

Section 3

Narratives for Selected Reportable Diseases/Conditions of Infrequent Occurrence

Anaplasmosis

Anaplasmosis is a tick-borne bacterial disease caused by *Anaplasma phagocytophilum*. It was previously known as human granulocytic ehrlichiosis (HGE), but was later renamed human granulocytic anaplasmosis (HGA) when the bacterium genus was changed from *Ehrlichia* to *Anaplasma*. Typical symptoms of anaplasmosis include fever, headache, chills, malaise, and muscle aches. More severe infections can be seen in the elderly and those who are immunosuppressed. Anaplasmosis is transmitted to humans by tick bites primarily from *Ixodes scapularis*, the black-legged tick, and *I. pacificus*, the western black-legged tick. Co-infection with other pathogens found in these vectors is possible. Unlike ehrlichiosis, most HGA cases reported in Florida are due to infections acquired in the northeastern and midwestern U.S. *Anaplasma* infections can be acquired in Florida but it is uncommon. Surveillance for anaplasmosis is intended to monitor incidence over time, estimate burden of illness, understand the epidemiology of each species, and target areas of high incidence for prevention education. See Table 1 for additional information on anaplasmosis cases reported in 2016.

All of six cases reported in 2016 were 60 years or older. Onset dates ranged from May to August of 2016. Five of the six cases were acquired in northeastern U.S. states where the vector is common, however one case was exposed in St. Johns County.

Table 1. Characteristics of Anaplasmosis Cases Reported in 2016, Florida

Summary		Case Classification	Number (Percent)
Number of cases in 2016	6	Confirmed	3 (50.0)
5-year trend (2012 to 2016)		Probable	3 (50.0)
Age (in Years)		Outcome	Number (Percent)
Mean	67	Interviewed	4 (67.0)
Median	66	Hospitalized	1 (16.7)
Min-max	60 - 75	Died	0 (0.0)
Gender		Number	(Percent)
Female	2 (33.3)	Sporadic	6 (100.0)
Male	4 (66.7)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	Number (Percent)
White	4 (66.7)	Maine	3 (50.0)
Black	0 (0.0)	Florida	1 (16.7)
Other	0 (0.0)	Massachusetts	1 (16.7)
Unknown race	2 (33.3)	New York	1 (16.7)
Ethnicity		County of Residence	Number (Percent)
Non-Hispanic	4 (66.7)	Miami-Dade	2 (33.3)
Hispanic	0 (0.0)	Alachua	1 (16.7)
Unknown ethnicity	2 (33.3)	Duval	1 (16.7)
		St. Johns	1 (16.7)
		Sumter	1 (16.7)

Brucellosis

Brucellosis is a systemic illness caused by several species of *Brucella* bacteria that can cause a range of symptoms in humans that may include fever, sweats, headaches, back pain, weight loss, and weakness. Brucellosis can also cause long-lasting or chronic symptoms that include recurrent fevers, joint pain, and fatigue. These bacteria are primarily transmitted among animal reservoirs, but people can be exposed when they come into contact with infected animals or animal products contaminated with the bacteria. Laboratorians can be at risk for exposure to *Brucella* species while working with human or animal cultures. Human infections in Florida are most commonly associated with exposure to feral swine infected with *B. suis*. Dogs and domestic livestock may also be infected with *B. suis*. Although dogs and dolphins may be infected with their own *Brucella* species, human illness is not commonly associated with them. Outside the U.S., unpasteurized milk products from infected goats, sheep, and cattle infected with *B. melitensis* and *B. abortus* are important sources of human infections. Brucellosis is reportable to public health authorities because there are a number of public health actions that can be taken to help reduce incidence of this infection. These actions include identifying populations at risk to allow for targeted prevention outreach; increasing health care provider awareness for earlier diagnosis and treatment of infected persons; intervening early and providing prophylaxis to prevent laboratory exposure-related infections from developing; detecting potentially contaminated products including food, transfusion, and organ transplant products; and detecting and responding to a bioterrorist incident. See Table 2 for additional information on brucellosis cases reported in 2016.

There was one confirmed and one probable case of brucellosis in Florida residents in 2016. The confirmed case was caused by *B. suis*. Risk factors included working in a slaughterhouse and hunting. This case had a pre-existing health condition (diabetes mellitus) and was culture-positive three times over a 12-month period. Thirty-one potential laboratory exposures involving laboratorians working with *Brucella* cultures resulted from this case. The probable case was a homeless man who recalled no exposure risks. In addition, a Texas resident was confirmed to be infected with *B. melitensis* while in Florida (note that non-Florida residents are not included in Table 2). The Texas resident reported eating unpasteurized soft cheeses.

Table 2. Characteristics of Brucellosis Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	2	Confirmed	1 (50.0)
5-year trend (2012 to 2016)		Probable	1 (50.0)
Age (in Years)		Outcome	
Mean	52	Interviewed	2 (100.0)
Median	52	Hospitalized	2 (100.0)
Min-max	50 - 54	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	0 (0.0)	Sporadic	2 (100.0)
Male	2 (100.0)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	1 (50.0)	Florida	2 (100.0)
Black	1 (50.0)	County of Residence	
Other	0 (0.0)		Number (Percent)
Unknown race	0 (0.0)	Gadsden	1 (50.0)
Ethnicity		Hillsborough	1 (50.0)
	Number (Percent)		
Non-Hispanic	2 (100.0)		
Hispanic	0 (0.0)		
Unknown ethnicity	0 (0.0)		

