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Influenza A(H3N2) Variant Virus Outbreak at Three Fairs — Maryland, 2017

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On September 17, 2017, the Maryland Department of Agriculture (MDA) was notified by fair and 4-H officials of ill swine at agricultural fair A, held September 14–17. That day, investigation of the 107 swine at fair A revealed five swine with fever and signs of upper respiratory tract illness. All five respiratory specimens collected from these swine tested positive for influenza A virus at the MDA Animal Health Laboratory, and influenza A(H3N2) virus was confirmed in all specimens by the U.S. Department of Agriculture National Veterinary Services Laboratory (NVSL). On September 18, MDA was notified by fair and 4-H officials that swine exhibitors were also ill. MDA alerted the Maryland Department of Health (MDH). A joint investigation with MDH and the local health department was started and later broadened to Maryland agricultural fairs B (September 13–17) and C (September 15–23). In total, 76 persons underwent testing for variant influenza, and influenza A(H3N2) variant (A(H3N2)v) virus infection was identified in 40 patients with exposure to swine at these fairs (Figure), including 30 (75%) who had more than one characteristic putting them at high risk for serious influenza complications; 24 (60%) of these were children aged <5 years. Twenty-six (65%) patients reported direct contact with swine (i.e., touching swine or swine enclosure), but 14 (35%) reported only indirect contact (e.g., walking through a swine barn). Two children required hospitalization; all patients recovered. This outbreak highlights the risk, particularly among children, for contracting variant influenza virus at agricultural fairs after direct or indirect swine contact. Publicizing CDC's recommendation that persons at high risk for serious influenza complications avoid pigs and swine barns might help prevent future variant influenza outbreaks among vulnerable groups (*1*).

Investigation and Results

Public health and agricultural officials met with fair and 4-H club leaders and swine exhibitors and identified an initial group of eight ill persons associated with fair A. They telephoned these persons and coordinated collection of nasopharyngeal (NP) swab specimens. On September 20, seven of eight NP specimens tested presumptively positive for A(H3N2)v virus by real-time reverse transcription–polymerase chain reaction (RT-PCR) testing at MDH Laboratories Administration.

A suspected case of variant influenza was defined as influenza-like illness (ILI) (fever and cough or sore throat) among persons with swine exposure ≤7 days before symptom onset. Case-finding activities included contacting swine exhibitors

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through in-person meetings, telephone calls, and e-mail. Through media outreach, persons with recent swine exposure and ILI were advised to seek medical testing. MDH sent an e-mail alert to clinicians and published an Epi-X* alert call for cases. NP swabs from ill persons were collected at local health departments, clinics, and hospitals; initial testing was performed at the MDH Laboratories Administration.

On September 21, MDH was notified by the local health department of an ill person with swine exposure at fair B, and specimen collection was conducted in the patient's home state of Delaware, in coordination with the Delaware Division of Public Health. No ill swine were detected at fair B, and no swine influenza testing was performed at this fair. The ill person had no other swine exposure and no sick contacts. On September 23, ill swine and ill persons with swine exposure at fair C were reported by fair officials. Among 294 swine at fair C, 11 were found to have fever and signs of upper respiratory tract illness. All 11 respiratory specimens collected from swine at fair C tested positive for influenza A at MDA Animal Health Laboratory and influenza A(H3N2) virus was confirmed in all specimens by NVSL. On September 27, MDH reported the first human A(H3N2)v virus presumptively positive cases associated with fairs B and C.

In total, 80 fair attendees reporting ILI were identified; 76 underwent influenza testing. Forty (52.6%) persons tested presumptively positive for influenza A(H3N2)v virus infection, including 39 Maryland residents who had NP swabs tested at the Maryland Laboratories Administration and one Delaware resident whose NP swab was tested at the Delaware Public Health Laboratory. All were confirmed to contain influenza A(H3N2)v virus by real-time RT-PCR testing and genetic sequencing analysis performed at CDC. Telephone interviews were conducted with all patients who tested presumptively positive using a novel influenza A virus case report form to collect demographic, health, and exposure information.

All patients reported attending one of three Maryland fairs (A [15], B [one], and C [24]); 52.5% were male. Patient age ranged from 9 months to 79 years; 37 (92.5%) were aged <15 years. Overall, 30 (75%) patients were at high risk for complications from influenza, including 24 aged <5 years, one aged ≥65 years, and six with a chronic medical condition. Twenty-six (65%) patients reported direct contact with swine. Fourteen (35%) patients reported only indirect contact with swine.

The median incubation period from last swine exposure to symptom onset was 2.5 days (range = 1–6 days). The most commonly reported signs and symptoms were fever (92.5%), cough (92.5%), and sore throat (40%). Eight patients reported vaccination against seasonal influenza in the past year. Two children were hospitalized; one of whom had an underlying medical condition and reported direct contact with swine. The other, admitted to an intensive care unit, was previously healthy and was wheeled in a stroller through a swine barn, but had no direct swine contact. Both recovered; there were no deaths.

* https://www.cdc.gov/mmwr/epix/epix.html.

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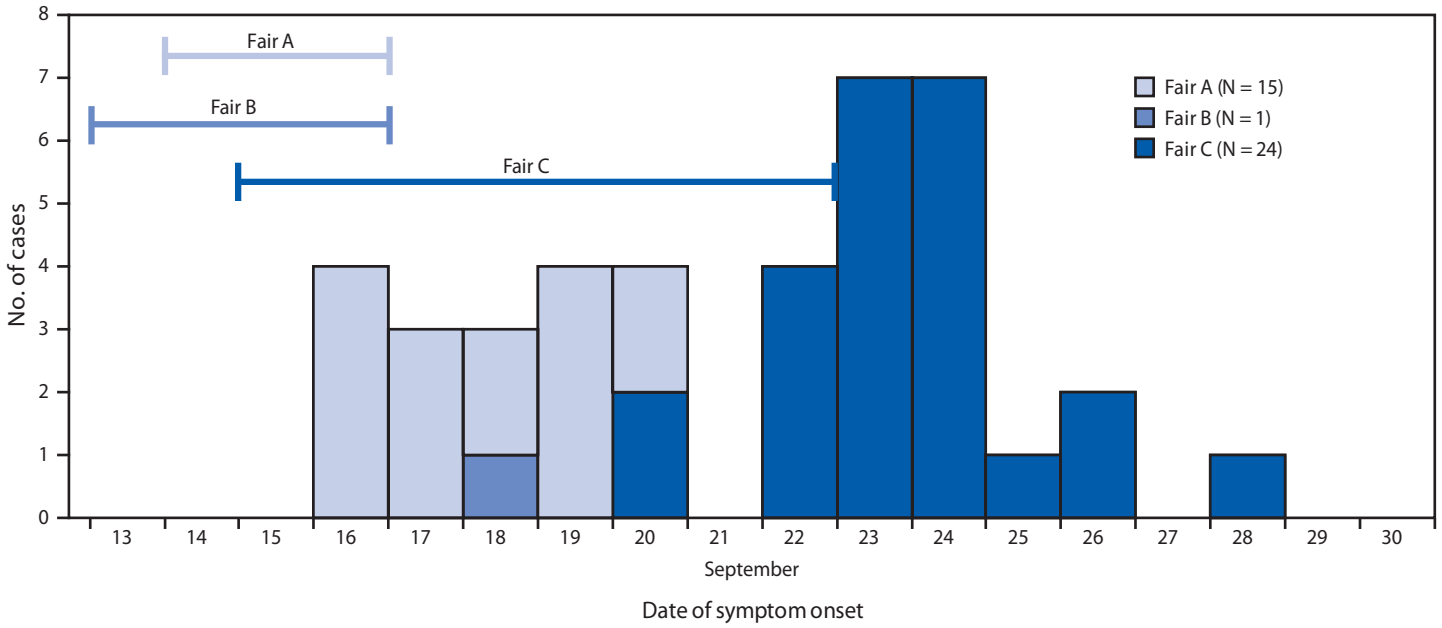
FIGURE. Human influenza A(H3N2) variant virus infections (N = 40), by date of symptom onset and associated agricultural fair — Maryland, September 2017



Laboratory Data

Viruses were isolated from two swine each at fairs A and C from clinical samples submitted from the MDA Animal Health Laboratory to NVSL. Whole-genome sequencing was performed on the four swine viruses at NVSL in accordance with guidelines stated in the National Surveillance Plan for influenza in pigs (*2*). All eight gene segments of the viruses were amplified using standard methods. Sequences were submitted to GenBank (*3*).[†]

Whole-genome sequences from human cases were generated for 34 viruses representing strains from each fair. Hemagglutinin (HA) and neuraminidase (NA) sequences only were available for one additional A(H3N2)v virus.[§] For phylogenetic analyses, nucleotide sequences were downloaded from GenBank for swine and from the Global Initiative on Sharing All Influenza Data (GISAID) for human A(H3N2)v viruses. Swine and human viruses from the Maryland fairs included in the investigation were highly similar to one another in each gene segment (>99% identity) and formed monophyletic clades in each of the gene trees. The Maryland A(H3N2)v and swine influenza viruses were also similar to other swine exhibit–associated variant cases detected during 2017 from other states (*4*).

[†] Nucleotide accession numbers: MG193837–MG193844 for A/swine/Maryland/A01764002/2017(H3N2); MG193875–MG193882 for A/swine/Maryland/A01764005/2017(H3N2); MG193883–MG193890 for A/swine/Maryland/A01764022/2017(H3N2); and MG193799–MG193806 for A/swine/Maryland/A01764024/2017(H3N2) for swine viruses.

[§] GISAID accession numbers: EPI_ISL_294259 to EPI_ISL_294289, EPI_ISL_294291, EPI_ISL_294294, EPI_ISL_294296, EPI_ISL_304787.

Public Health Response

In accordance with Maryland law and MDA's standard operating procedures for swine influenza, steps were taken to minimize transmission of influenza virus among swine and from swine to humans. At fair A, MDA allowed market swine to go to slaughter, and remaining nonmarket swine (i.e., breeder pigs) were quarantined on the fairgrounds until 7 days after the last swine showed signs of influenza illness. At fair C, MDA sent some breeder pigs home, increased surveillance of remaining pigs for illness, and closed swine exhibits to the public; when swine illness was later detected, market swine were allowed to go to slaughter and remaining swine were quarantined on the fairgrounds. The Maryland Secretary of Agriculture canceled swine exhibits at the final two fairs of the 2017 Maryland fair season.

Public health officials issued press releases, conducted media interviews, and created a variant influenza virus website to educate the public about risk, prevention, and treatment. A letter was sent advising preventive measures to schools and child care providers, particularly for field trips where children might be exposed to swine. In counties with canceled swine exhibits, MDA, MDH, and 4-H leaders held meetings with persons who had planned to exhibit swine to arrange for the safe sale and processing of market swine.

Discussion

This outbreak highlights the ongoing public health risk for variant influenza at agricultural fairs. In past outbreaks, most variant influenza virus infections and related hospitalizations have been among children (*4*,*5*). The proportion of ill children in this outbreak, including both hospitalized patients, underscores the vulnerability of children to variant influenza virus and its potential life-threatening complications.

Seventy-five percent of patients in this outbreak, including both hospitalized patients, were at high risk for influenza complications. CDC recommends that persons at high risk for serious influenza complications avoid pigs and swine barns (*1*). Increasing public awareness about these recommendations (e.g., through signage posted at swine barn entrances) might decrease variant influenza virus infection among these groups. Although immunization with seasonal influenza vaccine does not provide protection against infection with variant viruses, the low number of patients who reported seasonal influenza vaccination underscores the need to reinforce that seasonal influenza vaccination is recommended for all persons aged ≥6 months (*6*).

This outbreak also highlights the need to expand monitoring for swine and human respiratory illness to concurrent or upcoming agricultural fairs within the same region if swine influenza virus is detected at one fair. Influenza A viruses are endemic and circulate among most swine populations in North America (*7*). It is common for swine to be exhibited at multiple fairs (such as county and state fairs) and even in multiple states. Strategies to prevent potential influenza transmission at other ongoing or upcoming regional agricultural fairs might include enhanced surveillance for swine illness and public educational campaigns about variant influenza. In situations where the risk of variant influenza is high, such as when a variant influenza case at a nearby fair has been detected, closing ongoing swine exhibits to the public and canceling upcoming swine exhibits might also be considered.

Finally, this outbreak highlights the need for a One Health approach to investigating and responding to variant influenza virus outbreaks, including the application of both swine and human infection control measures, as well as collaboration between agricultural, environmental, and public health agencies on surveillance and communications strategies. This approach is collaborative, multisectoral, and transdisciplinary, used at the local, regional, national, and global levels, and recognizes the interconnection between humans, animals, plants, and their shared environment.

Summary

What is already known about this topic?

Outbreaks of variant influenza have occurred in agricultural fair settings in the United States.

What is added by this report?

In September 2017, 40 cases of influenza A(H3N2) variant virus infection were identified among persons with swine exposure at one of three Maryland agricultural fairs. Thirty cases (75%) occurred among persons at high risk for serious influenza complications. Thirty-five percent of patients reported only indirect swine contact.

What are the implications for public health practice?

Increased public education that groups at high risk for influenza complications should avoid pigs and swine barns is needed. When swine influenza virus is detected at one fair, enhanced surveillance should extend to all fairs in the region.

