPAI detections through wild bird surveillance within 3 months of the event.

H7N8 LPAI—Indiana

• OIE Immediate Report January 19, 2016—Resolved May 2, 2016

As part of existing avian influenza response plans, USDA-APHIS, in conjunction with the Indiana State Board of Animal Health, conducted a comprehensive epidemiological investigation and enhanced surveillance and testing in the Indiana H7N8 HPAI control area. Enhanced surveillance in the control area for the H7N8 HPAI Indiana event identified H7N8 LPAI in eight turkey flocks. The partial sequences of the H7N8 LPAI and HPAI viruses are nearly

identical except for the HA gene insertion, which imparts high pathogenicity to the HPAI virus. While the detection of AI in these additional flocks was of low pathogenicity, and the turkeys in these flocks were clinically healthy, this virus has a potential to mutate to HPAI, and, therefore, appropriate sanitary measures were implemented to mitigate the risk.

The last positive detection of H7N8 LPAI in poultry was made on January 16, 2016. In addition to having no further LPAI detections, the State of Indiana completed the following activities in resolution of the event:

- Completed all mandatory surveillance in the State and control areas with negative results for LPAI.
- Completed the depopulation of all infected premises and completed the appropriate disposal of birds and material.
- Completed the cleaning and disinfection of the infected premises (including, but not limited to, outside areas, equipment, trucks, and other fomites).
- Completed all testing of surveillance samples, which all tested negative for avian influenza virus.

H5N1 LPAI —Missouri

OIE Immediate Report May 2, 2016—Resolved August 9, 2016

Samples were initially collected from healthy, non-clinical turkeys as part of the routine, pre-slaughter surveillance that is done under the NPIP Avian Influenza Clean Program (H5 and H7). Through this routine surveillance, H5N1 LPAI of North American wild bird lineage was identified and confirmed by partial HA/NA sequence. A comprehensive epidemiological investigation of the event and enhanced surveillance was conducted by USDA-APHIS and the Missouri Department of Agriculture.

The last positive detection of H5N1 LPAI in poultry was made on April 30, 2016. In addition to having no further LPAI detections, the State of Missouri completed the following activities in resolution of the event:

- Completed all mandatory surveillance in the State and control areas with negative results for LPAI.
- Completed the depopulation of the infected premises and completed the appropriate disposal of birds and material.
- Finalized the cleaning and disinfection of the infected premises (including, but not limited to, outside areas, equipment, trucks, and other fomites).
- Completed all testing of surveillance samples, all of which tested negative for avian influenza virus.

H5N2 HPAI Wild Bird—Alaska

OIE Immediate Report August 26, 2016—Resolved November 10, 2016

The detection of H5N2 HPAI was from a wild mallard duck that was collected during a live bird banding program at a wildlife refuge in Alaska. This detection of H5N2 HPAI (EA/AM) virus in a wild bird was not associated with any poultry, commercial or backyard, anywhere in the United States. The event was considered resolved with no other detection of HPAI in wild birds.

New World Screwworm (Cochliomyia hominivorax)—Florida Keys, Florida

OIE Immediate Report October 3, 2016—Resolved March 23, 2017

The New World screwworm fly (NWS), *Cochliomyia hominivorax* (Coquerel), is in the subfamily Chrysomyinae of the dipteran family Calliphoridae (blowflies). New World screwworms are fly larvae (maggots) that can infest livestock and other warm-blooded animals, including people. They most often enter an animal through an open wound and feed on the animal's living flesh. If not treated, infestations can be fatal. While New World screwworm has not

been widely present in the United States since the 1960s, it is still found in most of South America and in five Caribbean countries.

In the 1950s, USDA developed a new method to help eradicate screwworm using a form of biological control called the sterile insect technique, which releases infertile male flies in infested areas. When they mate with local females, no offspring result. With fewer fertile mates available in each succeeding generation, the fly, in essence, breeds itself out of existence. USDA used this technique to eradicate screwworm from the U.S. and worked with other countries in Central America and the Caribbean to eradicate it there as well. Today, USDA and its partners maintain a permanent sterile fly barrier at the Darien Gap between Panama and Colombia to prevent the establishment of any screwworm flies that enter from South America.