Chikungunya Fever

Chikungunya fever is a mosquito-borne illness caused by the chikungunya virus. The most common symptoms of chikungunya virus infection are fever and joint pain. Other symptoms may include headache, muscle pain, joint swelling, or rash. Relapse of joint pain can occur and may persist for months or years. Chikungunya virus is transmitted to people through the bites of infected mosquitoes. Mosquitoes become infected when they feed on a person already infected with the virus. Chikungunya virus is most often spread to people by *Aedes aegypti* and *Aedes albopictus* mosquitoes (the same mosquitoes that transmit dengue and Zika viruses). Rarely the virus can be transmitted through blood transfusion or organ transplants. The first autochthonous transmission of chikungunya virus in the Americas was reported on the island of St. Martin in December 2013. Since then, local transmission has been identified in countries throughout the Caribbean and the Americas. In 2014, 442 cases were identified in Florida residents and Florida was the only continental U.S. state to report local cases of chikungunya fever, with 12 cases reported. No locally acquired cases were identified in 2015 or 2016. Overall incidence in Florida decreased dramatically in 2015 (121 cases) and 2016 (10 cases). Infection with chikungunya virus is believed to lead to lifetime immunity, which is considered to be the primary reason for this decrease. Extensive spread in Central and South America and the Caribbean in 2014 resulted in immunity for many people in those areas. Surveillance for chikungunya fever is important to identify individual cases and implement control measures to prevent introduction and ongoing transmission, monitor incidence over time, and estimate the burden of illness. See Table 3 for additional information on chikungunya fever cases reported in 2016.

Case counts in this report are based on report year and may differ from other reports that use different criteria to assemble the data (such as onset date). Two cases included as 2016 cases in this report had symptom onset near the end of 2015 but were not reported until 2016.

Table 3. Characteristics of Chikungunya Fever Cases Reported in 2016, Florida

Summary		Case Classification	Number (Percent)
Number of cases in 2016	10	Confirmed	2 (20.0)
5-year trend (2012 to 2016)		Probable	8 (80.0)
Age (in Years)		Outcome	Number (Percent)
Mean	40	Interviewed	8 (80.0)
Median	40	Hospitalized	2 (20.0)
Min-max	19 - 68	Died	0 (0.0)
Gender		Outbreak Status	Number (Percent)
	Number (Percent)	Sporadic	10 (100.0)
Female	7 (70.0)	Outbreak-associated	0 (0.0)
Male	3 (30.0)	Outbreak status unknown	0 (0.0)
Unknown gender	0 (0.0)	Location Where Exposed	
Race		Number (Percent)	
	Number (Percent)	South America	4 (40.0)
White	6 (60.0)	Asia	2 (20.0)
Black	1 (10.0)	Caribbean	2 (20.0)
Other	2 (20.0)	Central America	1 (10.0)
Unknown race	1 (10.0)	Mexico or Caribbean	1 (10.0)
Ethnicity		County of Residence	Number (Percent)
	Number (Percent)	Palm Beach	4 (40.0)
Non-Hispanic	3 (30.0)	Broward	2 (20.0)
Hispanic	6 (60.0)	Duval	1 (10.0)
Unknown ethnicity	1 (10.0)	Hillsborough	1 (10.0)
		Manatee	1 (10.0)
		Pinellas	1 (10.0)

Hansen’s Disease (Leprosy)

Hansen’s disease (also known as leprosy) is an infection caused by the slow-growing bacteria *Mycobacterium leprae*. It can affect the nerves, skin, eyes, and lining of the nose (nasal mucosa). With early diagnosis and treatment, the disease can be cured. However, if left untreated, the nerve damage can result in crippling of hands and feet, paralysis, and blindness. Leprosy was once feared as a highly contagious and devastating disease. Transmission is still not clearly defined, but it is hard to spread. Once recognized, treatment is effective. Bacteria are thought to spread person-to-person via respiratory droplets following extended close contact with an infected person. Historically, the disease was not thought to be endemic in Florida. More recently in Florida and nationally, the role of infected armadillos and possibly contaminated soil as a source of exposure is being investigated further. Surveillance is important to facilitate early diagnosis and appropriate treatment by an expert to minimize permanent nerve damage and prevent further transmission. See Table 4 for additional information on Hansen’s disease cases reported in 2016.

Due to the long incubation period for Hansen’s disease and a mobile population, location of exposure is often difficult to identify. However, seven infected people spent most or all their lives in Florida and were reported as Florida-acquired. Only three people reported direct armadillo contact and for one of those people, contact was 50 years earlier. The median age of infected people was 67 years and all except one were ≥53 years old. This older age distribution differs from overall national cases reported to the National Hansen’s Disease Program, which tend to have a younger median age. Case county of residence was primarily in counties in the central part of the state. It is unclear if this distribution is due to enhanced regional training and outreach efforts, population demographics, or other factors. Average time from onset to diagnosis was 1.1 years in 2016, which has improved from 1.75 years for cases reported from 2005 through 2014. Earlier diagnosis may in part be due to increased awareness in Florida health care providers.

Table 4. Characteristics of Hansen’s Disease (Leprosy) Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	18	Confirmed	18 (100.0)
5-year trend (2012 to 2016)		Probable	0 (0.0)
Age (in Years)		Outcome	
Mean	65	Interviewed	18 (100.0)
Median	67	Hospitalized	1 (5.6)
Min-max	37 - 81	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	7 (38.9)	Sporadic	17 (94.4)
Male	11 (61.1)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	1 (5.6)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	16 (88.9)	Unknown	11 (61.1)
Black	2 (11.1)	Florida	7 (38.9)
Other	0 (0.0)	County of Residence	
Unknown race	0 (0.0)		Number (Percent)
Ethnicity		Brevard	11 (61.1)
	Number (Percent)	Martin	2 (11.1)
Non-Hispanic	18 (100.0)	Alachua	1 (5.6)
Hispanic	0 (0.0)	Hillsborough	1 (5.6)
Unknown ethnicity	0 (0.0)	Orange	1 (5.6)
		Polk	1 (5.6)
		Seminole	1 (5.6)