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Translocation of a Stray Cat Infected with Rabies from North Carolina to a Terrestrial Rabies-Free County in Ohio, 2017

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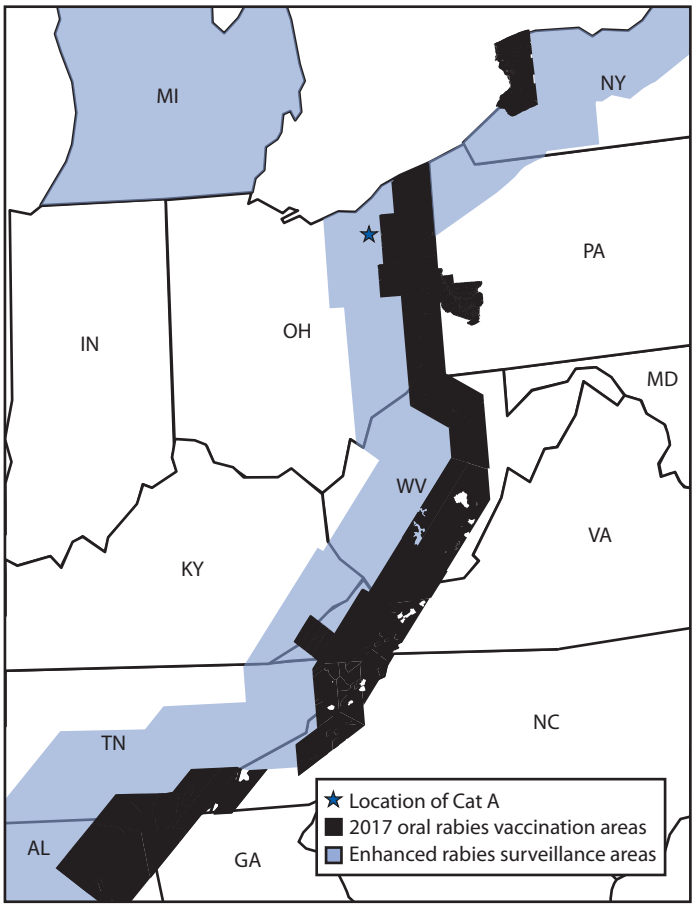
On July 24, 2017, the Ohio Department of Health (ODH) was notified of a positive rabies test result from a domestic cat in Summit County, a county considered free from terrestrial rabies. Oral rabies vaccination (ORV) of raccoons, in the form of consumable bait, is conducted each year along the Ohio-Pennsylvania border to prevent the westward expansion of the raccoon rabies virus variant (RVV). In the United States, several distinct rabies virus variants exist; raccoon RVV is enzootic along the eastern parts of the United States (from Florida to Maine), including several counties in northeast Ohio (*1*). Animal rabies vaccination is protective against all rabies virus variants. The rabid cat (cat A) was located west of the ORV barrier, raising concern that it had acquired the infection from a raccoon and suggesting a possible breach in the ORV barrier (Figure 1). ODH initiated an investigation to identify persons and animals exposed to the rabid cat during its viral shedding period and collaborated with CDC to determine the likely origin of the virus (Figure 2). Public health investigators later discovered that the cat originated in North Carolina. Phylogenetic analysis confirmed that the virus was most similar to the raccoon RVV that circulates in North Carolina (Figure 3); therefore, this ORV breach was likely the result of human-mediated movement of a rabid animal rather than natural expansion of the raccoon rabies virus enzootic area. This report summarizes the investigation and highlights the importance of owner compliance regarding rabies vaccination.

FIGURE 1. Oral rabies vaccination and enhanced rabies surveillance areas in Ohio and surrounding states, 2017



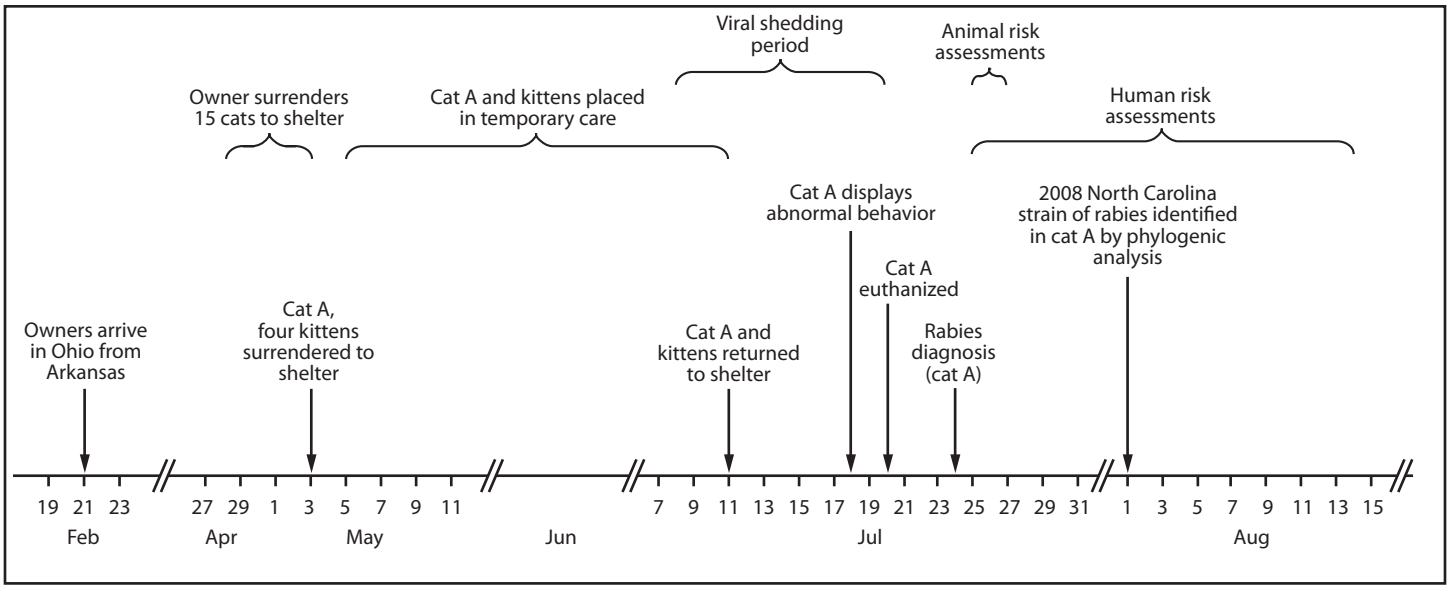
Abbreviations: AL = Alabama; GA = Georgia; IN = Indiana; KY = Kentucky; MD = Maryland; MI = Michigan; NC = North Carolina; NY = New York; OH = Ohio; PA = Pennsylvania; TN = Tennessee; VA = Virginia; WV = West Virginia.

Case Report

In early February 2017, two adults traveled from North Carolina to Arkansas with two dogs and 13 cats. The stray cats (including cat A) were taken in as personal pets while the couple lived in North Carolina. They departed Arkansas on February 17, and arrived in Summit County, Ohio, for temporary residence with family members on February 21. The cats were co-housed in a garage until May 3. During that time, the cats were not permitted out of the garage, and no known exposures to other mammals occurred. While housed in the garage, cat A and another cat gave birth to an unknown number of kittens, several of which died of unknown causes.

During April 28–May 3, because of inability to care for the animals, the owner surrendered 15 cats to the Humane Society of Summit County (a local nonprofit organization), including cat A and her four kittens. Upon intake, the animals received a physical exam, routine vaccines, an antihelminthic, flea and tick control, and feline immunodeficiency virus and feline leukemia virus testing. Because the rabies vaccine is administered at time of spay/neuter at this facility, cat A did not receive a rabies vaccine. Cat A and her four kittens were placed in a temporary home during May 5–July 11 to allow the kittens to be weaned. Cat A was examined by a veterinarian on May 24, June 1, and June 9 for an upper respiratory tract infection. On July 8, cat A was reported to be "making abnormal vocalizations," which were attributed to estrus. Upon return to the shelter on July 11, no abnormalities were noted in either cat A

FIGURE 2. Public health investigation of a rabid cat (Cat A) translocated from North Carolina to Ohio — February–August 2017*



* During human risk assessments, all potentially exposed persons were contacted by telephone. Three attempts were made by telephone and if no contact was made, a letter was sent to the residence. Three persons were lost to follow-up; 92% of the risk assessments were completed within 4 days of diagnosis of rabies in the cat. The remaining two were completed 7 days and 21 days after the diagnosis.

or the kittens. On July 18, almost 5 months after arriving in Ohio, cat A developed abnormal behavior including excessive panting, agitation, open-mouthed breathing, and hind-limb ataxia. Despite treatment, symptoms progressed rapidly and cat A was euthanized on July 20. Although no one was bitten and there was no evidence that cat A had been exposed to a rabies vector species, the cat's head was submitted for rabies testing. The ODH laboratory reported a positive rabies result on July 24, the same day the sample was received. After consultation with CDC, a brain tissue sample was submitted for further characterization to determine the likely origin of the virus. Antigenic typing confirmed that the virus was raccoon RVV, and molecular characterization of the rabies virus N-gene determined that it was most similar to a clade found in central North Carolina, suggesting that cat A had been infected before being translocated to Ohio.

Public Health Investigation

ODH developed a risk assessment tool to identify persons and animals potentially exposed to cat A during the viral shedding period (July 8–20), defined as 10 days before development of clinical signs (July 18) until the time of the cat's death (July 20) (*1*). Among 29 identified persons with potential contact, 26 (90%) were located and completed the risk assessment. Postexposure prophylaxis was recommended to three humane society staff members and one adult caring for cat A in the temporary home. Conditions of exposure included known and presumed exposure to saliva such as administration of oral medications, inability to determine if a bite or scratch had occurred, and possible breach of infection control during decapitation.

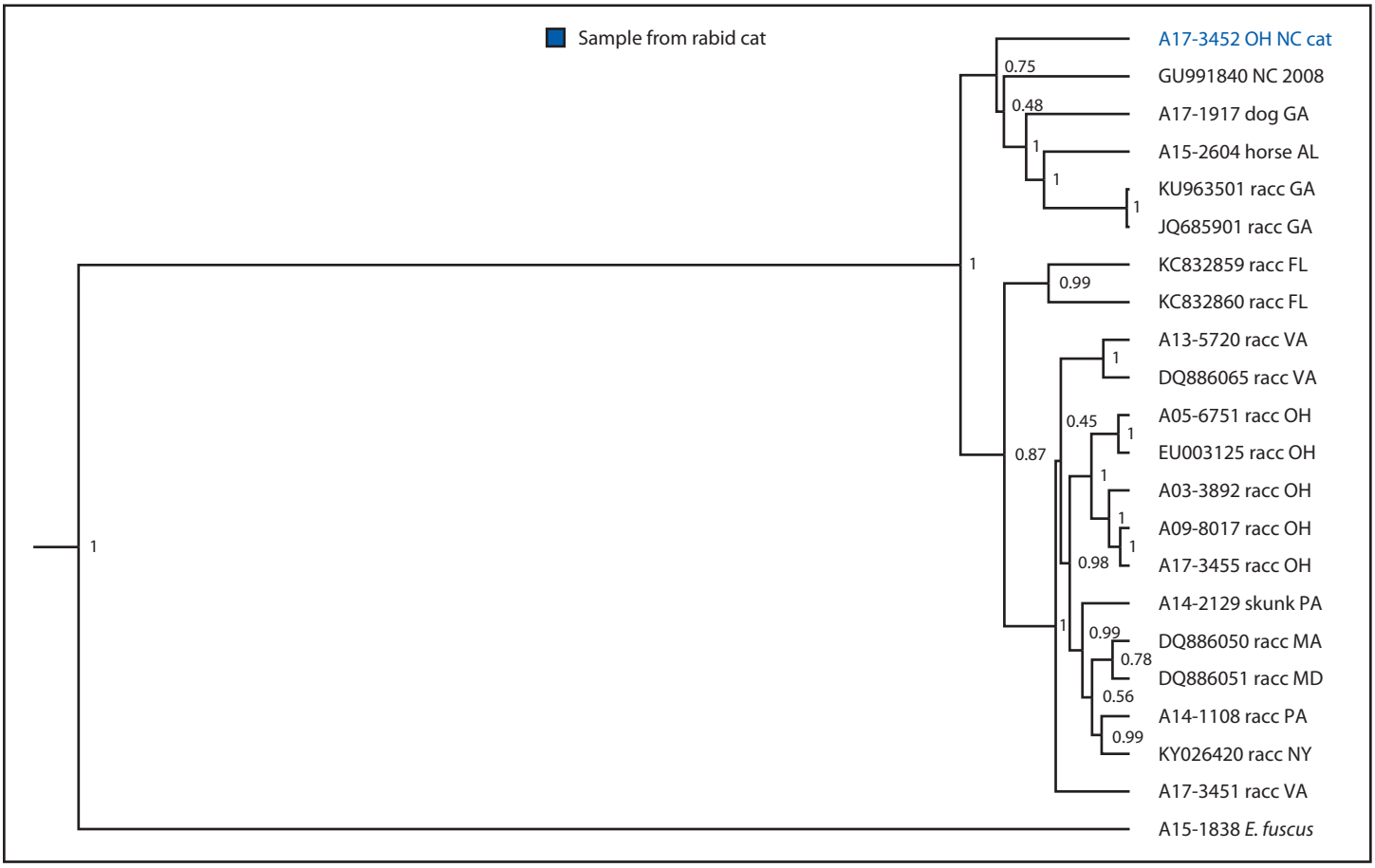
The 14 remaining cats had either been adopted or placed in temporary care among 12 households. Cat A's four kittens were presumed to be exposed because of contact with her saliva during grooming and nursing behaviors. The other 10 cats that had been co-housed in the garage with cat A were not considered exposed during the viral shedding period; however, exposure to a common source animal in North Carolina could not be ruled out, and all 10 cats were considered potentially exposed. Six of the 14 cats had not received rabies vaccine before adoption because they had been too young; owners were advised to vaccinate these animals at the appropriate age, according to veterinarian recommendations (*2*,*3*). In concordance with the 2011 Compendium of Animal Rabies Prevention and Control (*2*), all cats were placed under strict quarantine for 6 months to preclude the risk for further transmission.* Quarantine was managed either at the shelter or in their adoptive homes. As of May 7, 2018, no additional cases of rabies related to these animals were identified.

Discussion

The United States is host to five non-bat terrestrial rabies reservoir species, each with its own genetically distinct RVV and

* At the time of this event, the Ohio Administrative Code followed the 2011 Compendium of Animal Rabies Prevention and Control for quarantine recommendations.