In 2016, USDA-APHIS confirmed the presence of New World screwworm in Key deer from National Key Deer Refuge in Big Pine Key, Florida. This was the first local infestation in the United States in more than 30 years. Response activities included fly trapping, sterile fly release to prevent reproduction (sterile insect technique), and enhanced surveillance to look for additional cases. The response goal was to limit the infestation from spreading to any new areas and eradicate the New World screwworm flies from the affected Keys and local area.

On March 23, 2017, USDA-APHIS announced the successful eradication of the New World screwworm from Florida (United States). Additional information on the New World screwworm event can be found on the USDA-APHIS website: https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/cattle-disease-information/nws/new-world-screwworm.

Appendix 1. 2016 U.S. NLRAD-NAHRS Reportable Disease List

(* 2016 OIE Listed Diseases)

Changes from previous year:

Aquaculture - Crustacean:

OIE listed: N459 Acute hepatopancreatic necrosis Disease (AHPND) V. parahemolyticus (pVA-1 Plasmid)*

BOVINE	
A010	Foot-and-mouth disease (FMD)*
A020	Vesicular stomatitis (VS)
A040	Rinderpest*
A060	Contagious bovine pleuropneumonia (Mycoplasma mycoides mycoides)*
A070	Lumpy skin disease*
A080	Rift Valley fever*
A090	Bluetongue*
N001	Crimean Congo hemorrhagic fever*
2001	Akabane (congenital arthrogryposis-hydranencephalaly syndrome)
B051	Anthrax (Bacillus anthracis)*
B052	Aujesky's disease (Pseudorabies)*
B053	Echinococcosis / hydatidosis (<i>Echinococcus granulosus</i>)*
B055	Heartwater (Cowdria ruminantium)*
B057	Q Fever (Coxiella burnetti)*
B058	Rabies*
B059	Paratuberculosis (Johne's disease - (Mycobacterium avium paratuberculosis)*
B060	New World screwworm (Cochliomyia hominivorax)*
B061	Old World screwworm (<i>Chrysomya bezziana</i>)*
B101	Anaplasmosis (Anaplasma marginale, A. centrale)*
B102	Babesiosis (Babesia bovis, B.bigemina)*
B103	Bovine brucellosis (<i>B.abortus</i>)*
B152	Caprine and ovine brucellosis (B. melitensis)*
B253	Porcine brucellosis (<i>B.suis</i>)*
B104	Bovine genital campylobacteriosis (Campylobacter fetus venerealis)*
B105	Bovine tuberculosis (<i>Mycobacterium bovis</i>)*

N117	Bovine viral diarrhea (BVD)*		
B108	Enzootic bovine leukosis (BLV)*		
B109	Hemorrhagic septicemia (<i>Pasteurella multocida</i> , serotypes B/Asian or E/African)*		
B110	Infectious bovine rhinotracheitis/infectious pustular vulvovaginitis (IBR/IPV)*		
B111	Theileriasis (<i>Theileria annulata, T. parva</i>)*		
B112	Trichomoniasis (<i>Tritrichomonas [Trichomonas] foetus</i>)*		
B113	Trypanosomiasis (<i>Trypanosoma congolense, T. vivax, T. brucei brucei, T. evansi</i>))*		
B114	Malignant catarrhal fever (specify wildebeest or sheep form)		
B115	Bovine spongiform encephalopathy (BSE)*		
N158	Epizootic hemorrhagic disease (EHD)*		
C613	Melioidosis (Burkholderia pseudomallei)		
CAPRINE A	AND OVINE		
A010	Foot-and-mouth disease (FMD)*		
A020	Vesicular stomatitis (VS)		
A040	Rinderpest*		
A050	Peste des petits ruminants*		
A080	Rift Valley fever*		
A090	Bluetongue*		
A100	Sheep pox and goat pox*		
N001	Crimean Congo hemorrhagic fever*		
2001	Akabane (congenital arthrogryposis-hydranencephalaly syndrome)		
B051	Anthrax (Bacillus anthracis)*		
B052	Aujesky's disease (Pseudorabies)*		
B053	Echinococcosis / hydatidosis*		
B055	Heartwater (Cowdria ruminantium)*		
B057	Q Fever (Coxiella burnetti)*		
B058	Rabies*		
B059	Paratuberculosis (Johne's disease - <i>Mycobacterium avium paratuberculosis</i>)*		
B060	New World screwworm (Cochliomyia hominivorax)*		
B061	Old World screwworm (<i>Chrysomya bezziana</i>)*		