Hepatitis E

Hepatitis E is a liver disease caused by the hepatitis E virus (HEV). HEV is widespread in the developing world, causing large epidemics of acute hepatitis. Many infections are asymptomatic. When symptoms do occur, they are similar to those of other types of acute viral hepatitis and can include fever, fatigue, loss of appetite, nausea, vomiting, abdominal pain, jaundice, dark urine, clay-colored stool, and joint pain. Hepatitis E is usually self-limiting, but some cases may develop into acute liver failure, particularly among pregnant woman and persons with preexisting liver disease. HEV may also cause chronic infection, primarily in immunocompromised persons. The virus is shed in the stools of infected persons. Globally, HEV is transmitted mainly through contaminated drinking water. Although rare in developed countries, individual cases and outbreaks have been linked to exposure to pigs; consumption of undercooked pork, wild game, or shellfish; and blood transfusions. Most locally acquired infections report no specific risk factors. Surveillance for hepatitis E worldwide is important because it is a significant cause of morbidity with an estimated 20 million HEV infections, three million acute cases of hepatitis E, and over 57,000 hepatitis E-related deaths. Pregnant women with hepatitis E, particularly those in the second or third trimester, are at an increased risk of acute liver failure, fetal loss, and death. Surveillance in the U.S. is conducted to monitor incidence and trends. See Table 5 for additional information on hepatitis E cases reported in 2016.

Compared to 2015 when four of six reported infections were acquired in Florida, most infections were associated with exposures in other countries in 2016. Only one infection was acquired in Florida. One case was lost to follow-up and exposures were unknown. No commonalities were identified among cases.

Table 5. Characteristics of Hepatitis E Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	5	Confirmed	4 (80.0)
5-year trend (2012 to 2016)		Probable	1 (20.0)
Age (in Years)		Outcome	
Mean	46	Interviewed	4 (80.0)
Median	50	Hospitalized	1 (20.0)
Min-max	20 - 58	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	1 (20.0)	Sporadic	4 (80.0)
Male	4 (80.0)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	1 (20.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	3 (60.0)	Florida	1 (20.0)
Black	0 (0.0)	Bangladesh	1 (20.0)
Other	1 (20.0)	Mauritius	1 (20.0)
Unknown race	1 (20.0)	Saudi Arabia	1 (20.0)
Ethnicity		County of Residence	
	Number (Percent)		Number (Percent)
Non-Hispanic	3 (60.0)	Manatee	1 (20.0)
Hispanic	1 (20.0)	Miami-Dade	1 (20.0)
Unknown ethnicity	1 (20.0)	Okaloosa	1 (20.0)
		Orange	1 (20.0)
		Palm Beach	1 (20.0)

Influenza-Associated Pediatric Mortality

Influenza, or flu, is a respiratory infection caused by a variety of influenza viruses. The Centers for Disease Control and Prevention estimate that influenza has resulted in between 9.2 million and 60.8 million illnesses, 140,000 to 710,000 hospitalizations, and 12,000 to 56,000 deaths annually since 2010.¹ Most experts believe that influenza viruses spread mainly by droplets made when infected people cough, sneeze, or talk. Less often, a person might become infected with influenza by touching a surface or object contaminated with influenza virus then touching their own mouth, eyes, or possibly nose. The best way to prevent influenza and prevent severe complications or outcomes from infection is to get vaccinated each year. Influenza surveillance is conducted to detect changes in the influenza virus, which helps determine the vaccine composition each year and prepare for epidemics and pandemics. Surveillance is also conducted to identify unusually severe presentations of influenza; detect outbreaks; and determine the onset, peak, and wane of influenza season to assist with influenza prevention, particularly in high-risk populations like the very young, the elderly, and pregnant women. Individual cases of novel influenza (a new subtype of influenza) and influenza-associated pediatric deaths are reportable in Florida. Additional surveillance of influenza and influenza-like illness activity is conducted using a variety of surveillance systems, including laboratory-based surveillance and syndromic surveillance. For additional information about influenza surveillance and the 2016-17 influenza season, see Section 6: Influenza and Influenza-Like Illness Surveillance. Note that influenza season starts in October each year and continues through May of the following year. During the 2016-17 influenza season, 10 deaths were reported. Data summarized here are based on report year rather than influenza season. See Table 6 for additional information on the six influenza-associated pediatric mortalities reported in the 2016 report year.

Table 6. Characteristics of Influenza-Associated Pediatric Mortality Cases Reported in 2016, Florida

Summary		Case Classification	Number (Percent)
Number of cases in 2016	6	Confirmed	6 (100.0)
5-year trend (2012 to 2016)		Probable	0 (0.0)
Age (in Years)		Outcome	Number (Percent)
Mean	11	Interviewed	3 (50.0)
Median	11	Hospitalized	4 (66.7)
Min-max	5 - 16	Died	6 (100.0)
Gender		Outbreak Status	Number (Percent)
	Number (Percent)	Sporadic	6 (100.0)
Female	4 (66.7)	Outbreak-associated	0 (0.0)
Male	2 (33.3)	Outbreak status unknown	0 (0.0)
Unknown gender	0 (0.0)	Location Where Exposed	
Race		Number (Percent)	
	Number (Percent)	Florida	5 (83.3)
White	4 (66.7)	New Hampshire	1 (16.7)
Black	0 (0.0)	County of Residence	
Other	2 (33.3)	Number (Percent)	
Unknown race	0 (0.0)	Broward	1 (16.7)
Ethnicity		Collier	1 (16.7)
	Number (Percent)	Monroe	1 (16.7)
Non-Hispanic	4 (66.7)	Orange	1 (16.7)
Hispanic	2 (33.3)	Palm Beach	1 (16.7)
Unknown ethnicity	0 (0.0)	Sarasota	1 (16.7)

1 Rolfes MA, Foppa IM, Garg S, Flannery B, Brammer L, Singleton JA, et al. 2016. Estimated Influenza Illnesses, Medical Visits, Hospitalizations, and Deaths Averted by Vaccination in the United States. Available at www.cdc.gov/flu/about/disease/2015-16.htm.