FIGURE 3. Phylogenetic analysis* of rabies virus variant from a rabid cat — Ohio, 2017



* Branch length is related to the number of nucleotide substitutions. The more substitutions, the longer the branch. More evolved variants are further from their ancestor.

geographic distribution. The raccoon RVV is found in 19 states in the eastern United States, but in only several counties in northeast Ohio that border Pennsylvania; Summit County is not considered enzootic for rabies RVV. The U.S. Department of Agriculture (USDA), Animal and Plant Health Inspection Service Wildlife Services commits over $20 million annually to oral rabies vaccine (ORV) programs in the eastern United States. In Ohio, the ORV zone covers several counties in the northeastern part of the state. Vaccine-laden baits are dropped in these areas to create a barrier of immunized animals that aids in reducing the number of animal rabies cases and prevents the westward spread of raccoon RVV. Enhanced rabies surveillance is conducted along the ORV zone, which includes Summit County, to ensure that ORV breaches are quickly recognized and confirmed; risk assessments are conducted to guide the necessity and scope for emergency management action. When breaches occur, emergency vaccination operations are typically conducted by USDA in collaboration with federal, state, and local partners.

Phylogenetic and epidemiologic evidence was used to rule out a breach by natural expansion; in this case, human intervention appears to have been responsible for the translocation of raccoon RVV from North Carolina (an enzootic state) into Summit County, Ohio, a county free from the viral variant. Molecular characterization of the virus variant was essential in determining the source of the virus, which guided public health intervention efforts on local, state, and federal levels. Had the evidence suggested a natural expansion event, an emergency ORV baiting operation would likely have been initiated. However, given that the translocation event was likely human-mediated, and the event was quickly contained, additional ORV baiting was deemed unnecessary.

Human-mediated translocation (movement of an animal from its home range to a new area) of rabid animals has occurred in the past. These events can have profound public health implications, as seen by the translocation of a rabid raccoon from Florida to Virginia in the 1970s and the translocation of a rabid raccoon from Vermont to Hamilton, Canada,

in 2015 (*3*,*4*). Both events triggered large-scale wildlife rabies epizootics and control measures that continue to this day. CDC estimates the cost of public health expenditures on rabies disease diagnostics, prevention, and control in the United States at $245 to $510 million annually (*5*). Expansion of rabies enzootic zones, either through translocation or natural expansion, could substantially increase both the cost and the burden on public health resources.

The rabies virus isolated from this cat was determined to be associated with a viral clade found only in central North Carolina, the same location where cat A was procured as a stray. No other cats in the captured cohort were reported to have developed signs of rabies from the time the owner left North Carolina (February) up to the time of surrender in May. Therefore, cat A likely was infected with the raccoon RVV as a stray followed by a minimum 5-month incubation period, which is longer than the typical incubation period of 3 weeks to 3 months (*2*). During this time, cat A passed through eight states, three of which (Arkansas, Indiana, and Mississippi) are terrestrial-rabies–free; USDA enhanced rabies surveillance does not occur in these states. Had the cat died while passing through any of these three states, it is unlikely that, in the absence of a clear human exposure, routine rabies public health surveillance would have detected the case[†] (*3*).

None of the 13 translocated cats had a known history of rabies vaccination. Because of the public health and agriculture risks associated with translocation of unvaccinated rabies-susceptible animals, numerous federal and state animal movement laws have been enacted. These include requirements for rabies vaccination before interstate travel and procurement of a health certificate from a veterinarian (*2*,*6*). These requirements are difficult to enforce, highlighting the importance of responsible pet ownership. It is important for stray animals to receive appropriate veterinary care, with special regard to rabies vaccination, when adopted into a home. Rabies is rare in vaccinated animals (*2*); had cat A been vaccinated upon acquisition and before interstate travel, this event could have been prevented. Phylogenetic analysis and molecular characterization of the virus variant played a major role in making an evidence-based decision that prevented a costly USDA emergency response.

[†] Ohio Administrative Code (OAC) 901:1–17–01: Importation and Health of Animals, General requirements; OAC 901:1–17–05: Dogs and Cats (http://codes.ohio.gov/oac/901%3A1-17); OAC 3701–3-29: Biting animal to be confined (http://codes.ohio.gov/oac/3701-3).

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Summary

What is already known about this topic?

Translocation of wildlife is responsible for spreading rabies in the United States, and has led to the introduction of new rabies variants and establishment of terrestrial rabies in areas where it was previously undetected.

What is added by this report?

While incubating the rabies virus, a cat potentially traveled through eight states, three of which are terrestrial rabies free. If the cat had become infectious during travel, a rabies epizootic could have occurred.

What are the implications for public health practice?

Local rabies vaccination laws vary greatly and animals frequently cross state lines without proper veterinary care and medical documentation. Animal rabies testing, prompt investigation, interagency collaboration, and the utilization of molecular epidemiology are important in determining proper public health interventions.

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Update: Influenza Activity — United States and Worldwide, May 20–October 13, 2018

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During May 20–October 13, 2018,* low levels of influenza activity were reported in the United States, with a mix of influenza A and B viruses circulating. Seasonal influenza activity in the Southern Hemisphere was low overall, with influenza A(H1N1)pdm09 predominating in many regions. Antigenic testing of available influenza A and B viruses indicated that no significant antigenic drift in circulating viruses had emerged. In late September, the components for the 2019 Southern Hemisphere influenza vaccine were selected and included an incremental update to the A(H3N2) vaccine virus used in egg-based vaccine manufacturing; no change was recommended for the A(H3N2) component of cell-manufactured or recombinant influenza vaccines. Annual influenza vaccination is the best method for preventing influenza illness and its complications, and all persons aged ≥6 months who do not have contraindications should receive influenza vaccine, preferably before the onset of influenza circulation in their community, which often begins in October and peaks during December–February. Health care providers should offer vaccination by the end of October and should continue to recommend and administer influenza vaccine to previously unvaccinated patients throughout the 2018–19 influenza season (*1*). In addition, during May 20–October 13, a small number of nonhuman influenza "variant" virus infections† were reported in the United States; most were associated with exposure to swine. Although limited human-to-human transmission might have occurred in one instance, no ongoing community transmission was identified. Vulnerable populations, especially young children and other persons at high risk for serious influenza complications, should avoid swine barns at agricultural fairs, or close contact with swine.§

United States

The U.S. influenza surveillance system¶ is a collaboration between CDC and federal, state, local, and territorial partners and uses eight data sources to collect influenza information, six of which operate year-round. During May 20–October 13, U.S. clinical laboratories tested 197,295 respiratory specimens for influenza, and 2,763 (1.4%) were positive (Figure 1), including 1,801 (65.2%) that were positive for influenza A viruses and 962 (34.8%) that were positive for influenza B viruses. Public health laboratories in the United States tested 5,863 respiratory specimens for influenza viruses; among these, 587 were positive for seasonal influenza viruses (Figure 2), including 442 (75.34%) positive for influenza A viruses and 145 (24.7%) for influenza B viruses. Influenza B viruses were more commonly detected than influenza A viruses from May until mid-June, whereas influenza A predominated from late June onward. A total of 400 (90.5%) of the seasonal influenza A viral specimens were subtyped by public health laboratories; among these, 233 (58.3%) were influenza A(H1N1)pdm09, and 167 (41.8%) were influenza A(H3N2). Of the 118 (81.4%) influenza B viruses for which lineage was determined, 94 (79.7%) belonged to the B/Yamagata lineage and 24 (20.3%) to the B/Victoria lineage. CDC received reports of a small number of influenza outbreaks during the summer, including domestic origin outbreaks along with influenza virus infection identified in returning international travelers.

During May 20–October 13, data obtained from the U.S. Outpatient Influenza-Like Illness Surveillance Network (ILINet) indicated that the weekly percentage of outpatient visits to health care providers for influenza-like illness (ILI)**

* Data as of October 19, 2018.

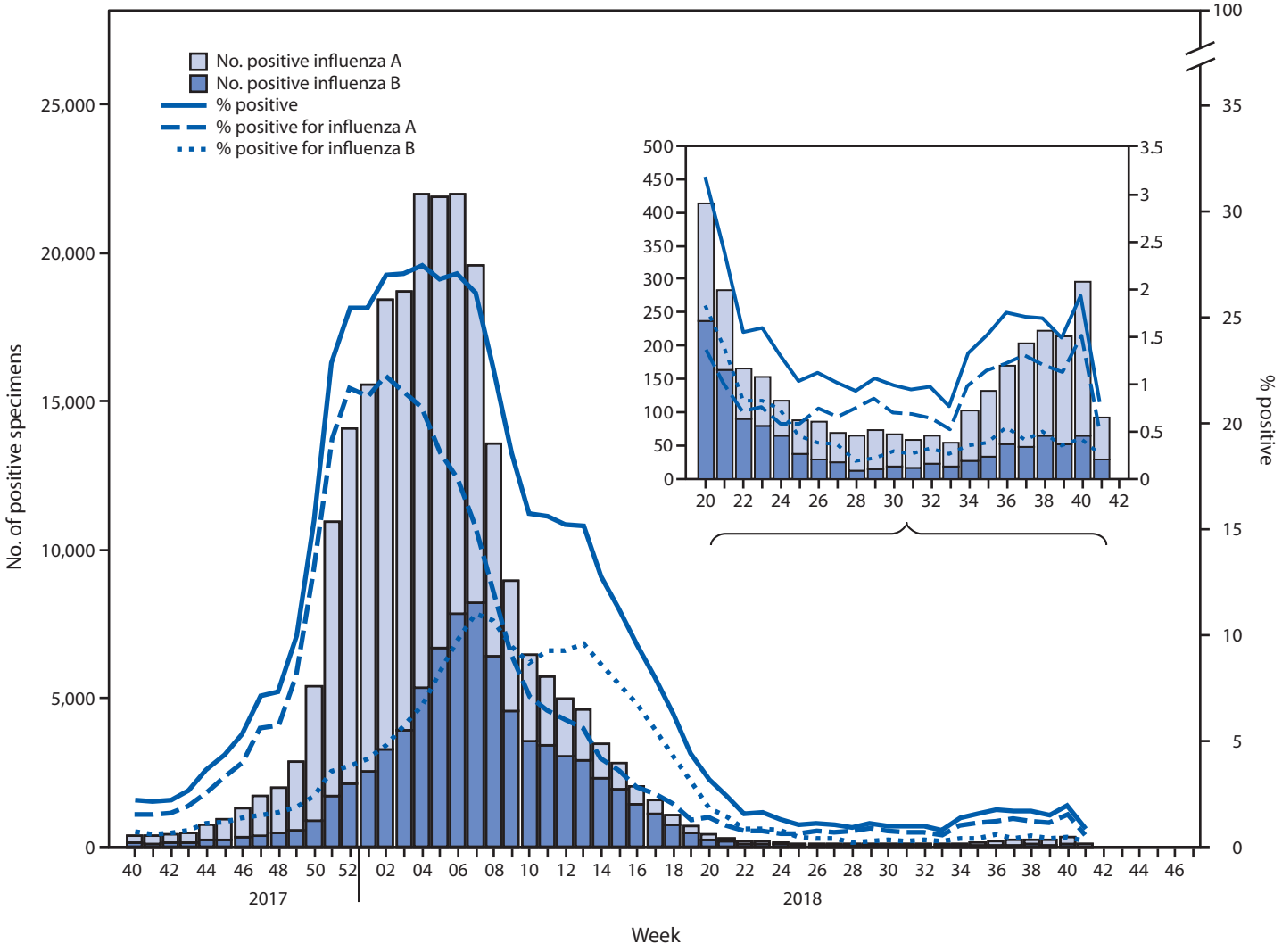
† Influenza viruses that circulate in swine are called swine influenza viruses when isolated from swine, but are called variant influenza viruses when isolated from humans. Seasonal influenza viruses that circulate worldwide in the human population have important antigenic and genetic differences from influenza viruses circulating in swine.

§ https://www.cdc.gov/flu/swineflu/variant/preventspreadfactsheet.htm.

¶ The U.S. influenza surveillance system collects five categories of information from eight data sources: 1) viral surveillance (U.S. World Health Organization collaborating laboratories, the National Respiratory and Enteric Virus Surveillance System, and novel influenza A virus case reporting); 2) outpatient illness surveillance (U.S. Outpatient Influenza-Like Illness Surveillance Network); 3) mortality (the National Center for Health Statistics Mortality Surveillance System and influenza-associated pediatric mortality reports); 4) hospitalizations (FluSurv-NET, which includes the Emerging Infections Program and surveillance in three additional states); and 5) summary of the geographic spread of influenza (state and territorial epidemiologist reports). https://www.cdc.gov/flu/weekly/overview.htm.

** Defined as a fever (temperature ≥100°F [≥37.8°C]), oral or equivalent, and cough and/or sore throat, without a known cause other than influenza.