B103	Bovine brucellosis (B.abortus)*			
B105	Bovine tuberculosis (<i>Mycobacterium bovis</i>)*			
B111	Theileriasis (<i>Theileria annulata, T. parva</i>)			
B152	Caprine and ovine brucellosis (B. melitensis)*			
B151	Ovine epididymitis (<i>Brucella ovis</i> infection)*			
B153	Caprine arthritis / encephalitis (CAE)*			
B154	Contagious agalactia (<i>Mycoplasma agalactiae, M. Capricolum capricolum, M. putrefaciens, M. mycoides mycoides, M. mycoides mycoides LC</i>)*			
B155	Contagious caprine pleuropneumonia (Mycoplasma capricolum capripneumoniae)*			
B156	Enzootic abortion of ewes (Ovine psittacosis, Chlamydia psittaci)*			
B158	Nairobi sheep disease*			
B159	Salmonellosis (Salmonella abortus ovis)*			
B160	Scrapie*			
B161	Maedi-visna/ovine progressive pneumonia*			
B352	Tularemia (Francisella tularensis)*			
N002	West Nile fever*			
	Melioidosis (<i>Burkholderia pseudomallei</i>)			
C613	Melioidosis (Burkholderia pseudomallei)			
C613 C706	Melioidosis (Burkholderia pseudomallei) Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis)			
	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi,			
C706	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi,			
C706	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis)			
C706 EQUINE A020	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS)			
C706 EQUINE A020 A110	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS) African horse sickness*			
C706 EQUINE A020 A110 B051	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS) African horse sickness* Anthrax (Bacillus anthracis)*			
C706 EQUINE A020 A110 B051 B053	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS) African horse sickness* Anthrax (Bacillus anthracis)* Echinococcosis / hydatidosis*			
C706 EQUINE A020 A110 B051 B053 B058	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS) African horse sickness* Anthrax (Bacillus anthracis)* Echinococcosis / hydatidosis* Rabies*			
C706 EQUINE A020 A110 B051 B053 B058 B060	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS) African horse sickness* Anthrax (Bacillus anthracis)* Echinococcosis / hydatidosis* Rabies* New World screwworm (Cochliomyia hominivorax)*			
C706 EQUINE A020 A110 B051 B053 B058 B060 B061	Mange (Sarcoptes scabiei var ovis, Chorioptes bovis, Psoroptes ovis, Psoroptes cuniculi, Psoregates ovis) Vesicular stomatitis (VS) African horse sickness* Anthrax (Bacillus anthracis)* Echinococcosis / hydatidosis* Rabies* New World screwworm (Cochliomyia hominivorax)* Old World screwworm (Chrysomya bezziana)*			

Equine encephalomyelitis (Eastern)*

N220

N221	Equine encephalomyelitis (Western)*		
B205	Equine infectious anemia (EIA)*		
B206	Equine influenza (Virus Type A)*		
B207	Equine piroplasmosis (babesiosis, Babesia [Piroplasma] equi, B. caballi)*		
B208	Equine rhinopneumonitis (EHV- 1)*		
B208a	Equine herpesvirus myeloencephalopathy (EHV1 - EHM)		
B209	Glanders (<i>Pseudomonas mallei</i>)*		
B211	Equine viral arteritis (EVA)*		
B212	Japanese encephalitis*		
B215	Surra (<i>Trypanosoma evansi</i>)*		
B216	Venezuelan equine encephalomyelitis*		
B352	Tularemia (Francisella tularensis)*		
N002	West Nile fever*		
W075	Hendra		
C613	Melioidosis (Burkholderia pseudomallei)		
PORCINE			
PORCINE A010	Foot-and-mouth disease (FMD)*		
	Foot-and-mouth disease (FMD)* Vesicular stomatitis (VS)		
A010			
A010 A020	Vesicular stomatitis (VS)		
A010 A020 A030	Vesicular stomatitis (VS) Swine vesicular disease		
A010 A020 A030 A040	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest*		
A010 A020 A030 A040 A120	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever*		
A010 A020 A030 A040 A120 A130	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever* Classical swine fever (hog cholera)*		
A010 A020 A030 A040 A120 A130 N258	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever* Classical swine fever (hog cholera)* Nipah virus encephalitis*		
A010 A020 A030 A040 A120 A130 N258 B051	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever* Classical swine fever (hog cholera)* Nipah virus encephalitis* Anthrax (Bacillus anthracis)*		
A010 A020 A030 A040 A120 A130 N258 B051 B052	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever* Classical swine fever (hog cholera)* Nipah virus encephalitis* Anthrax (Bacillus anthracis)* Aujesky's disease (Pseudorabies)*		
A010 A020 A030 A040 A120 A130 N258 B051 B052 B053	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever* Classical swine fever (hog cholera)* Nipah virus encephalitis* Anthrax (Bacillus anthracis)* Aujesky's disease (Pseudorabies)* Echinococcosis / hydatidosis*		
A010 A020 A030 A040 A120 A130 N258 B051 B052 B053 B058	Vesicular stomatitis (VS) Swine vesicular disease Rinderpest* African swine fever* Classical swine fever (hog cholera)* Nipah virus encephalitis* Anthrax (Bacillus anthracis)* Aujesky's disease (Pseudorabies)* Echinococcosis / hydatidosis* Rabies*		