Measles (Rubeola)

Measles, also known as rubeola, is a vaccine-preventable respiratory disease caused by the measles virus. Before a routine vaccination program was introduced in the U.S., measles was a common illness in infants, children, and young adults. Most people have now been vaccinated in the U.S. and the disease has become rare. Measles is still common in many parts of the world where vaccination rates are low, including some countries in Africa, Asia, Europe, and the Pacific. In recent years, measles has been imported into the U.S. from frequently visited countries, including the United Kingdom, France, Germany, India, and the Philippines, where large outbreaks have been reported. Most measles cases imported into the U.S. have come from unvaccinated U.S. residents who became infected while traveling abroad, became symptomatic after returning to the United U.S., and in some cases infected others in their communities, causing outbreaks. Additional information on global measles control efforts is available on the Measles & Rubella Initiative website at www.measlesrubellainitiative.org. A typical case of measles begins with mild to moderate fever, cough, runny nose, red eyes, and sore throat, possibly followed by tiny white spots inside the mouth, a red or reddish-brown generalized maculopapular rash, and high fever. Measles is highly contagious among susceptible people and can spread to others from four days before to four days after the rash appears. Measles is only found in humans, and is spread by aerosolized droplets of saliva or mucus from the mouth, nose, or throat of an infected person, usually when the person coughs, sneezes, or talks. Surveillance for measles is important to identify infected people and prevent them from transmitting the virus to others by isolating the infected person and identifying and vaccinating any susceptible contacts. It is also important to educate potentially exposed people about the signs and symptoms of measles to facilitate early diagnosis and reduce the risk of further transmission. See Table 7 for additional information on measles cases reported in 2016.

Out of the five confirmed cases in 2016, four were epidemiologically linked and three of those were from the same household. The cluster resulted from a vaccinated adult exposed in Illinois to an internationally acquired measles case. That adult infected an unvaccinated child in Florida, who in turn infected two family members. The Centers for Disease Control and Prevention conducted sequencing on specimens collected during the investigation and identified identical genotype D8 measles virus from the international case and the Florida cluster of cases.

Table 7. Characteristics of Measles (Rubeola) Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	5	Confirmed	5 (100.0)
5-year trend (2012 to 2016)		Probable	0 (0.0)
Age (in Years)		Outcome	
Mean	24	Interviewed	5 (100.0)
Median	30	Hospitalized	2 (40.0)
Min-max	3 - 48	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	2 (40.0)	Sporadic	1 (20.0)
Male	3 (60.0)	Outbreak-associated	4 (80.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	5 (100.0)	Florida	4 (80.0)
Black	0 (0.0)	Illinois	1 (20.0)
Other	0 (0.0)	County of Residence	
Unknown race	0 (0.0)		Number (Percent)
Ethnicity		Miami-Dade	4 (80.0)
	Number (Percent)	Collier	1 (20.0)
Non-Hispanic	2 (40.0)		
Hispanic	3 (60.0)		
Unknown ethnicity	0 (0.0)		

Meningococcal Disease

Meningococcal disease is caused by *Neisseria meningitidis* bacteria. About 1 in 10 people have these bacteria in the back of their nose and throat with no signs or symptoms of disease (i.e., colonized). Sometimes the bacteria invade the body and cause certain illnesses, including infections of the lining of the brain and spinal cord (meningitis) and bloodstream infections (bacteremia or septicemia). These illnesses are often severe and can be deadly. Bacteria spread from person to person by direct contact or inhalation of respiratory droplets from the nose or throat of a colonized or infected person. Five *N. meningitidis* serogroups cause almost all invasive disease (A, B, C, Y and W). Vaccines provide protection against these serogroups. Serogroup W continued to be the most frequently identified serogroup causing infection in Florida, which differs significantly from national trends where serogroup B is the most frequently identified serogroup. Beginning in late 2008, a dominant clone of *N. meningitidis* serogroup W emerged in south Florida. This *N. meningitidis* clone has caused the majority of invasive meningococcal disease cases in south Florida over the past eight years and has also caused a multi-year increase in invasive meningococcal disease in the region, which has now diminished.¹ Surveillance for meningococcal disease is important because immediate public health actions are taken in response to every suspected meningococcal disease case to prevent secondary transmission. Surveillance is also conducted to monitor effectiveness of immunization programs and vaccines. See Table 8 for additional information on meningococcal disease cases reported in 2016.

Table 8. Characteristics of Meningococcal Disease Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	18	Confirmed	18 (100.0)
5-year trend (2012 to 2016)		Probable	0 (0.0)
Age (in Years)		Outcome	
Mean	40	Interviewed	17 (94.0)
Median	34	Hospitalized	18 (100.0)
Min-max	0 - 96	Died	1 (5.6)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	10 (55.6)	Sporadic	17 (94.4)
Male	8 (44.4)	Outbreak-associated	1 (5.6)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	15 (83.3)	Florida	15 (83.3)
Black	1 (5.6)	Chile	1 (5.6)
Other	2 (11.1)	North Carolina	1 (5.6)
Unknown race	0 (0.0)	Saint Martin	1 (5.6)
Ethnicity		County of Residence	
	Number (Percent)		Number (Percent)
Non-Hispanic	16 (88.9)	Broward	3 (16.7)
Hispanic	2 (11.1)	Hillsborough	2 (11.1)
Unknown ethnicity	0 (0.0)	Palm Beach	2 (11.1)
Serogroup		Bay	1 (5.6)
	Number (Percent)	Collier	1 (5.6)
Group W	6 (33.3)	Duval	1 (5.6)
Group B	5 (27.8)	Lee	1 (5.6)
Group C	3 (16.7)	Leon	1 (5.6)
Group Y	1 (5.6)	Marion	1 (5.6)
Unknown	3 (16.7)	Miami-Dade	1 (5.6)
		Okaloosa	1 (5.6)
		Pasco	1 (5.6)
		Polk	1 (5.6)
		St. Johns	1 (5.6)

1 Doyle TJ, Mejia-Echeverry A, Fiorella P, Leguen F, Livengood J, Kay R, et al. 2010. Cluster of Serogroup W135 Meningococci, Southeastern Florida, 2008–2009. *Emerging Infectious Diseases*, 16(1):113-115. Available at https://wwwnc.cdc.gov/eid/article/16/1/09-1026_article.