FIGURE 1. Number* and percentage of respiratory specimens testing positive for influenza reported by clinical laboratories, by influenza virus type and surveillance week — United States, October 1, 2017–October 13, 2018†



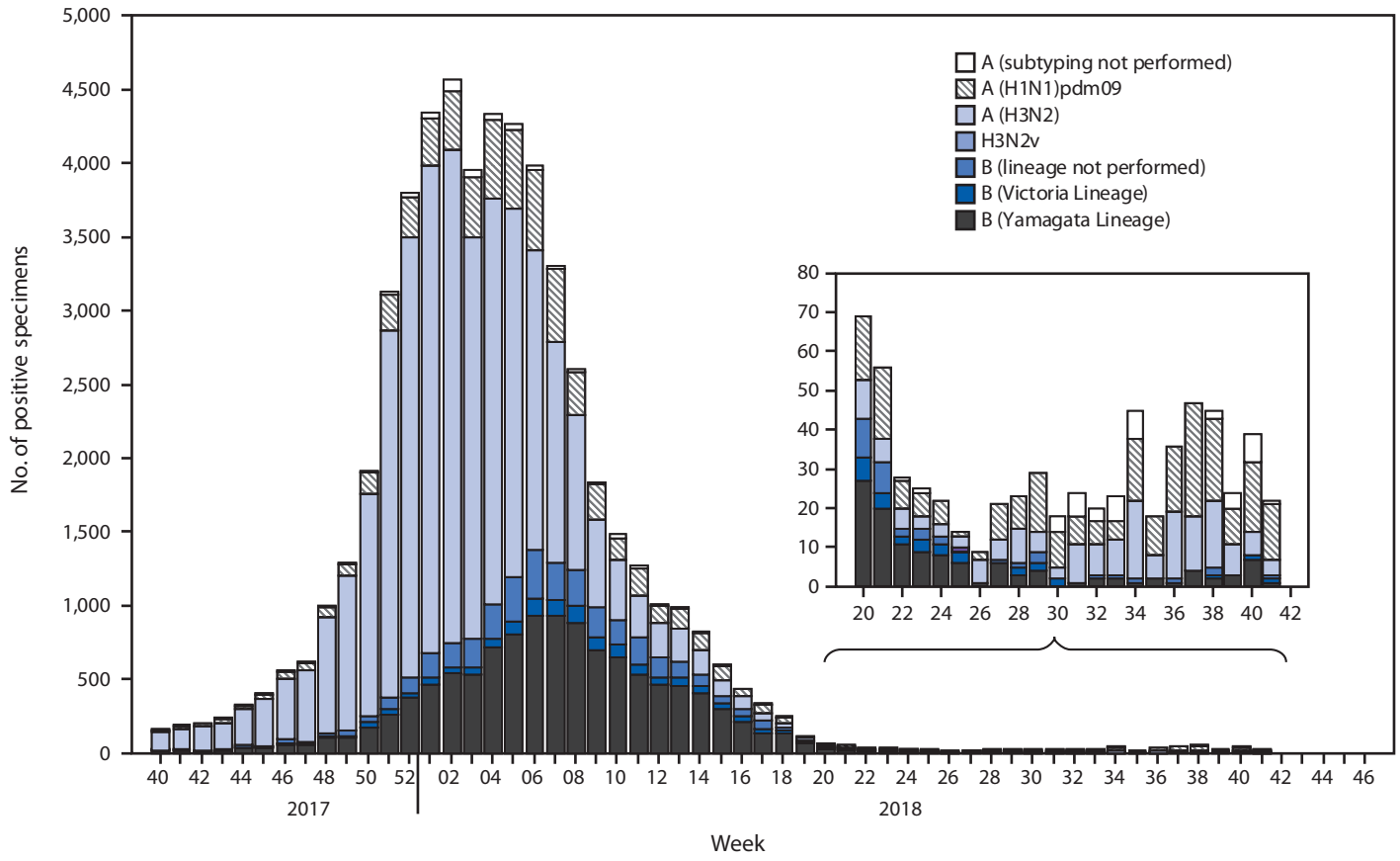
* A total of 238,440 (16.4%) of 1,452,986 specimens tested were positive during October 1, 2017–October 13, 2018.
† As of October 19, 2018.

remained below the national baseline†† of 2.2%, ranging from 0.6% to 1.4%. All regions remained below their region-specific ILI baselines. During the first 2 weeks of October, ILI activity levels§§ for all reporting jurisdictions were minimal and, although a small number of jurisdictions have reported

†† The national and regional baselines are the mean percentage of visits for influenza-like illness (ILI) during noninfluenza weeks for the previous three seasons plus two standard deviations. Noninfluenza weeks are defined as periods of ≥2 consecutive weeks in which each week accounted for <2% of the season's total number of specimens that tested positive for influenza in public health laboratories. National and regional percentages of patient visits for ILI are weighted based on state population. Use of the national baseline for regional data are not appropriate.

§§ Activity levels are based on the percentage of outpatient visits in a jurisdiction attributed to ILI and are compared with the average percentage of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, corresponding to ILI activity from outpatient clinics at or below the average, to high, corresponding to ILI activity from outpatient clinics much higher than the average. Because the clinical definition of ILI is nonspecific, not all ILI is caused by influenza; however, when combined with laboratory data, the information on ILI activity provides a clearer picture of influenza activity in the United States.

FIGURE 2. Number* of respiratory specimens testing positive for influenza reported by public health laboratories, by influenza virus type, subtype/lineage, and surveillance week— United States, October 1, 2017–October 13, 2018†



* N = 54,920.
† As of October 19, 2018.

the geographic spread of influenza activity¶¶ as local, approximately 60% of all reporting jurisdictions reported sporadic activity. Data from CDC's National Center for Health Statistics Mortality Surveillance System indicated that the percentage of deaths attributed to pneumonia and influenza remained below the epidemic threshold*** during this period. Of the 183 influenza-associated pediatric deaths reported to CDC that occurred during the 2017–18 influenza season, five occurred during May 20–September 29. The first influenza-associated pediatric death occurring during the 2018–19 season was reported to CDC in mid-October.

Worldwide

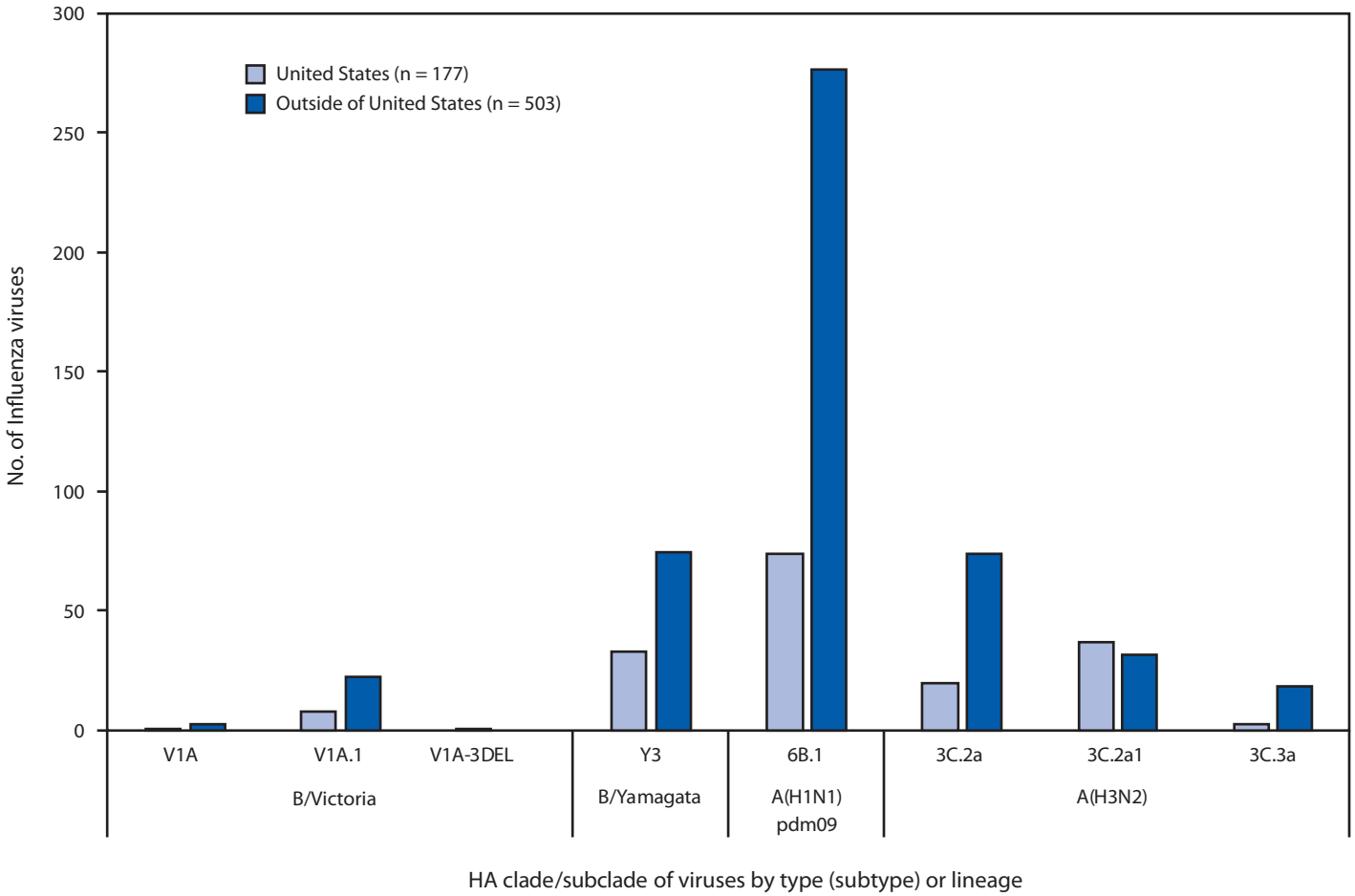
CDC serves as the WHO Collaborating Center for Surveillance, Epidemiology, and Control of Influenza, one of six WHO Collaborating Centers for Influenza in the WHO Global Influenza Surveillance and Response System (GISRS).††† CDC, along with other international public health partners, provides surveillance and virus characterization data to WHO. The timing of influenza activity and the predominant circulating virus around the world can vary by

¶¶ Levels of activity are 1) no activity; 2) sporadic: isolated laboratory-confirmed influenza cases or a laboratory-confirmed outbreak in one institution, with no increase in activity; 3) local: increased ILI, or two or more institutional outbreaks (ILI or laboratory-confirmed influenza) in one region of the state, with recent laboratory evidence of influenza in that region; virus activity no greater than sporadic in other regions; 4) regional: increased ILI activity or institutional outbreaks (ILI or laboratory-confirmed influenza) in two or more outbreaks, but less than half of the regions in the state with recent laboratory evidence of influenza in those regions; and 5) widespread: increased ILI activity or institutional outbreaks (ILI or laboratory-confirmed influenza) in at least half of the regions in the state, with recent laboratory evidence of influenza in the state.

*** The seasonal baseline proportion of pneumonia and influenza (P&I) deaths is projected using a robust regression procedure, in which a periodic regression model is applied to the observed percentage of deaths from P&I that were reported by the National Center for Health Statistics Mortality Surveillance System during the preceding 5 years. The epidemic threshold is set at 1.645 standard deviations above the seasonal baseline.

††† http://www.who.int/influenza/gisrs_laboratory/collaborating_centres/en.

FIGURE 3. Genetic characterization of influenza viruses collected in and outside of the United States during May 20–October 13, 2018



region.[§§§] Overall, reported Southern Hemisphere influenza activity has been relatively low and fairly mild, with influenza A(H1N1)pdm09 viruses predominating in most regions.[¶¶¶] Influenza data from GISRS during May 20–September 30 in temperate climate South American countries suggest that activity began to increase in mid-May and peaked in August. Influenza A(H3N2) predominated in Chile and Paraguay. In temperate Southern Africa, influenza activity increased in April and peaked in June, with A(H1N1)pdm09 predominating. A second wave of elevated activity in Southern Africa of mostly influenza B began in late August and peaked in September. Influenza activity in Australia and New Zealand was below seasonal threshold with A(H1N1)pdm09 predominating. Influenza activity in regions with more tropical climates (Central America and the Caribbean, tropical South America, Southern Asia, and Southeast Asia) was more variable, but A(H1N1)pdm09 virus predominated in most countries. Influenza A(H1N1)pdm09, A(H3N2), and B viruses cocirculated in Eastern Africa, and influenza A(H1N1)pdm09 and A(H3N2) viruses cocirculated in Southern Asia.

[§§§] In temperate climates, the onset and peak of influenza activity might vary substantially from one influenza season to the next, but generally begins to increase in the late fall. In the Northern Hemisphere's temperate regions, annual epidemics of influenza typically occur during October–February, but the peak of influenza activity can occur as late as April or May. In temperate regions of the Southern Hemisphere, influenza activity typically peaks during May through August. Although temperate regions of the world experience a seasonal peak in influenza activity, influenza viruses can be isolated year-round. The timing of seasonal peaks in influenza activity in tropical and subtropical countries varies by region. Multiple peaks of activity during the same year have been seen in some areas and influenza infection can occur year-round.

[¶¶¶] http://www.who.int/influenza/surveillance_monitoring/updates/en/.

Genetic and Antigenic Characterization of Influenza Viruses

The components for the Northern Hemisphere 2018–19 influenza vaccines were selected in February 2018, during one of the twice-yearly WHO-sponsored vaccine consultation meetings. The recommended Northern Hemisphere 2018–19 trivalent influenza vaccine composition included an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Singapore/INFIMH-16–0019/2016 (H3N2)-like virus,

and a B/Colorado/06/2017-like virus (B/Victoria lineage), with an additional influenza B virus (B/Phuket/3073/2013-like [B/Yamagata lineage]) recommended for quadrivalent vaccines.**** Data obtained from antigenic characterization are important in the assessment of the similarity between reference vaccine viruses and circulating viruses. In vitro antigenic characterization data acquired through hemagglutination inhibition (HI) assays or virus neutralization-based focus reduction assays (FRAs) evaluate whether genetic changes in circulating viruses affect antigenicity; substantial differences could affect vaccine effectiveness. Nearly all influenza viruses received by CDC are genomically characterized using next generation sequencing, and the genomic data are analyzed and submitted to public databases (GenBank: https://www.ncbi.nlm.nih.gov/genbank or EpiFlu: https://www.gisaid.org/). CDC antigenically or genetically characterized 680 influenza viruses collected and submitted by U.S. laboratories and laboratories outside the United States during May 20–October 13, including 351 influenza A(H1N1)pdm09 viruses, 185 influenza A(H3N2) viruses, and 144 influenza B viruses.