B212	Japanese encephalitis*		
B252	Cysticercosis (Cysticercus cellulosae metacestode stage of Taenia solium)*		
B253	Porcine brucellosis (B. suis)*		
B254	Transmissible gastroenteritis (TGE)*		
B257	Porcine reproductive and respiratory syndrome (PRRS)*		
B352	Tularemia (Francisella tularensis)*		
C613	Melioidosis (Burkholderia pseudomallei)		
C801	Swine erysipelas (Erysipelothrix rhusiopathiae)		
2006	Vesicular exanthema		
2010	Swine Enteric Coronavirus Disease (SECD) (Porcine epidemic diarrhea virus –PEDV; Porcine delta coronavirus (PDCoV)		
AVIAN			
A150h	Highly pathogenic avian influenza*		
A150i	Low pathogenic avian influenza (H5 or H7 subtypes- poultry)*		
A160	Newcastle disease (Exotic)*		
N315	Turkey rhinotracheitis*		
B301	Avian infectious bronchitis*		
B302	Avian infectious laryngotracheitis*		
B304	Duck viral hepatitis*		
B308	Fowl typhoid (Salmonella gallinarum)*		
B309	Infectious bursal disease (Gumboro disease)*		
B311	Mycoplasmosis (M. gallisepticum)*		
B312	Avian chlamydiosis (psittacosis and ornithosis, Chlamydia psittaci)*		
B313	Pullorum disease (Salmonella pullorum)*		
N316	Mycoplasmosis (<i>M. synoviae</i>)*		
AQUACUL	TURE		
B401	Fish: Viral hemorrhagic septicemia (VHS)*		
B402	Fish: Infectious pancreatic necrosis		
N416	Fish: Infectious salmon anemia (ISA)(HPR-deleted or HPR0)*		
B404	Fish: Spring viremia of carp (SVC)*		
B405	Fish: Infectious hematopoietic necrosis (IHN)*		

B408	Fish: Bacterial kidney disease (Renibacterium salmoninarium)			
N412	Fish: Viral encephalopathy and retinopathy			
B413	Fish: Epizootic hematopoietic necrosis*			
B415	Fish: Oncorhynchus masou virus disease (herpesvirosis of salmonids)			
N417	Fish: Epizootic ulcerative syndrome (EUS)*			
N418	Fish: Gyrodactylosis (<i>Gyrodactylus salaris</i>)*			
N419	Fish: Red sea bream iridoviral disease*			
N420	Fish: Koi herpesvirus disease*			
N415	Fish: Piscirickettsiosis (<i>Piscirickettsia salmonis</i>)			
2002	Fish: Whirling disease (Myxobolus cerbralis)			
2003	Fish: White sturgeon iridoviral disease			
2011	Fish: Infection with salmonid alphavirus*			
N430	Mollusc: Infection with Bonamia ostreae*			
N431	Mollusc: Infection with Bonamia exitiosa/roughleyi*			
N432	Mollusc: Infection with Marteilia refringens*			
N433	Mollusc: Infection with <i>Perkinsus marinus*</i>			
N434	Mollusc: Infection with Perkinsus olseni/atlanticus*			
N435	Mollusc: Infection with Xenohaliotis californiensis*			
N436	Mollusc: Infection with abalone herpes-like virus*			
N463	Mollusc: Abolone viral mortality			
2004	Mollusc: Infection with Marteilia chungmuensis			
2005	Mollusc: Infection with Marteilia sydneyi			
N438	Mollusc: Infection with <i>Haplosporidium nelson</i> (MSX) or <i>Haplosporidium costale</i> (sea side organism)			
2007	Mollusc: QPX (Quahog parasite unknown)			
N441	Crustacean: Spherical baculovirosis (Penaeus monodon-type baculovirus)			
N442	Crustacean: Tetrahedral baculovirosis (Baculovirus penaei)			
N450	Crustacean: Taura syndrome*			
N451	Crustacean: White spot disease*			
N452	Crustacean: Yellowhead disease*			
N455	Crustacean: Infectious hypodermal and haematopoietic necrosis*			