Mercury Poisoning

Mercury is a naturally occurring element distributed in the environment as a result of both natural and man-made processes. There are three forms of mercury (elemental or metallic mercury, organic mercury compounds, inorganic mercury compounds), each with unique characteristics and potential health threats. Mercury exposures are typically due to ingestion of mercury or inhalation of mercury vapors. Forms of mercury most likely encountered by the general public include elemental mercury vapor (found in some thermometers and dental amalgam), methylmercury (associated with fish consumption), ethylmercury (found in some medical preservatives), and inorganic mercury (mercuric salts). Methylmercury is created when microorganisms in the environment convert inorganic mercury into its organic form, which can build up in the environment and accumulate in fish and marine mammals. Eating fish is healthy and can reduce the risk of heart attack and strokes, but eating too much of certain fish can increase exposure to mercury. Developing fetuses and young children are more sensitive to the effects of mercury, which can impact brain development. Mercury cannot be cut away, cleaned, or cooked out of fish. Methylmercury is the most likely source of mercury leading to adverse health effects in the general population and can cause impaired neurological development; impaired peripheral vision; disturbed sensations (e.g., “pins and needles feelings” usually in the hands, feet, and around the mouth); lack of coordinated movements; impaired speech, hearing, and walking; and muscle weakness. Surveillance for mercury poisoning is important to determine if there is a source of mercury exposure of public health concern (e.g., fish, broken thermometer, dental amalgams), prevent further or continued exposure through remediation or elimination of sources when possible, and to inform the public about how to reduce the risk of exposure. See Table 9 for additional information on mercury poisoning cases reported in 2016.

All people with reported mercury poisoning in 2016 reported fish consumption as the source of poisoning. One of the affected people ate ≤17 ounces of fish per week; six people ate 18-35 ounces, six people ate 36-65 ounces, two people ate 66-95 ounces, and two people ate ≥126 ounces. Two people did not report the amount of fish consumed. The Florida Department of Health guidelines for fish consumption are available at www.doh.state.fl.us/FloridaFishAdvice. Women of childbearing age and young children should not eat more than one meal per week of fish with *very low* mercury or one meal per month of fish with *low* mercury, and they should avoid eating any fish with *moderate* mercury. Women not planning to be pregnant and men should not eat more than two meals a week of fish with *very low* mercury, one meal per week of fish with *low* mercury, or one meal per month of fish with *moderate* mercury.

Table 9. Characteristics of Mercury Poisoning Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	19	Confirmed	19 (100.0)
5-year trend (2012 to 2016)		Probable	0 (0.0)
Age (in Years)		Outcome	
Mean	57	Interviewed	18 (95.0)
Median	60	Hospitalized	0 (0.0)
Min-max	24 - 83	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	6 (31.6)	Sporadic	19 (100.0)
Male	13 (68.4)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	18 (94.7)	Florida	18 (94.7)
Black	1 (5.3)	Unknown	1 (5.3)
Other	0 (0.0)	County of Residence	
Unknown race	0 (0.0)		Number (Percent)
Ethnicity		Lee	5 (26.3)
	Number (Percent)	Palm Beach	5 (26.3)
Non-Hispanic	18 (94.7)	Broward	3 (15.8)
Hispanic	1 (5.3)	Bay	1 (5.3)
Unknown ethnicity	0 (0.0)	Indian River	1 (5.3)
		Pasco	1 (5.3)
		Polk	1 (5.3)
		Sarasota	1 (5.3)
		St. Lucie	1 (5.3)

Mumps

Mumps is a vaccine-preventable disease caused by the mumps virus. Mumps typically starts with a few days of fever, headache, muscle aches, tiredness and loss of appetite, followed by swelling of salivary glands. Before a routine vaccination program was introduced in the U.S., mumps was a common illness in infants, children and young adults. Despite routine vaccination, the number of cases in the U.S. has been increasing mainly due to outbreaks in young adults in settings with close contact, like college campuses. Waning immunity is thought to play a role in these outbreaks. Mumps is only found in humans, and is spread by droplets of saliva or mucus from the mouth, nose or throat of an infected person, usually when the person coughs, sneezes or talks. Surveillance for mumps is important to identify infected people and prevent them from transmitting the infection to others by isolating the infected person and identifying and vaccinating any susceptible contacts. It is important to educate potentially exposed people about the signs and symptoms of mumps to facilitate early diagnosis and reduce the risk of further transmission. Surveillance data are also used to evaluate prevention programs and vaccine effectiveness. See Table 10 for additional information on mumps cases reported in 2016.

Of the 16 reported cases, six cases acquired mumps from international travel or had close contact to someone with symptoms who recently traveled. One case was identified as part of an out-of-state college campus outbreak. Two cases that were initially reported as acquired in Florida and acquired in an unknown location were later determined to have traveled outside the country before the onset of symptoms after the close of the 2016 morbidity dataset. These cases were acquired in Colombia and England. One case initially reported as sporadic was later found to be outbreak-associated after the close of the 2016 morbidity dataset.