Phylogenetic analysis of the A(H1N1)pdm09 hemagglutinin (HA) genes of viruses collected globally since May 20, 2018, identified viruses belonging to HA genetic subgroup 6B.1 (Figure 3). All of the A(H1N1)pdm09 viruses tested (57 in and 87 outside the United States) were antigenically similar (analyzed using HI tests with ferret antisera) to egg and cell-propagated A/Michigan/45/2015 viruses, which are in genetic group 6B.1 and are reference viruses representing the influenza A(H1N1) component of the Northern Hemisphere 2018–19 influenza vaccine.

Among 185 influenza A(H3N2) viruses collected and sequenced since May 20, 2018, phylogenetic analyses indicated cocirculation of multiple clades and subgroups of HA genes. The HA genes of the viruses belonged to genetic groups 3C.2a, 3C.2a1, and 3C.3a, with 3C.2a predominating (Figure 3). The majority of genetic group 3C.2a viruses (89% [86/94]) belonged to subclade 3C.2a2. A subset of 111 influenza A(H3N2) viruses was antigenically characterized by HI or FRA (43 in and 68 outside the United States); 102 (91.9%) were well inhibited by ferret antisera raised against cell-propagated A/Singapore/INFIMH-16–0019/2016 (3C.2a1), the reference virus representing the A(H3N2) component of Northern Hemisphere 2018–19 influenza vaccines. However, combined data generated by the WHO GISRS Collaborating Centers demonstrated that ferret antisera raised against egg-propagated A/Singapore/INFIMH-16–0019/2016-like viruses inhibited a smaller proportion of recently circulating viruses. In contrast, ferret antisera raised against egg-propagated A/Switzerland/8060/2017 inhibited the majority of viruses belonging to the globally-predominant subclade 3C.2a2, which was a factor leading to an update of the recommended influenza A(H3N2) component for egg-based vaccines for the 2019 Southern Hemisphere influenza vaccine.††††

Thirty-six influenza B/Victoria-lineage viruses were phylogenetically analyzed. All HA genes belonged to genetic group V1A and 31 (86.1%), belonged to subgroup V1A.1, represented by B/Colorado/06/2017, the reference virus representing the B/Victoria lineage component of Northern Hemisphere 2018–19 influenza vaccines. The V1A.1 subgroup is characterized by a two amino acid deletion in the HA at residues 162–163. One virus belonging to the genetic group V1A-3DEL was identified. This virus had a three amino acid deletion (amino acid residues 162–164) in the HA; similar viruses were identified sporadically in several countries in recent months. Eighteen of 19 antigenically characterized B/Victoria lineage viruses (10 in and nine outside the United States) were well inhibited by ferret antisera raised against cell-propagated B/Colorado/06/2017-like viruses.

Phylogenetic analysis of the influenza B/Yamagata lineage viruses sequenced showed that all HA genes belonged to genetic group Y3 (Figure 3). Among 65 influenza B/Yamagata lineage viruses antigenically characterized (32 in and 33 outside the United States), all were well inhibited by ferret antisera raised against cell-propagated B/Phuket/3073/2013-like viruses, the reference virus representing the influenza B/Yamagata lineage component of the Northern Hemisphere 2018–19 quadrivalent vaccines.

Antiviral Resistance of Influenza Viruses

The WHO Collaborating Center for Surveillance, Epidemiology, and Control of Influenza at CDC tested 347 influenza virus specimens collected during May 20–October 13 from the United States and worldwide for resistance to oseltamivir, peramivir, and zanamivir, the influenza virus neuraminidase inhibitor antiviral medications currently approved for use against seasonal influenza. Among 134 influenza A(H1N1)pdm09 viruses (63 in and 71 outside the United States), 132 influenza A(H3N2) viruses (57 in and 75 outside the United States), and 81 influenza B viruses (44 in and 37 outside the United States) tested, all were susceptible to all three medications. High levels of resistance to the adamantanes (amantadine and rimantadine) persisted among influenza A(H1N1)pdm09 and influenza A(H3N2) viruses, which is consistent with the

****http://www.who.int/influenza/vaccines/virus/recommendations/2018_19_north/en/.

†††† http://www.who.int/influenza/vaccines/virus/recommendations/201809_recommendation_report.pdf?ua.

current recommendation to avoid use of these medications against influenza at this time.[§§§§]

Composition of the 2019 Southern Hemisphere Influenza Vaccine

The WHO recommendations for influenza vaccine composition for the Southern Hemisphere 2019 season were made at the WHO Consultation and Information Meeting on the Composition of Influenza Virus Vaccines held September 24–27, 2018, in Atlanta, Georgia. The recommended components for the 2019 Southern Hemisphere egg-based influenza trivalent vaccines are an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Switzerland/8060/2017 (H3N2)-like virus, and a B/Colorado/06/2017-like virus (B/Victoria lineage). For egg-based quadrivalent vaccines, an additional component, B/Phuket/3073/2013-like virus (B/Yamagata lineage), is recommended. It was recommended that the A(H3N2) component of non–egg-based vaccines be an A/Singapore/INFIMH-16–0019/2016-like virus. Compared with the composition of the 2018 Southern Hemisphere influenza vaccine formulation, these recommendations reflect an update to the influenza A(H3N2) component for egg-based vaccines, a change in the influenza B lineage included in the trivalent vaccine and a change in the influenza B/Victoria component. Compared with the composition of the Northern Hemisphere 2018–19 influenza vaccines, these recommendations reflect only one change, an update to the A(H3N2) component used in egg-based manufacturing.

Novel Influenza A Virus Infections

Fourteen human infections with novel influenza A viruses were reported in the United States during May 20–October 13. Influenza viruses that normally circulate in swine and not humans are called "variant" viruses when detected in humans and designated with the letter v after the subtype. One infection was associated with an influenza A(H3N2)v virus, and 13 were associated with influenza A(H1N2)v viruses. All but one infection occurred among persons aged <18 years. The A(H3N2)v virus infection was reported from Indiana in a patient who reported swine contact at an agricultural fair in the week before symptom onset. All A(H1N2)v virus infections were reported in August from three states: California (six cases), Ohio (four), and Michigan (three). Eleven of the 13 patients reported contact with swine at agricultural fairs, one reported attendance at an agricultural fair but no contact with swine, and one reported neither contact with swine nor attendance at an agricultural fair. Limited human-to-human transmission might have taken place with this last A(H1N2)v infection; however, no ongoing or sustained human-to-human transmission associated with any of these infections was identified. None of the novel influenza A virus infections resulted in hospitalization, and all patients recovered.

The genome of the one A(H3N2)v virus(A/Indiana/27/2018) was closely related to A(H3N2)v viruses detected during 2017 and viruses known to circulate in the U.S. swine population. Antigenic testing showed reduced inhibition by ferret antisera raised to the nearest A(H3N2)v candidate vaccine virus (CVV), but postvaccination antisera from adults vaccinated with the 2017–18 influenza vaccine reacted with the virus at titers that were within fourfold of those against the homologous reference virus, A/Michigan/15/2014, representing the A(H3N2) component of the 2017–18 seasonal influenza vaccines. Postvaccination sera collected from children, however, had lower titers to this virus than to the A/Michigan/15/2014 homologous virus titer. These studies indicate that vaccination with the 2017–18 seasonal influenza vaccine might offer less protection against this A(H3N2)v virus for children than adults.

All of the A(H1N2)v viruses detected had HA gene segments from the delta 2 sublineage of the swine influenza virus H1 HA lineage. The HA and neuraminidase gene segments of these viruses were closely related to 2017 and 2018 A(H1N2) influenza viruses circulating in the U.S. swine population, including swine identified at the agricultural fairs attended by infected persons and viruses sporadically detected in previous A(H1N2)v zoonotic infections. Antigenic testing demonstrated that all of the 2018 A(H1N2)v viruses were well inhibited by ferret antisera raised to the nearest CVV. HI reactivity of pooled, child and adult postvaccination antisera from persons vaccinated with the 2017–18 vaccine was below the limit of detection for all viruses tested. These studies indicate that vaccine viruses specially developed to prevent A(H1N2)v virus infections would be protective; however, vaccination with the seasonal vaccine would not offer any protection.

Discussion

In the United States, ILI activity remained below baseline levels during May 20–October 13, 2018; low levels of laboratory-confirmed influenza were reported as a result of a mix of influenza A and B. In the Southern Hemisphere, low levels of influenza activity were observed with a predominance of A(H1N1)pdm09 viruses. Analysis of available viruses suggests that minimal drift of viruses has occurred.

Vaccination before the onset of influenza activity is the primary strategy to prevent influenza-associated illness and its potentially serious complications. A recent report indicated the high prevalence of influenza illnesses resulted in approximately 79,000 deaths and 960,000 hospitalizations during the

[§§§§] https://www.cdc.gov/flu/professionals/antivirals/links.htm.

2017–18 influenza season (https://www.cdc.gov/flu/about/disease/burden.htm). Influenza vaccination prevents millions of medical visits, tens of thousands of hospitalizations, and thousands of deaths each year, even with vaccine effectiveness estimates in the range of 40%–60%. Health care providers should urge their patients to get vaccinated by the end of October, if they have not already been vaccinated. Vaccination efforts should continue throughout the influenza season.

In late September, WHO issued its recommendations for the 2019 Southern Hemisphere influenza vaccine. Surveillance has shown that there has been no significant evidence of antigenic drift among circulating A(H3N2) viruses since the selection of viruses for the 2018–19 Northern Hemisphere vaccines was made in February. However, the influenza A(H3N2) component for egg-based vaccines was updated to address genetic and antigenic changes that occur when A(H3N2) vaccine viruses are propagated in eggs. The A(H3N2) component was updated because sera against egg-propagated A/Switzerland/8060/2017 (H3N2) virus showed better reactivity with an increasing number of circulating A(H3N2) viruses than sera generated against egg-propagated A/Singapore/INFIMH-16-0019/2016. No changes were recommended for the A(H3N2) component of cell-manufactured or recombinant vaccines. It is difficult to predict which influenza virus will predominate or what the season will be like, but there will likely be cocirculation of influenza A(H1N1), A(H3N2), and B influenza viruses.

Annual influenza vaccination is the best method for preventing influenza infection and its potentially serious complications. In the United States, annual influenza vaccine is recommended for all persons aged ≥6 months who do not have a contraindication (*1*). Influenza vaccination has been shown to reduce the risk for influenza illness, and a growing body of evidence suggests that vaccination also reduces the risk for serious influenza outcomes that can result in hospitalization and even death. A CDC study in 2017 showed influenza vaccination reduced the risk for influenza-associated death by 51% among children with underlying high-risk medical conditions and by 65% among healthy children (*2*). Most recently, an August 2018 study showed that influenza vaccination lessened the risk for severe influenza among adults, including reducing the risk for hospitalization and admission to the intensive care unit, and also lessened severity of illness (https://www.cdc.gov/flu/spotlights/vaccine-reduces-risk-severe-illness.htm). These benefits are especially important for persons at high risk for serious influenza complications, including persons aged ≥65 years, children aged <5 years, pregnant women, and persons with certain underlying long-term medical conditions, including heart and lung disease, or diabetes.

Ideally, influenza vaccination should be administered before the start of community influenza activity. However, health care providers should continue to offer annual influenza vaccine to unvaccinated persons as long as influenza viruses continue to circulate. For the 2018–19 influenza season, multiple influenza vaccines are approved and recommended for use; there is no preferential recommendation for one influenza vaccine product over another for persons for whom more than one is suitable (*1*). Children aged 6 months–8 years require 2 doses of influenza vaccine administered ≥4 weeks apart if they have not received at least 2 doses of influenza vaccine before July 1, 2018 (*3*). Those who have previously received at least 2 doses before this date only require a single dose for 2018–19, even if the 2 previous doses were not received during the same or consecutive seasons (*1*). For the 2018–19 season, interim supply projections by manufacturers for the U.S. market range from 163 to 168 million doses of influenza vaccine.

Influenza antiviral medications can serve as a valuable adjunct to annual influenza vaccination. Early treatment with influenza antiviral medication is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at high risk for influenza-related complications.¶¶¶¶ Early treatment has been shown to decrease time to symptom improvement (*4*–*7*) and to reduce secondary complications associated with influenza (*8*,*9*). Providers should not delay treatment until test results become available because treatment is most effective when given early in the illness, especially within 48 hours of symptom onset (*10*). Providers should also not rely on less sensitive assays such as rapid antigen detection influenza diagnostic tests to inform treatment decisions (*10*).

During May 20–October 13, fewer human infections with variant viruses were reported compared with most previous seasons.***** Most of these variant viruses were influenza A(H1N2)v viruses, and A(H1N2) viruses have predominated in swine in some regions of the United States.†††††† All but two of the patients with variant virus infections reported

¶¶¶¶ Persons at high risk include 1) children aged <2 years; 2) adults aged ≥65 years; 3) persons with chronic pulmonary conditions (including asthma), cardiovascular disease (except hypertension alone), renal, hepatic, hematologic (including sickle cell) disease, metabolic disorders (including diabetes mellitus), or neurologic and neurodevelopmental conditions (including disorders of the brain, spinal cord, peripheral nerves, and muscles, such as cerebral palsy, epilepsy [seizure disorders], stroke intellectual disability [mental retardation], moderate to severe developmental delay, muscular dystrophy, or spinal cord injury); 4) persons with immunosuppression, including that caused by medications or by human immunodeficiency virus infection; 5) women who are pregnant or postpartum (within 2 weeks after delivery); 6) persons aged ≤18 years who are receiving long-term aspirin therapy; 7) American Indians/Alaska Natives; 8) persons with extreme obesity (i.e., body mass index ≥40); and 9) residents of nursing homes and other chronic care facilities.

***** https://gis.cdc.gov/grasp/fluview/Novel_Influenza.html.

†††††† https://www.aphis.usda.gov/animal_health/animal_dis_spec/swine/downloads/fy2018quarter1swinereport.pdf.

Summary

What is already known about this topic?

CDC compiles, collects, and analyzes data on influenza activity to monitor the timing and severity of each influenza season.

What is added by this report?