N456	Crustacean: Crayfish plague (Aphanomyces astaci)*
N457	Crustacean: Infectious myonecrosis*
N458	Crustacean: White tail disease*
N459	Crustacean: Acute hepatopancreatic necrosis disease (<i>V.parahemolyticus</i> pVA-1 plasmid)*

FARMED CERVIDS Foot-and-mouth disease (FMD)* A010 A020 Vesicular stomatitis (VS) A040 Rinderpest* A080 Rift Valley fever* N001 Crimean Congo hemorrhagic fever* 2001 Akabane (congenital arthrogryposis-hydranencephalaly syndrome) A090 Bluetongue* B051 Anthrax (Bacillus anthracis)* B052 Aujesky's disease (Pseudorabies)* B053 Echinococcosis / hydatidosis* B055 Heartwater (Cowdria ruminantium)* Q Fever (Coxiella burnetti)* B057 B058 Rabies* B059 Paratuberculosis (Johne's dsease - Mycobacterium avium paratuberculosis)* B060 New World screwworm (Cochliomyia hominivorax)* B061 Old World screwworm (Chyrsomya bezziana)* B103 Bovine brucellosis (B. abortus)* B152 Caprine and ovine brucellosis (B. melitensis)* B253 Porcine brucellosis (B. suis)* B105 Bovine tuberculosis (Mycobacterium bovis)* B114 Malignant catarrhal fever N156 Chronic wasting disease (CWD)

Epizootic hemorrhagic disease (EHD)*

Melioidosis (Burkholderia pseudomallei)

N158

C613

LAGOMORPH (Rabbits & Hares) B351 Myxomatosis* Tularemia (Francisella tularensis)* B352 B353 Rabbit hemorrhagic disease* **OTHER DISEASES** B501 Leishmaniosis* N502 Camelpox* **AMPHIBIAN DISEASES** N601 Infection with Batrachochytrium dendrobatidis* N602 Infection with ranavirus* BEE (APIARY) (optional reporting requirement; other agencies responsible) B451 Acarapisosis of honey bees* American foulbrood of honey bees* B452 B453 European foulbrood of honey bees* B455 Varroosis of honey bees*

2008

2009

Tropilaelaps infestation of honey bees*

Small hive beetle infestation (Aethina tumida)*

Appendix 2. OIE-Reportable Diseases: U.S. Status through CY 2016

Disease	Status	Date of Last Occurrence / Notes
Multiple species diseases		
Anthrax	Present	Sporadic / limited distribution
Aujeszky's disease	Present	Sporadic / limited distribution to feral and-or non-commercial production swine. Non-commercial swine: swine managed under biosecurity conditions that allow for potential exposure to feral swine that may be infected with swine diseases, such as pseudorabies / national eradication program / no commercial production swine herd detections in 2016
Bluetongue	Present	Sporadic
Brucellosis (<i>Brucella abortus</i>)	Present	Sporadic / limited distribution-primarily limited to wildlife in the Greater Yellowstone National Park area/national eradication program
Brucellosis (Brucella melitensis)	Free	1999
Brucellosis (<i>Brucella suis</i>)	Present	Sporadic / limited distribution to feral and-or non-commercial production swine. Non-commercial swine: swine managed under biosecurity conditions that allow for potential exposure to feral swine that may be infected with swine diseases, such as brucellosis / national eradication program / no commercial production swine herd detections in 2016
Crimean Congo haemorrhagic fever	Free	Never occurred
Echinococcosis/hydatidosis (Echinococcosis granulosus, E. multilocularis)	Present?	Sporadic (uncommon in all species)/2008
Epizootic hemorrhagic disease (EHD)	Present	Sporadic and limited distribution.
Equine encephalomyelitis (Eastern)	Present	Sporadic / limited distribution
Foot-and-mouth disease	Free	1929
Heartwater	Free	Never occurred
Japanese encephalitis	Free	Never occurred
New world screwworm	Present	One event in 2016 limited to the Florida Keys – infestation in Key Deer. There was no NWS myiasis in any production