Table 10. Characteristics of Mumps Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	16	Confirmed	6 (37.5)
5-year trend (2012 to 2016)		Probable	10 (62.5)
Age (in Years)		Outcome	
Mean	38	Interviewed	15 (94.0)
Median	42	Hospitalized	4 (25.0)
Min-max	14 - 62	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	7 (43.8)	Sporadic	12 (75.0)
Male	9 (56.3)	Outbreak-associated	3 (18.8)
Unknown gender	0 (0.0)	Outbreak status unknown	1 (6.3)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	7 (43.8)	Florida	9 (56.3)
Black	3 (18.8)	Unknown	2 (12.5)
Other	2 (12.5)	Bangladesh	1 (6.3)
Unknown race	4 (25.0)	Iowa	1 (6.3)
Ethnicity		Indiana	1 (6.3)
	Number (Percent)	India	1 (6.3)
Non-Hispanic	9 (56.3)	Europe	1 (6.3)
Hispanic	2 (12.5)	County of Residence	
Unknown ethnicity	5 (31.3)		Number (Percent)
		Miami-Dade	5 (31.3)
		Broward	3 (18.8)
		Hillsborough	2 (12.5)
		Alachua	1 (6.3)
		Citrus	1 (6.3)
		Gadsden	1 (6.3)
		Okaloosa	1 (6.3)
		Orange	1 (6.3)
		Palm Beach	1 (6.3)

Rocky Mountain Spotted Fever and Spotted Fever Rickettsiosis

Spotted fever rickettsioses (SFRs) are a group of tick-borne diseases caused by closely related *Rickettsia* bacteria. The most serious and commonly reported spotted fever group rickettsiosis in the U.S. is Rocky Mountain spotted fever (RMSF) caused by *R. rickettsii*. Examples of other causes of SFR include *R. parkeri*, *R. africae*, and *R. conorii*. RMSF symptoms include fever, headache, and rash and can be fatal if not treated early with the correct antibiotic. Other SFRs have similar signs and symptoms, including fever, headache, and rash, but are often less severe than RMSF. Unlike RMSF, an eschar often develops at the site of the tick bite following infection with other SFRs. Most infections reported in Florida are acquired in the northern and central regions of the state. Imported cases also occur regularly, particularly in people traveling to countries in southern Africa. Cases are reported year-round without distinct seasonality, though peak transmission typically occurs during the summer months. The principal tick vectors in Florida are the American dog tick (*Dermacentor variabilis*) and the Gulf Coast tick (*Amblyomma maculatum*). In 2010, the national reporting criteria were expanded to include both RMSF and other SFRs. Florida adopted this change in June 2014. Human antibodies to spotted fever rickettsial species such as *R. parkeri*, *R. amblyommii*, *R. africae*, and *R. conorii* cross-react with serologic tests for the RMSF organism *R. rickettsii*. Commercial antibody testing to differentiate other SFRs from RMSF is currently limited, though PCR testing of eschar swabs performed at reference laboratories can provide species. Surveillance for SFRs is important to monitor incidence over time, estimate burden of illness, monitor geographical and temporal occurrence, and target areas of high incidence for prevention education. See Table 11 for additional information on SFR cases reported in 2016.

All three confirmed cases were exposed during international travel to South Africa and were unrelated to each other. Eschar swabs from two of the confirmed cases tested PCR positive for SFR; one was positive for *R. conorii* and one for *R. africae*. The third case was confirmed using serologic assays so species could not be determined.

Table 11. Characteristics of Rocky Mountain Spotted Fever and Spotted Fever Rickettsiosis Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	12	Confirmed	3 (25.0)
5-year trend (2012 to 2016)		Probable	9 (75.0)
Age (in Years)		Outcome	
Mean	53	Interviewed	10 (83.0)
Median	53	Hospitalized	8 (66.7)
Min-max	14 - 83	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)	Sporadic	12 (100.0)
Female	4 (33.3)	Outbreak-associated	0 (0.0)
Male	8 (66.7)	Outbreak status unknown	0 (0.0)
Unknown gender	0 (0.0)	Location Where Exposed	
Race			Number (Percent)
	Number (Percent)	Florida	7 (58.3)
White	9 (75.0)	South Africa	3 (25.0)
Black	1 (8.3)	Pennsylvania	1 (8.3)
Other	0 (0.0)	South Carolina	1 (8.3)
Unknown race	2 (16.7)	County of Residence	
Ethnicity			Number (Percent)
	Number (Percent)	Duval	2 (16.7)
Non-Hispanic	7 (58.3)	Miami-Dade	2 (16.7)
Hispanic	2 (16.7)	Okaloosa	2 (16.7)
Unknown ethnicity	3 (25.0)	Broward	1 (8.3)
		Clay	1 (8.3)
		Manatee	1 (8.3)
		Marion	1 (8.3)
		Palm Beach	1 (8.3)
		Suwannee	1 (8.3)

Staphylococcus aureus Infection, Vancomycin-Intermediate and Vancomycin-Resistant

Staphylococcus aureus is a bacterium commonly found on the skin and in the noses of healthy people. Most *S. aureus* infections are minor, but sometimes serious or fatal bloodstream infections, wound infections, or pneumonia can occur. *S. aureus* is also an important cause of health care-associated infections, especially among chronically ill patients who have recently had invasive procedures or who have indwelling medical devices. *S. aureus* is transmitted person-to-person by direct contact. Commonly found among health care workers, *S. aureus* is spread by hands that become contaminated by contact with colonized or infected patients; colonized or infected body sites of the health care workers themselves; or devices, items, or other environmental surfaces contaminated with body fluids containing *S. aureus*.