Reported Southern Hemisphere influenza activity was relatively low and fairly mild, with influenza A(H1N1)pdm09 viruses predominating in most regions. In the United States, influenza activity was low in all regions, typical for this time of year. Fourteen influenza variant virus infections were reported in the United States, and most were associated with exposure to swine.

What are the implications for public health practice?

Annual influenza vaccination is recommended for all persons aged ≥6 months who do not have a contraindication. Providers should encourage influenza vaccination now prior to the increase of influenza activity.

swine exposure and attendance at an agricultural fair; one only attended an agricultural fair, and another reported neither swine exposure nor attendance at an agricultural fair. Vulnerable populations, especially young children and other persons at high risk for serious influenza complications, should avoid swine barns at agricultural fairs or close contact with swine. Health care providers should consider novel influenza virus infections in persons with ILI and swine or poultry exposure, or with severe acute respiratory infection after travel to areas where avian influenza viruses have been detected.

Influenza surveillance reports for the United States are posted online weekly and are available at https://www.cdc.gov/flu/weekly. Additional information regarding influenza viruses, influenza surveillance, influenza vaccines, influenza antiviral medications, and novel influenza A virus infections in humans is available at https://www.cdc.gov/flu.

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Measles Outbreak in a Highly Vaccinated Population — Israel, July–August 2017

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On August 6, 2017, the Israeli Defense Force Public Heath Branch (IDFPHB) was notified of two suspected measles cases. IDFPHB conducted an epidemiologic investigation, which identified nine measles cases in a population with high measles vaccination coverage. All measles patients had signs and symptoms consistent with modified measles (i.e., less severe disease with milder rash, fever, or both, with or without other mild typical measles symptoms). A total of 1,392 contacts were identified, and 162 received postexposure prophylaxis (PEP) with measles-mumps-rubella (MMR) vaccine; the remaining contacts were followed for 21 days (one incubation period). No tertiary cases were identified.

Investigation and Findings

The first two cases (in patients A and B) were reported on August 6, 2017. Both cases occurred in soldiers who developed mild symptoms (fever and maculopapular rash) on August 4 and subsequently were hospitalized in isolation at a civilian hospital. Urine and serum specimens were sent to Israel's National Measles and Rubella Laboratory (NMRL). Neither patient had traveled or had a known exposure to measles, nor was any epidemiologic link evident between the cases. Both patients had self-reported history of receipt of 2 doses of MMR vaccine. The cases in patients A and B were laboratory-confirmed serologically and by urine polymerase chain reaction (PCR) testing on August 7 and August 9, respectively (Table). A third patient with mild symptoms (patient C) was reported by NMRL staff members to IDFPHB on August 7 after urine PCR confirmation. Patient C, a soldier aged 19 years, was the partner of patient A and reported having received 2 doses of measles vaccine.

IDFPHB undertook an epidemiologic investigation to determine the source of infection, to identify contacts, and to recommend PEP. Because all three cases appeared within days of one another, a common source of infection was suspected.

Investigators learned that patients A, B, and C had visited the same crowded, mixed civilian-military clinic on July 24 during the same hour; therefore, the clinic was suspected to be the site of exposure. To evaluate that hypothesis, investigators reviewed medical records of all patients treated at the clinic on July 24 during the same time that patients A, B, and C visited. One patient examined in the clinic was a Ukraine-born soldier, aged 21 years, who was evaluated for fever and rash; measles was not suspected at the time. The investigation found that he had returned to Israel 3 days before visiting the clinic, having traveled to three European countries (France, Germany, and Ukraine) with ongoing measles outbreaks (*1*). Because he was suspected to be the primary patient, his serum specimen was forwarded to NMRL, where measles was serologically confirmed.

The primary patient would have been infectious from approximately 4 days before until 4 days after the onset of rash. Because more than 14 days had passed from the July 24 clinic exposure, it was anticipated that some exposed clinic contacts (in addition to patients A, B, and C) might have already developed measles. Therefore, the medical records of all soldiers who went to the clinic on July 24, as well as other military contacts of the primary patient, were reviewed daily for the 21 days beginning July 24. The aim was to identify occurrence of fever, rash, conjunctivitis, or Koplik spots among the contacts.

For the purpose of the investigation, a suspected case of measles was defined as the presence of a febrile rash illness. Confirmed measles was defined as positive test for measles by urine PCR or positive/equivocal measles immunoglobulin M, and a probable case was defined as a suspected case with suggestive laboratory results (positive immunoglobulin G [IgG] with high IgG avidity, indicative of a past immunologic response to measles vaccine or infection).

The review of medical records led to further evaluation of 14 patients, including vaccination history, exposure history, inquiries regarding potential contacts, and a physical examination by a general practitioner. Among the 14 patients, eight measles cases were identified in addition to the primary case, seven of which were laboratory-confirmed (Table). The median patient age was 20 years (range = 19–37 years). All patients had mild disease with rash, fever, or both and minimal or no conjunctivitis or Koplik spots, consistent with modified measles (*2*). There were no known complications. Two patients (A and B) were hospitalized, primarily to establish the diagnosis and provide isolation.

Patients were residents of central Israel and served on different military bases. Four patients had documentation of receipt of 2 doses of measles-containing vaccine, four reported receiving 2 doses during childhood (with no documentation), and the primary patient had documentation of receipt of 3 doses

TABLE. Age, measles vaccination history, and laboratory results for nine patients with measles — Israel, July–August, 2017

Patient	Age (yrs)	Measles vaccination history	Rash onset date	Urine PCR	IgM	IgG	Avidity†	Confirmation
Primary	21	3 doses*	Jul 24	Not available	Positive	Positive	62	Confirmed
A§	20	2 doses¶	Aug 4	Positive	Positive	Negative	Not applicable	Confirmed
B	20	2 doses¶	Aug 5	Positive	Positive	Positive	70	Confirmed
C	20	2 doses¶	Aug 6	Positive	Negative	Positive	77	Confirmed
D§	20	2 doses¶	Aug 4	Negative**	Equivocal	Positive	74	Confirmed
E	37	2 doses††	Aug 7	Negative**	Negative	Positive	71	Probable
F	19	2 doses*	Aug 7	Positive	Equivocal	Positive	65	Confirmed
G	19	2 doses*	Aug 7	Positive	Positive	Positive	75	Confirmed
H	19	2 doses*	Aug 10	Positive	Negative	Positive	76	Confirmed

Abbreviations: IgG = immunoglobulin G; IgM = immunoglobulin M; PCR = polymerase chain reaction.
* Documentation of vaccination.
† >60% = high avidity.
§ Ring vaccination (vaccination of all susceptible persons in the unit) was performed.
¶ Reported history of vaccination.
** PCR sample not appropriately transported to laboratory.
†† 1 dose documented; second reported.

of MMR in Ukraine, one each in 1997, 1998, and 2002. Patient A's report of receipt of 2 doses of measles-containing vaccine was inconsistent with the negative IgG test result. Laboratory testing confirmed high avidity (>60% IgG) in all patients except patient A (Table), suggesting a previous immune response (*3*). The epidemiologic investigation identified 1,392 contacts of these nine patients. No measles cases were diagnosed among contacts of patients A–H.

Phylogenetic analysis of virus isolates from three patients identified B3 genotype. Concurrent with this outbreak, three measles cases with no apparent connection to the military cases were diagnosed in civilians in the Tel Aviv district. Measles genotype B3 was identified in these cases as well, and the sequence of 450nt region of the N gene was identical to that from the military isolates, supporting the suspicion of epidemiologic linkage among all Israeli cases. According to GenBank, the U.S. National Institute of Health's open-access, annotated collection of all publicly available nucleotide sequences, measles virus B3 genotype with the identical 450nt N gene sequence was detected in Hungary (MG323532.1), Germany (MF593154.1), Belgium (MF490426.1), and Italy (KY801730.1) during the same period, strengthening the evidence that the primary case was acquired while traveling in Europe.

Public Health Response

During the active search for contacts of patients A–H, a total of 1,392 military contacts were identified and located, and their physicians were notified. All contacts were instructed to seek medical care or call IDFPHB if they developed fever or rash during the subsequent 21 days. Contacts identified within 72 hours of exposure who had received fewer than 2 doses of MMR vaccine were given an MMR dose for PEP. By August 27, a total of 162 soldiers had received PEP with MMR vaccine. Among the remaining contacts who were not offered PEP, most had documentation of receipt of 2 doses of measles-containing vaccine; some were not identified until >72 hours after exposure. Because of the crowded nature of the military units of two patients (A and D), vaccination of all susceptible persons in the unit (ring vaccination) was performed. After consultation with Israel's Ministry of Health (MOH) public health and laboratory specialists, and because of the low attack rate, a decision was made to not recommend a third MMR dose for contacts. No quarantine was recommended for contacts.

As mandated, IDFPHB notified MOH about the cases. Because more than 2 weeks had elapsed from the airline flight taken by the primary patient until the diagnosis of measles was made, it was not possible to administer PEP to the passengers of the flight. MOH was not notified of any Israeli measles cases among contacts from the flight. Additional measures taken during the outbreak were confirmation of vaccination status of health care workers in the clinics and in military units with confirmed cases and issuance of an alert for military health care practitioners about the outbreak.

Discussion

This measles outbreak occurred in an adult population with high 2-dose measles vaccination coverage. The primary patient had documentation of receipt of 3 doses of measles-containing vaccine, one each at ages 1, 2, and 6 years, per the vaccination schedule in Ukraine. Although it is possible that the vaccination record contained an error, the high IgG avidity suggests secondary vaccine failure (*2*). All patients except one had high measles IgG avidity, which is an indicator of previous vaccination or previous infection. Because all the serum specimens (except that from the primary patient) were collected 2–3 days after the onset of symptoms, the high avidity IgG was assumed to be a result of patients' previous vaccination.

Summary

What is already known about this topic?

Measles occurs sporadically in Israel and can be imported by travelers. Measles outbreaks occurred in 15 European countries during the summer of 2017.

What is added by this report?

During July and August 2017, nine measles cases occurred among vaccinated Israeli soldiers. The primary patient had recently traveled to Europe. All other cases occurred in his direct contacts. All patients had mild illness; no tertiary cases occurred.

What are the implications for public health practice?

Modified measles might not be suspected in persons with documentation of vaccination. In outbreak settings, health care providers should maintain a high index of suspicion for measles, even in vaccinated patients, and conduct a thorough epidemiologic and laboratory investigation of suspected measles cases.

Although outbreaks of measles among vaccinated populations have been reported worldwide (*4*–*7*), most outbreaks in Israel have occurred in unvaccinated or partially vaccinated populations (*8*,*9*). Measles transmission from a vaccinated person with documented secondary vaccine failure also has been described in New York City in 2011, including among vaccinated health care providers (*4*), and in the Marshall Islands (*10*). Waning of vaccine-induced immunity is a phenomenon that needs to be addressed, especially in regions where circulation of wild measles virus is low. Further studies, which might include seroepidemiologic studies of the dynamics of IgG levels by age, are needed to assess measles immunity and incidence of measles in populations with high 2-dose vaccination coverage. Demonstrating waning immunity with age could guide development of recommended vaccination regimens.

This outbreak highlights the importance of a thorough epidemiologic and laboratory investigation of suspected cases of measles, regardless of vaccination status, as well as the need for active surveillance of contacts. The symptoms reported by patients with secondary measles cases were modified from the typical signs of fever; rash; and coryza, conjunctivitis, or cough. Without active surveillance, the possibility of measles likely would not have been considered, and circulation of the virus might have continued. Health care providers should include measles in the differential diagnosis of fever and rash even in a vaccinated patient and obtain appropriate laboratory testing.

Absence of tertiary cases in this outbreak is consistent with the lower risk for transmission reported in other cases of measles in vaccinated persons, possibly owing to their milder symptoms, including lack of or reduced cough (*4*,*5*). In this outbreak, most contacts being fully vaccinated probably contributed to rapid containment.

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Update on Vaccine-Derived Polioviruses — Worldwide, January 2017–June 2018

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Since the Global Polio Eradication Initiative was launched in 1988 (*1*), the number of polio cases worldwide has declined by >99.99%. Among the three wild poliovirus (WPV) serotypes, only type 1 (WPV1) has been detected since 2012. This decline is attributable primarily to use of the live, attenuated oral poliovirus vaccine (OPV) in national routine immunization schedules and mass vaccination campaigns. The success and safety record of OPV use is offset by the rare emergence of genetically divergent vaccine-derived polioviruses (VDPVs), whose genetic drift from the parental OPV strains indicates prolonged replication or circulation (*2*). Circulating VDPVs (cVDPVs) can emerge in areas with low immunization coverage and can cause outbreaks of paralytic polio. In addition, immunodeficiency-associated VDPVs (iVDPVs) can emerge in persons with primary immunodeficiencies and can replicate and be excreted for years. This report presents data on VDPVs detected during January 2017–June 2018 and updates previous VDPV summaries (*3*). During this reporting period, new cVDPV outbreaks were detected in five countries. Fourteen newly identified persons in nine countries were found to excrete iVDPVs. Ambiguous VDPVs (aVDPVs), isolates that cannot be classified definitively, were found among immunocompetent persons and environmental samples in seven countries.

Global eradication of type 2 WPV (WPV2) was declared in 2015; type 3 WPV (WPV3) was last detected in 2012. The number of detected WPV1 cases has reached a historic low (22 cases in 2017 and 18 as of September 2018) in two of the three countries with endemic WPV1 transmission (Afghanistan and Pakistan); in Nigeria, WPV1 was last detected in September 2016. After the emergence of multiple cVDPV2 outbreaks during the preceding 15 years, in April 2016, all OPV-using countries switched from using trivalent OPV (tOPV; Sabin types 1, 2, and 3) to bivalent OPV (bOPV; Sabin types 1 and 3). To control and prevent cVDPV2 outbreaks, approximately 100 million doses of monovalent type 2 OPV (mOPV2) have been distributed in 11 countries (*4*). To maintain protection from poliovirus type 2 paralysis, 176 OPV-using countries have introduced at least 1 dose of injectable inactivated polio vaccine beginning in 2015.