		livestock. Eradicated in early 2017 using sterile flies.
Old world screwworm	Free	Never occurred
Paratuberculosis (Johne's disease)	Present	Voluntary control program
Q fever	Present	Sporadic
Rabies	Present	
Rift Valley fever	Free	Never occurred
Rinderpest	Free	Never occurred
Surra (<i>Trypanosoma evansi</i>)	Free	Never occurred
Trichinellosis	Present?	Sporadic (backyard and wild animals) / no commercial production swine herd detections in 2016
Tularemia	Present (wild)	Sporadic
West Nile fever/encephalitis	Present	
Cattle diseases		
Bovine anaplasmosis	Present	
Bovine babesiosis	Free	Limited distribution (endemic in territories of Puerto Rico and the U.S. Virgin Islands; last occurrence on the U.S. mainland was in 1943)
Bovine genital campylobacteriosis	Present	Sporadic
Bovine spongiform encephalopathy	OIE-Negligible Risk status	2012 detection of atypical BSE, an uncommon form of the agent not generally associated with an animal consuming infected feed
Bovine tuberculosis	Present	Sporadic / limited distribution / national eradication program
Bovine viral diarrhea	Present	
Contagious bovine pleuropneumonia (<i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC)	Free	1892
Enzootic bovine leukosis	Present	

Haemorrhagic septicaemia (<i>Pasteurella multocida</i> , serotypes B/Asian or E/African)	Absent	1969
Infectious bovine rhinotracheitis/infectious pustular vulvovaginitis	Present	
Lumpy skin disease	Free	Never occurred
Theileriosis	Free	Never occurred
Trichomonosis	Present	
Trypanosomosis (tsetse-transmitted)	Free	Never occurred
Sheep and goat diseases		
Caprine arthritis/encephalitis	Present	
Contagious agalactia	Present	Sporadic/ limited distribution
Contagious caprine pleuropneumonia	Free	Never occurred
Enzootic abortion of ewes (ovine chlamydiosis, <i>Chlamydophila abortus</i>)	Present	Sporadic
Maedi-visna	Present	Sporadic
Nairobi sheep diseases	Free	Never occurred
Ovine epididymitis (Brucella ovis)	Present	
Peste des petits ruminants	Free	Never occurred
Salmonellosis (S. abortus ovis)	Present?	Sporadic / no detections reported in 2016
Scrapie	Present	National eradication program/ no detections May 2016 – May 2017
Sheep pox and goat pox	Free	Never occurred
Equine diseases		
African horse sickness	Free	Never occurred
Contagious equine metritis	Absent	No detections since 2013
Dourine	Free	1934
Equine encephalomyelitis (Western)	Present?	No equine detections reported the last 20 years

Equine infectious anemia	Present	Sporadic / limited distribution / national control program
Equine influenza	Present	Sporadic
Equine piroplasmosis	Present	Sporadic / limited distribution. latrogenic transmission cases only; No cases of natural tick-borne transmission identified since 2009 (single outbreak – eradicated).
Equine herpesvirus-1 (EHV-1)	Present	
Equine viral arteritis	Present	Sporadic
Glanders	Free	1942
Venezuelan equine encephalomyelitis	Free	1971
Swine diseases		
African swine fever	Free	Never occurred
Classical swine fever (hog cholera)	Free	1976
Nipah virus encephalitis	Free	Never occurred
Porcine cysticercosis	Absent	2004
Porcine reproductive and respiratory syndrome	Present	
Transmissible gastroenteritis	Present	
Avian diseases		
Avian chlamydiosis	Present	Sporadic (wild birds, pet birds, backyard) / no commercial production flock detections in 2016
Avian infectious bronchitis	Present	
Avian infectious laryngotracheitis	Present	Sporadic (primarily vaccine-related)
Avian mycoplasmosis (M. gallisepticum)	Present	Sporadic / all commercial poultry breeding flocks are under a surveillance program to confirm infection-free status. Commercial table-egg laying hens may be vaccinated.
Avian mycoplasmosis (<i>M. synoviae</i>)	Present	Sporadic / all commercial poultry breeding flocks are under a surveillance program to confirm infection-free status.