S. aureus with resistance to many antibiotics has become more common in the last decade. Consequently, physicians rely heavily on vancomycin as the primary antibiotic for treating patients infected with bacteria that are resistant to many antibiotics. When the bacteria become resistant to vancomycin as well, treatment options are limited. Vancomycin-intermediate *S. aureus* (VISA) and vancomycin-resistant *S. aureus* (VRSA) have acquired intermediate or complete resistance to vancomycin. VISA emerges when a patient with preexisting *S. aureus* infection or colonization is exposed to repeated vancomycin use and the *S. aureus* strain develops a thicker cell wall. This resistance mechanism is not transferrable to susceptible strains. In contrast, VRSA emerges when a strain of *S. aureus* acquires the *vanA* gene from a vancomycin-resistant *Enterococcus* (VRE) organism. Recent exposure to vancomycin is not necessary. This type of gene-mediated resistance is theoretically transferable to susceptible strains or organisms, so there is potential for person-to-person transmission. No VRSA infection has ever been detected in Florida. Surveillance for VISA and VRSA is intended to identify infected people, evaluate their risk factors for infection, assess the risk of a patient transmitting infection to others, and to prevent such transmission. Additionally, it is important to track the emergence of a relatively new and rare clinically important organism. See Table 12 for additional information on VISA cases reported in 2016.

Of the four reported cases in 2016, three were admitted from the community, each with significant past medical histories that increase the risk for infections. One person’s risk factors were unknown.

Table 12. Characteristics of *Staphylococcus aureus* Infection, Intermediate Resistance to Vancomycin Cases Reported in 2016, Florida

Summary		Case Classification	Number (Percent)
Number of cases in 2016	4	Confirmed	4 (100.0)
5-year trend (2012 to 2016)		Outcome	Number (Percent)
Age (in Years)		Interviewed	1 (25.0)
Mean	56	Hospitalized	4 (100.0)
Median	56	Died	0 (0.0)
Min-max	40 - 74	Outbreak Status	
Gender		Sporadic	4 (100.0)
	Number (Percent)	Outbreak-associated	0 (0.0)
Female	1 (25.0)	Outbreak status unknown	0 (0.0)
Male	3 (75.0)	Location Where Exposed	
Unknown gender	0 (0.0)	Florida	4 (100.0)
Race		County of Residence	
	Number (Percent)	Lake	1 (25.0)
White	3 (75.0)	Pasco	1 (25.0)
Black	1 (25.0)	Pinellas	1 (25.0)
Other	0 (0.0)	Suwannee	1 (25.0)
Unknown race	0 (0.0)		
Ethnicity			
	Number (Percent)		
Non-Hispanic	4 (100.0)		
Hispanic	0 (0.0)		
Unknown ethnicity	0 (0.0)		

Tetanus

Tetanus is a life-threatening disease caused by the toxin produced by *Clostridium tetani* bacteria. Tetanus is entirely preventable through immunization. Another name for tetanus is "lockjaw" because it often causes a person's neck and jaw muscles to lock, making it hard to open the mouth or swallow. Other symptoms may include headache, muscle spasms, painful muscle stiffness all over the body, seizures, fever and sweating, high blood pressure, and fast heart rate. Tetanus is rare in the U.S. because vaccination rates are high. Tetanus vaccines are available for children and adults in several different formulations. Booster tetanus vaccines are recommended at least every 10 years. Nearly all cases of tetanus are among people who have never received a tetanus vaccine or adults who do not stay up-to-date on their 10-year booster shots. Unlike other vaccine-preventable diseases, tetanus is not spread from person to person. *C. tetani* bacteria are found in high concentrations in soil and animal excrement and people can become infected when contaminated soil, dust, or manure enter the body through breaks in the skin (usually cuts or puncture wounds caused by contaminated objects). The purpose of tetanus surveillance is to monitor the effectiveness of immunization programs and vaccines and to collect information on the temporal, geographic, and demographic occurrence to facilitate its prevention and control. See Table 13 for additional information on tetanus cases reported in 2016.

Of the five cases reported in 2016, the exposures leading to illness included a man who cut his finger while painting outdoors, a man who cut his hand while towing a car, and a woman who stepped on a nail while outdoors. One woman had no known acute injuries and information about one man's injury was limited. One woman died; the cause of death was unknown. Four people did not recall receiving a tetanus toxoid vaccination within the past 10 years, and one person had a previous dose of tetanus toxoid vaccine within the past year.

Table 13. Characteristics of Tetanus Cases Reported in 2016, Florida

Summary		Case Classification	Number (Percent)
Number of cases in 2016	5	Probable	5 (100.0)
5-year trend (2012 to 2016)		Outcome	Number (Percent)
Age (in Years)		Interviewed	3 (60.0)
Mean	52	Hospitalized	4 (80.0)
Median	43	Died	1 (20.0)
Min-max	36 - 77	Outbreak Status	
Gender		Number (Percent)	
Female	2 (40.0)	Sporadic	5 (100.0)
Male	3 (60.0)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
Number (Percent)		Number (Percent)	
White	4 (80.0)	Florida	5 (100.0)
Black	1 (20.0)	County of Residence	
Other	0 (0.0)	Number (Percent)	
Unknown race	0 (0.0)	Pinellas	2 (40.0)
Ethnicity		Broward	1 (20.0)
Number (Percent)		Miami-Dade	1 (20.0)
Non-Hispanic	4 (80.0)	Okaloosa	1 (20.0)
Hispanic	1 (20.0)		
Unknown ethnicity	0 (0.0)		

Typhoid Fever

Typhoid fever is a systemic illness caused by *Salmonella enterica* serotype Typhi (*Salmonella* Typhi) bacteria. People with typhoid fever typically have a sustained high fever and may also experience weakness, stomach pains, headache, loss of appetite, or rash. Typhoid fever can be severe. *Salmonella* Typhi lives only in humans. People get typhoid fever after eating food or drinking beverages that have been handled by a person who is shedding *Salmonella* Typhi in their stool or when sewage contaminated with *Salmonella* Typhi bacteria gets into the water used for drinking or washing food. Typhoid fever is common in most parts of the world except in industrialized regions such as the U.S., Canada, Western Europe, Australia, and Japan. Good sanitation and aggressive case follow-up help prevent typhoid fever from becoming endemic in industrialized regions. Surveillance for typhoid fever is intended to determine if there is a source of infection of public health concern (e.g., an infected food handler or contaminated commercially distributed food product) and to stop transmission from such a source, assess the risk of infected people transmitting infection to others and prevent such transmission, and identify other unrecognized cases. See Table 14 for additional information on typhoid fever cases reported in 2016.