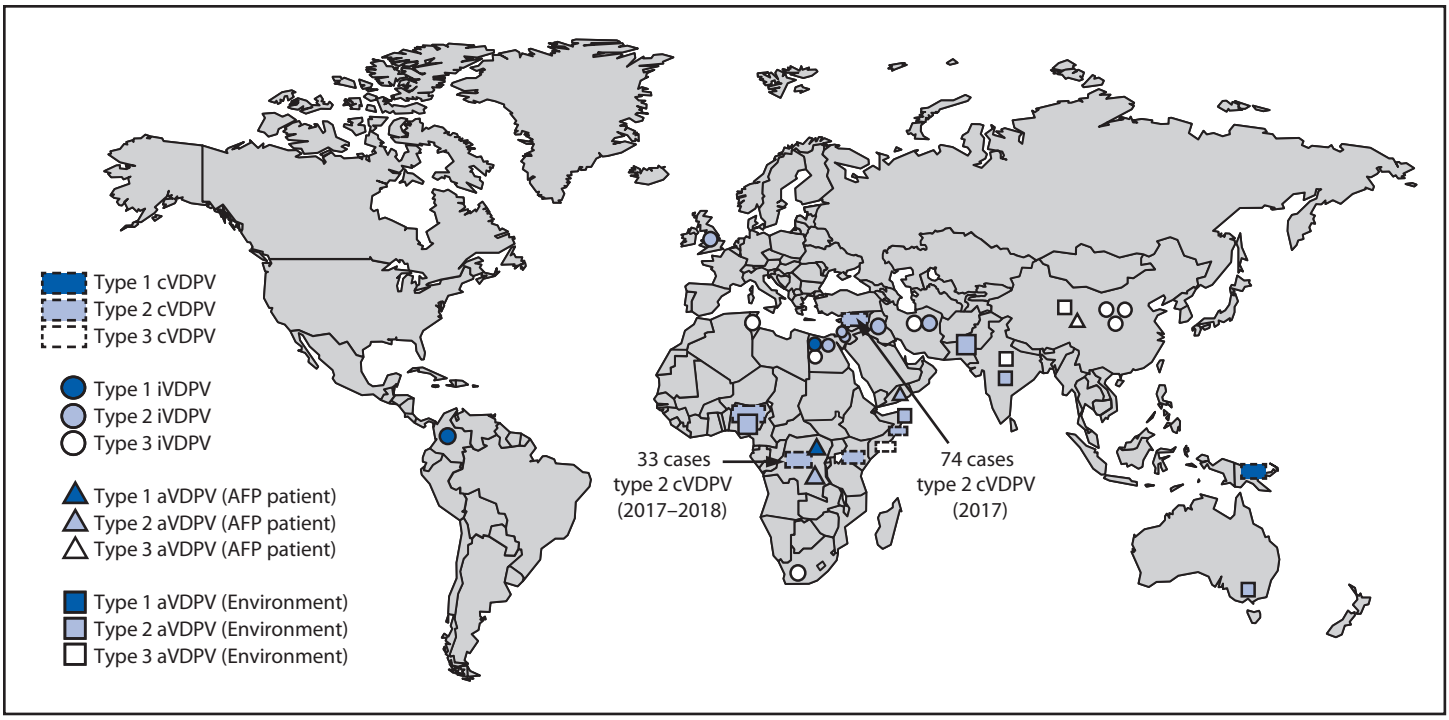
Properties and Virologic Characterization of VDPVs

Poliovirus isolates are characterized by laboratories of the Global Polio Laboratory Network. VDPV screening is conducted using real-time reverse transcription–polymerase chain reaction nucleic acid amplification, followed by sequencing of the VP1 region. VDPVs are isolates that are >1% divergent (for PV1 and PV3) or >0.6% divergent (for PV2) in VP1 nucleotide sequences from the corresponding OPV strain (*3*). Starting August 1, 2016, use of the VDPV2 screening assay was discontinued, and all PV2 isolates have been sequenced. VDPVs are further classified as 1) cVDPVs, when evidence of person-to-person transmission in the community exists; 2) iVDPVs, when they are isolated from persons with primary immunodeficiencies; and 3) aVDPVs, when they are clinical isolates from persons with no known immunodeficiency and no evidence of transmission, or they are sewage isolates that are unrelated to other known VDPVs and whose source is unknown (*2*).

Detection of cVDPVs

During January 2017–June 2018, cVDPV circulation was detected in six countries, an increase of one since the previous reporting period (*3*) (Figure 1); five countries reported cVDPV2 circulation (Democratic Republic of the Congo [DRC], Kenya, Nigeria, Somalia, and Syria); cVDPV1 was reported in Papua New Guinea (Table). Cases of cVDPV (in patients with acute flaccid paralysis [AFP]) continued to be identified from the previously reported (*3*) cVDPV2 outbreaks in Syria and DRC (*5*,*6*). No additional cases were reported from the cVDPV2 outbreaks first reported in Nigeria and Pakistan in 2016. New outbreaks were reported in DRC (three cVDPV2 emergences); Somalia (one cVDPV2 emergence and one cVDPV3 emergence) with linked cVPDV2 isolation in sewage in Kenya (*7*); Nigeria (two cVDPV2 emergences); and Papua New Guinea (one cVDPV1 emergence) (Table). During the reporting period, 113 cVDPV2 cases were detected (Table), including 74 in Syria, 33 in DRC, four in Nigeria, and two in Somalia. The large cVDPV2 outbreak in Syria (*3*) was apparently interrupted in 2017; the last reported cases had

FIGURE 1. Vaccine-derived polioviruses (VDPVs) detected — worldwide, January 2017–June 2018



Abbreviations: AFP = acute flaccid paralysis; aVDPV = ambiguous VDPV; cVDPV = circulating VDPV; iVDPV = immunodeficiency-associated VDPV.

paralysis onset in September 2017. Three cVDPV1 cases were detected in Papua New Guinea, and three cVDPV3 cases were detected in Somalia (Table). Sixty-two cVDPVs were isolated from sewage sampling in environmental surveillance sites in Kenya, Nigeria, and Somalia. After June 2018, newly identified VDPVs linked to emergences during the reporting period were detected in all outbreak countries except Syria. During January 2017–June 2018, among 119 cVDPV cases, 113 (95%) were cVDPV2, which represented a serotype profile similar to that of the previous 12 years (Figure 2).

Selected cVDPV Emergences from the Reporting Period

Democratic Republic of the Congo. Three distinct cVDPV2 emergences (designated HLO-1, MAN-1, and MON-1, per detection location and number of emergences in a geographic region) were detected during February 2017–June 2018. The HLO-1 emergence circulated in Haut Katanga, Haut Lomami, Ituri, and Tanganyika provinces. The MAN-1 and MON-1 emergences had limited circulation in Maniema and Mongala provinces, respectively. Multiple supplementary immunization rounds with mOPV2 were conducted in outbreak provinces and adjacent high-risk areas in response to the cVDPV2 emergences.

Horn of Africa (Kenya and Somalia). Two distinct cVDPV emergences were detected during October 2017–May 2018. A cVDPV2 emergence (designated BAN-1) was detected in three environmental sites in Mogadishu, Somalia, (Banaadir province) and in one environmental site in Nairobi, Kenya. Two cVDPV2 cases linked to BAN-1 also were detected in Gedo and Hiran provinces of Somalia. A cVDPV3 emergence (BAN-2) also was detected in the same three environmental sites; during February–May 2018, cVDPV3s associated with BAN-2 emergence were detected in three environmental sites in Mogadishu and in three cases in Middle Shabelle and Hiran provinces of Somalia. The launch of a new environmental sampling site in Mogadishu, Somalia, in October 2017 led to the immediate detection of type 2 cVDPV and subsequent detection of two type 3 cVDPVs and one aVDPV2. Outbreak response included three supplementary immunization rounds with mOPV2 in Somalia (December 2017–May 2018) and one mOPV2 round in Kenya (May 2018).

Nigeria. During January–June 2018, two concurrent cVDPV2 emergences were detected in Nigeria, one in the states of Gombe, Jigawa, and Yobe (designated JIS-1), and the other in Sokoto state (SOS-3). The JIS-1 emergence was detected in 18 cVDPV2 isolates from environmental samples and in isolates from four persons with AFP. Seventeen SOS-3 cVDPV2s were isolated from sewage samples collected in Sokoto. Outbreak response included two supplementary immunization rounds with mOPV2 conducted in four states (Bauchi, Gombe, Jigawa, and Sokoto) in May 2018.

TABLE. Vaccine-derived polioviruses (VDPVs) detected, by classification and other selected characteristics — worldwide, January 2017–June 2018

Category	Country	Year(s) detected*	Source†	Serotype	Source of isolates§ January 2017–June 2018 (no.) AFP cases	Non-AFP cases¶	Environmental surveillance	Capsid protein VP1 divergence from Sabin OPV strain** (%)	Coverage with 3 OPV doses (%)††	Estimated duration of VDPV replication§§ (yrs)	Date of last outbreak case, patient isolate, or environmental sample
cVDPV	DRC	2017–2018	Outbreak HLO-1	2	27	10	0	1.5–3.2	79	2.9	May 27, 2018
	DRC	2017	Outbreak MAN-1	2	2	1	0	0.7–1.0	79	0.9	Apr 18, 2017
	DRC	2018	Outbreak MON-1	2	4	3	0	2.1–2.4	79	2.2	Jun 24, 2018
	Kenya	2018	Outbreak BAN-1	2	0	0	2	4.9–5.2	81	4.7	May 29, 2018
	Nigeria	2018	Outbreak JIS-1	2	4	2	18	1.4–2.5	40	2.3	Jun 29, 2018
	Nigeria	2018	Outbreak SOS-3	2	0	0	17	0.7–1.2	40	1.3	Jun 26, 2018
	Papua New Guinea	2018	Outbreak	1	3	2	0	1.4–2.5	60	2.0	Jun 25, 2018
	Somalia	2017–2018	Outbreak BAN-1	2	2	0	16	3.7–4.8	47	4.7	May 29, 2018
	Somalia	2018	Outbreak BAN-2	3	3	1	9	1.6–2.1	47	1.9	May 18, 2018
	Syria	2017	Outbreak	2	74	60	0	2.4–3.7	53	3.3	Sep 21, 2017
Total cVDPV	—¶¶	—¶¶	—¶¶	—¶¶	**119**	**79**	**62**	—¶¶	—¶¶	—¶¶	—¶¶
iVDPV	China	2017	AFP patient	3	1	0	0	1.4	99	1.2	Oct 15, 2017
	China	2018	AFP patient	3	1	0	0	1.1	99	1.0	May 10, 2018
	China	2018	AFP patient	3	1	0	0	1.3	99	1.1	Jun 8, 2018
	Colombia	2018	AFP patient	1	1	0	0	1.4	92	1.2	May 16, 2018
	Egypt	2017	Non-AFP SCID	1	0	1	0	2.4	94	2.1	Oct 23, 2017
	Egypt	2017	AFP patient	2	1	0	0	1.9	94	1.7	Feb 13, 2017
	Egypt	2017–2018	AFP patient	3	1	0	0	2.1	94	1.9	Feb 13, 2017
	Iran	2017	Non-AFP PID	3	0	1	0	1.3	99	1.1	May 18, 2017
	Iran	2015–2017	Non-AFP PID	2	0	1	0	4.1	99	3.7	Mar 13, 2017
	Israel	2016–2017	Non-AFP SCID	2	0	1	0	1.8	98	1.6	Jun 3, 2017
	South Africa	2017–2018	AFP patient	3	1	0	0	2.0	66	1.8	Jun 29, 2018
	Tunisia	2016–2017	AFP patient XLA	3	1	0	0	1.2	98	1.1	Jan 11, 2017
	United Kingdom	2015–2017	Non-AFP PID	2	0	1	0	17.94	94	>30	May 11, 2017
	West Bank and Gaza Strip	2016–2017	Non-AFP SCID	2	0	1	0	1.0	94	0.9	Feb 8, 2017
Total iVDPV	—¶¶	—¶¶	—¶¶	—¶¶	**8**	**6**	**0**	—¶¶	—¶¶	—¶¶	—¶¶

See table footnotes on the next page.

Papua New Guinea. During April–June 2018, circulating VDPV1s were isolated from three patients with AFP and two contacts in the provinces of Easter Highlands and Morobe. Reported routine vaccine coverage at the subnational level has been low (50%) for years; bOPV outbreak response campaigns are ongoing.

Detection of iVDPVs

During January 2017–June 2018, 14 iVDPVs were reported from nine countries, including seven type 3 iVDPVs (iVDPV3), five type 2 iVDPVs (iVDPV2), and two type 1 iVDPVs (iVDPV1). (Table). Six of the iVDPV isolates were newly detected since the last report. Since introduction of OPV in 1961, the cumulative iVDPV serotype distribution is iVDPV2 (66%), iVDPV3 (17%), iVDPV1 (12%), and heterotypic mixes (i.e., types 1 and 2 or types 2 and 3) (5%).

Detection of aVDPVs

During January 2017–June 2018, the number of countries with detected aVDPVs decreased to seven from 11 described in the previous report (*3*) (Table). Among 28 detected aVDPVs, 23 were type 2 (aVDPV2) (predominantly after mOPV2 responses to cVDPV outbreaks), four were type 3 (aVDPV3), and one was type 1 (aVDPV1); 23 (82%) aVDPVs were isolated from environmental samples. Detection of aVDPVs in settings with <60% polio vaccination coverage might indicate a risk for cVDPV emergence and further spread. A highly divergent aVDPV2 (8.4% VP1 divergence) was isolated from an environmental sample collected in metropolitan Melbourne, Australia on November 21, 2017. This environmental isolate had genomic sequence characteristics compatible with iVDPVs.