Duck viral hepatitis	Free	1998
Fowl typhoid (Salmonella gallinarum)	Free	1981
Highly pathogenic avian influenza	Present	Two events reported to the OIE in 2016: 1) H7N8 in commercial turkey flock, Closed 4/2016; 2) identification of H5N2 in a wild mallard duck
Low pathogenic avian influenza (poultry) Notifiable H5 and H7	Identification of the presence of infection	Identified sporadically in backyard poultry and in live-bird-markets which serve local ethnic communities. Two LPAI detections in commercial turkey flocks (H7N8 and H5N1) reported to the OIE in 2016.
Infectious bursal disease (Gumboro disease)	Present	Sporadic
	- (W.D	
Newcastle disease (Neurotropic and viscerotropic strains)	Present (wild)	2003-domestic poultry are considered Free / sporadic detections in wild birds
Pullorum disease (Salmonella pullorum)	Present	Sporadic (backyard) / no commercial production flock detections since 1991, considered absent in them
Turkey rhinotracheitis	Present?	Disease suspected but not confirmed limited to certain zones / regions of the country
Lagomorph diseases		
Myxomatosis	Present?	Sporadic / limited distribution in wild rabbits
Rabbit hemorrhagic disease	Absent	2010
Bee diseases		
Acarapisosis of honey bees (<i>Acarapis</i> woodi)	Present	Sporadic / limited distribution
American foulbrood of honey bees (Paenibacillus larvae)	Present	
European foulbrood of honey bees (Melissococcus plutonius)	Present	

Small hive beetle infestation (Aethina tumida)	Present	
Tropilaelaps infestation of honey bees (<i>Tropilaelaps</i> spp.)	Free	Never occurred
Varroosis of honey bees (Varroa spp.)	Present	
Other listed disease		
Leishmaniosis	Present	Sporadic occurrence in canines
Camelpox	Free	Never occurred

Status of aquatic animal diseases in the United States of America

Disease	Status	Date of Last Occurrence/Notes
Fish		
Epizootic hematopoietic necrosis (EHN)	Free	Never occurred
Infection with <i>Aphanomyces invadans</i> (Epizootic ulcerative syndrome, EUS)	Present	2004-Domestic absent / sporadic occurrence in wild species
Gyrodactylosis (Gyrodactylus salaries)	Free	Never occurred
Infectious hematopoietic necrosis (IHN)	Present	2015-Domestic/ sporadic / limited distribution
Infectious salmon anemia, ISA (HPR-deleted or HPR0)	Absent HPR-deleted	2016- OIE reported detection of HPRO ISA in healthy fish, no detections of ISAV HPR- deleted
Koi herpesvirus disease (KHV)	Present	Limited distribution
Red sea bream iridoviral disease	Free	Never occurred
Salmonid alphavirus (SAV)	Free	Never occurred
Spring viremia of carp (SVC)	Present? (Wild)	2004-Domestic absent
Viral hemorrhagic septicaemia (VHS)	Present (Wild)	Domestic absent / Sporadic (wild species)- / limited distribution
Molluscs		
Infection with abalone herpes virus	Free	Never occurred
Infection with Bonamia exitiosus	Present (wild)	2015-Domestic/ Sporadic – limited distribution (wild species).

Infection with Bonamia ostreae	Present? (wild)	2006-domestic/ limited distribution
Infection with Marteilia refringens	Free	Never occurred
Infection with <i>Perkinsus marinus</i>	Present	Sporadic /limited distribution
Infection with Perkinsus olseni	Free	Never occurred
Infection with Xenohaliotis californiensis	Present	Sporadic/ limited distribution
Crustaceans		
Ciustaceans		
Acute hepatopancreatic necrosis disease	Absent	
Crayfish plague (Aphanomyces astaci)	Absent	
Infectious hypodermal and haematopoietic necrosis	Absent	
Infectious myonecrosis	Free	Never occurred
Necrotising hepatopancreatitis	Free	
Taura syndrome	Free	2007-Domestic
White spot disease	Present? (wild)	2012-domestic /wild present? – limited distribution
White tail disease	Free	Never occurred
Yellowhead disease	Free	Never occurred
Amphibians		
Infection with Batrachochytrium dendrobatidis	Present (wild)	
Infection with ranavirus	Present (wild)	

Present = occurrence of the disease reported

Free= no occurrence in the U.S. of the OIE-listed disease

Present? = occurrence suspected but not confirmed

Absent = disease absent during the reporting period/no detections reported

Sporadic = occurring only occasionally

Limited distribution = limited geographic distribution

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