Typically, about 80% of infections are acquired in other countries; however, in 2016, all cases were acquired in other countries. One infection was acquired in Haiti before immigrating to the U.S., one case was acquired in Haiti or Mexico while traveling for business, and the other 10 cases were acquired in various countries while visiting family or friends. While nine of the cases were in U.S. citizens, three cases were in citizens of other countries who were currently living in Florida (two Haitian citizens, one Indian citizen).

Table 14. Characteristics of Typhoid Fever Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	12	Confirmed	12 (100.0)
5-year trend (2012 to 2016)		Probable	0 (0.0)
Age (in Years)		Outcome	
Mean	21	Interviewed	12 (100.0)
Median	16	Hospitalized	11 (91.7)
Min-max	4 - 38	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	4 (33.3)	Sporadic	12 (100.0)
Male	8 (66.7)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	0 (0.0)	Haiti	5 (41.7)
Black	6 (50.0)	India	2 (16.7)
Other	6 (50.0)	Pakistan	2 (16.7)
Unknown race	0 (0.0)	Bangladesh	1 (8.3)
Ethnicity		County of Residence	
	Number (Percent)		Number (Percent)
Non-Hispanic	11 (91.7)	Broward	3 (25.0)
Hispanic	1 (8.3)	Miami-Dade	2 (16.7)
Unknown ethnicity	0 (0.0)	Palm Beach	2 (16.7)
		Collier	1 (8.3)
		Duval	1 (8.3)
		Hillsborough	1 (8.3)
		Orange	1 (8.3)
		St. Johns	1 (8.3)

West Nile Virus Disease

West Nile virus (WNV) is a mosquito-borne flavivirus that was first introduced to the northeastern U.S. in 1999 and first detected in Florida in 2001. Since its initial detection, WNV activity has been reported in all 67 Florida counties. People infected with WNV can experience a wide range of symptoms. Approximately 80% of those infected show no clinical symptoms, 20% have mild symptoms (headache, fever, pain, fatigue), and less than 1% suffer from the neuroinvasive form of illness, which may involve meningitis and encephalitis and can cause irreversible neurological damage, paralysis, coma, or death. *Culex* species (mosquitoes) and wild birds are the natural hosts. Humans and horses can become infected when they are bitten by a mosquito infected with WNV. WNV can also be transmitted to humans via contaminated blood transfusions and less frequently through organ transplantation. Since 2003, all blood donations are screened for the presence of WNV prior to transfusion. Symptoms typically appear from 2 to 14 days after the exposure. People spending large amounts of time outside (due to occupation, hobbies, or homelessness) or not using insect repellent or other forms of prevention are at higher risk of becoming infected. Surveillance for WNV infections is important to identify areas where WNV is being transmitted to target prevention education for the public, monitor incidence over time, and estimate the burden of illness. See Table 15 for additional information on WNV disease cases reported in 2016.

Six of the eight cases reported in 2016 had neuroinvasive symptoms. Two infected people were first identified by blood donor screening tests. One person developed symptoms after blood donation and the other had a febrile illness prior to blood donation and later developed neuroinvasive symptoms.

While asymptomatic WNV infections do occur, they do not meet the Florida surveillance case definition. In 2016, two asymptomatic infections in blood donors were identified in Florida residents of Gulf (October) and Pinellas (July) counties. The Pinellas blood donor was lost to follow-up and it is unknown if the WNV infection was acquired in Florida. A fatal neuroinvasive WNV infection was also identified in a non-Florida resident who was visiting Florida (note that this report only includes Florida residents in case counts). It is unknown whether or not the infection was acquired in Florida as the person was unavailable for interview. Information provided by family members indicated that the person spent part of their incubation period in their state of residence and part in Florida. This was the only fatal infection identified in Florida in 2016.

Table 15. Characteristics of West Nile Virus Disease Cases Reported in 2016, Florida

Summary		Case Classification	
Number of cases in 2016	8	Confirmed	4 (50.0)
5-year trend (2012 to 2016)		Probable	4 (50.0)
Age (in Years)		Outcome	
Mean	44	Interviewed	8 (100.0)
Median	41	Hospitalized	6 (75.0)
Min-max	16 - 72	Died	0 (0.0)
Gender		Outbreak Status	
	Number (Percent)		Number (Percent)
Female	2 (25.0)	Sporadic	8 (100.0)
Male	6 (75.0)	Outbreak-associated	0 (0.0)
Unknown gender	0 (0.0)	Outbreak status unknown	0 (0.0)
Race		Location Where Exposed	
	Number (Percent)		Number (Percent)
White	8 (100.0)	Florida	8 (100.0)
Black	0 (0.0)	County of Residence	
Other	0 (0.0)		Number (Percent)
Unknown race	0 (0.0)	Bay	3 (37.5)
Ethnicity		Escambia	2 (25.0)
	Number (Percent)	Duval	1 (12.5)
Non-Hispanic	7 (87.5)	Okaloosa	1 (12.5)
Hispanic	1 (12.5)	Santa Rosa	1 (12.5)
Unknown ethnicity	0 (0.0)		