TABLE. (*Continued*) Vaccine-derived polioviruses (VDPVs) detected, by classification and other selected characteristics — worldwide, January 2017–June 2018

Category	Country	Year(s) detected*	Source†	Serotype	Source of isolates§ January 2017–June 2018 (no.)			Capsid protein VP1 divergence from Sabin OPV strain** (%)	Coverage with 3 OPV doses (%)††	Estimated duration of VDPV replication§§ (yrs)	Date of last outbreak case, patient isolate, or environmental sample
					AFP cases	Non-AFP cases¶	Environmental surveillance				
aVDPV	Australia	2017	Environmental sample	2	0	0	1	8.4	95	7.2	Nov 21, 2017
	China	2017	AFP patient	3	1	0	0	1.1	99	1.0	Feb 14, 2017
	China	2018	Environmental sample	3	0	0	1	1.4	99	1.3	Apr 18, 2018
	China	2018	Environmental sample	3	0	0	1	1.2	99	1.1	Feb 7, 2018
	DRC	2017	AFP patient	1	1	0	0	2.7	79	2.5	Apr 1, 2017
	DRC	2017	AFP patient	2	2	0	0	1.1–1.9	79	1.0–1.8	Dec 29, 2017
	India	2017	Environmental sample	2	0	0	1	1.2	88	1.1	Mar 29, 2017
	India	2018	Environmental sample	3	0	0	1	1.1	88	1.0	May 16, 2018
	Nigeria	2017	Non-AFP	2	0	1	0	0.7	40	0.7	Mar 2, 2017
	Nigeria	2017	Environmental sample	2	0	0	12	0.7–1.1	40	0.6–1.0	Apr 17, 2017
	Pakistan	2017	Environmental sample	2	0	0	5	0.7–0.8	75	0.6–0.7	Jul 15, 2017
	Somalia	2018	Environmental sample	2	0	0	1	0.7	47	0.6	Mar 1, 2018
Total aVDPV	—¶¶	—¶¶	—¶¶	—¶¶	**4**	**1**	**23**	—¶¶	—¶¶	—¶¶	—¶¶

Abbreviations: AFP = acute flaccid paralysis; aVDPV = ambiguous VDPV; cVDPV = circulating VDPV; DRC = Democratic Republic of the Congo; IPV = inactivated poliovirus vaccine; iVDPV = immunodeficiency-associated VDPV; OPV = oral poliovirus vaccine; PID = primary immunodeficiency; SCID = severe combined immunodeficiency; XLA = X-linked agammaglobulinemia.

* Total years detected for previously reported cVDPV outbreaks (DRC and Syria).

† Outbreaks list total cases clearly associated with cVDPVs. Some VDPV case isolates from outbreak periods might be listed as aVDPVs. HLO-1, MAN-1, MON-1, BAN-1, BAN-2, JIS-1, and SOS-3 indicate independent cVDPV emergences and designate the location of the emergence and the number of emergences in a particular geographic region.

§ Total cases for VDPV-positive specimens from AFP cases and total VDPV-positive samples for environmental (sewage) samples.

¶ Contacts and healthy child sampling.

** Percentage of divergence is estimated from the number of nucleotide differences in the VP1 region from the corresponding parental OPV strain.

†† Coverage with 3 doses of OPV; data from the 2017 World Health Organization (WHO) Vaccine Preventable Diseases Monitoring System (2017 global summary) and WHO-United Nations Children's Fund coverage estimates, http://www.who.int/gho/immunization/poliomyelitis/en/. National data might not reflect weaknesses at subnational levels.

§§ Duration of cVDPV circulation was estimated from extent of VP1 nucleotide divergence from the corresponding Sabin OPV strain; duration of iVDPV replication was estimated from clinical record by assuming that exposure was from initial receipt of OPV; duration of aVDPV replication was estimated from sequence data.

¶¶ Not cumulative data.

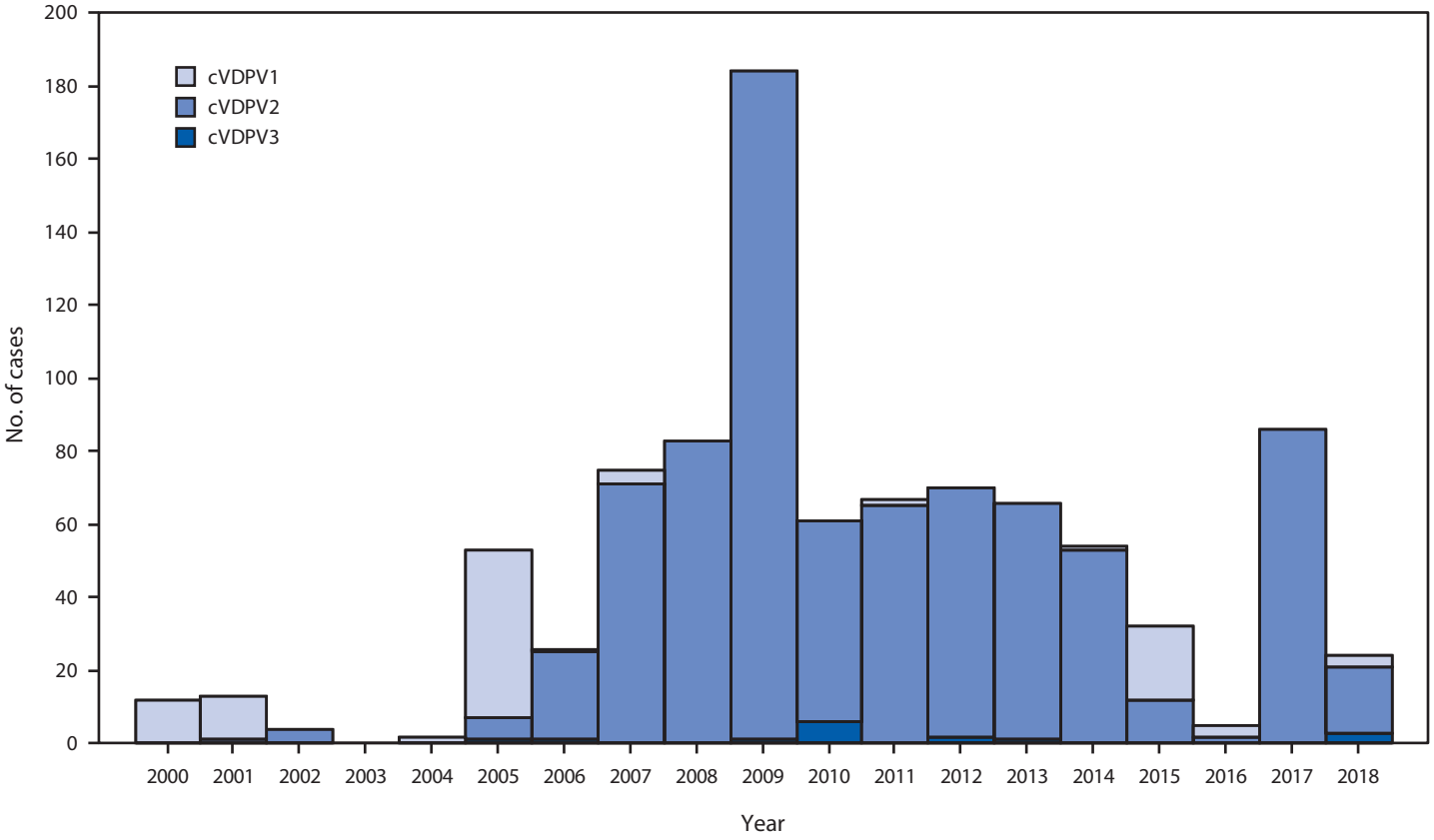
Discussion

During January 2017–June 2018, the number of reported cVDPV outbreaks and the total number of reported cVDPV cases in these outbreaks increased from the January 2016–June 2017 reporting period (*3*); new cVDPVs were detected in DRC, Kenya, Nigeria, Papua New Guinea, and Somalia during the January 2017–June 2018 reporting period. Cases have continued to be identified in 2018 after this reporting period in DRC, Nigeria, Papua New Guinea, and Somalia.

The continued expansion of sewage sampling (244 sites in 41 countries) (*8*) has increased the frequency of detection of WPV, VDPV, and residual PV2 excretion after mOPV2 vaccination during outbreak responses. As of April 2018, the number of environmental sites in countries with recent active WPV transmission (Afghanistan, Nigeria, and Pakistan) increased from 21 at the end of 2011 to 153. Partially as a result of supplemental surveillance measures for VDPVs among patients with primary immunodeficiencies (*9*), the number of known iVDPV excretors has increased; the antiviral pocapavir has recently been used to treat iVDPV excretors under compassionate use protocols in three countries (Task Force for Global Health, personal communication, October 2018).

Gaps in immunity to poliovirus type 2 remain in high-risk areas and continue to increase with time after the 2016 tOPV-to-bOPV switch. Continued detection of VDPV2s in 2017 and into 2018 underscores the existence of substantial populations of children who missed PV2 immunization before the switch. Some cVDPV2 detections occurred in or

FIGURE 2. Circulating vaccine-derived poliovirus (cVDPV) cases detected, by serotype (N = 917) — worldwide, January 2000–June 2018*



* Data through June 2018; available by September 18, 2018.

near security-compromised areas (DRC, Somalia, and Syria), where surveillance quality is uncertain. Likewise, new type 1 and type 3 cVDPV outbreaks highlight the importance of maintaining high levels of poliovirus immunity against these serotypes, as well as sensitive AFP surveillance. During the reporting period, VDPV cases outnumbered WPV cases; however, documentation of eradication of WPV is required before global OPV use can cease. Cessation of all OPV use after certification of polio eradication will eliminate the risk for VDPV emergence.

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The World Health Organization Global Polio Laboratory Network; Qi Chen, Chadi Agha, Hongmei Liu, Naomi Dybdahl-Sissoko, Hong Pang, Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, CDC.

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All authors have completed and submitted the ICMJE form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

Summary

What is already known about this topic?

Vaccine-derived polioviruses (VDPVs) can circulate in settings of low population immunity or during outbreaks.

What is added by this report?

After the 2016 synchronized switch from trivalent oral poliovirus vaccine (OPV) (types 1, 2, and 3) to bivalent OPV (types 1 and 3), transmission of type 2 circulating VDPVs (cVDPVs) was detected in countries with subpopulations of children who missed immunization to type 2 poliovirus before the switch. Types 1 and 3 cVDPVs were identified in Papua New Guinea and Somalia, respectively.

What are the implications for public health practice?

All countries must maintain high population immunity to polio. Cessation of all OPV use after certification of polio eradication will eliminate the risk for VDPV emergence.

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Notes from the Field

Recurrence of a Multistate Outbreak of *Salmonella* Enteritidis Infections Linked to Contact with Guinea Pigs — Eight States, 2015–2017

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In December 2017, the Colorado Department of Public Health and Environment reported two human *Salmonella* Enteritidis infections in persons with exposure to pet guinea pigs. The guinea pigs had been purchased from two separate pet stores, belonging to a single chain, and supplied by a common distributor located in California. Clinical isolates were indistinguishable by pulsed-field gel electrophoresis (PFGE), suggesting the infections were related. This PFGE pattern was previously seen in a 2010 multistate outbreak linked to contact with pet guinea pigs (*1*). An investigation was initiated to determine the number of patients affected and to identify the source of human illnesses.

A case was defined as *Salmonella* Enteritidis infection with a clinical isolate having an identical PFGE pattern to those from the Colorado isolates and closely related to a guinea pig isolate by whole genome sequencing (WGS), and with onset of clinical signs on or after January 1, 2015. State health departments were asked to review recent *Salmonella* Enteritidis illness records for patient exposure to guinea pigs. In addition, the U.S. Department of Agriculture's National Veterinary Services Laboratories was queried for isolates from guinea pigs that matched the outbreak strain. All isolates underwent WGS using high-quality single nucleotide polymorphism (SNP) analysis. An isolate from the 2010 outbreak was sequenced for comparison. Guinea pig purchase invoices were used to trace guinea pigs with an epidemiologic link to human illness back to the distributor of origin.

Nine cases in humans were identified from eight states, including two cases in Colorado and one each in Iowa, Indiana, Massachusetts, Michigan, New York, Vermont, and Virginia. Five of eight patients reported exposure to guinea pigs. Onset dates ranged from July 15, 2015, to December 15, 2017. The median patient age was 12 years (range = 1–70 years). Five patients were female. One patient was hospitalized, and no deaths were reported. Six isolates submitted to veterinary diagnostic laboratories from ill guinea pigs and one isolate from a patient's guinea pig were sequenced and found to be closely related to the outbreak strain. Including the 2010 isolate tested for comparison, all isolates were within 38 SNPs by WGS.

Traceback information was available for four guinea pigs purchased from two large pet store chains (Figure). The two distributors supplying guinea pigs to pet stores during this outbreak received guinea pigs from multiple wholesalers; however, a single common wholesaler was mentioned by both. This wholesaler also supplied guinea pigs that were associated with cases during the 2010 outbreak.

Following the 2010 outbreak, recommendations including environmental testing were made to the wholesaler regarding *Salmonella* prevention; however, the actions were not implemented. Failure to implement recommended prevention measures might have contributed to recurrence of the outbreak. To enhance compliance with recommendations made in this outbreak, CDC developed a document containing prevention measures aimed at reducing the prevalence of *Salmonella* in guinea pig colonies intended for use in the pet industry. Content was also posted on the CDC website to increase consumer awareness of risk for *Salmonella* infection linked to pet guinea pigs. Recommendations to pet owners during this outbreak focused on proper hand hygiene. Recommendations to distributors and wholesalers included routine monitoring of guinea pigs for *Salmonella* through diagnostic testing, recordkeeping to aid in traceback, and evaluating husbandry and environmental sanitation practices of guinea pig breeders to reduce the prevalence of *Salmonella* and other zoonotic diseases of concern to the pet industry (*2*).

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All authors have completed and submitted the ICMJE form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

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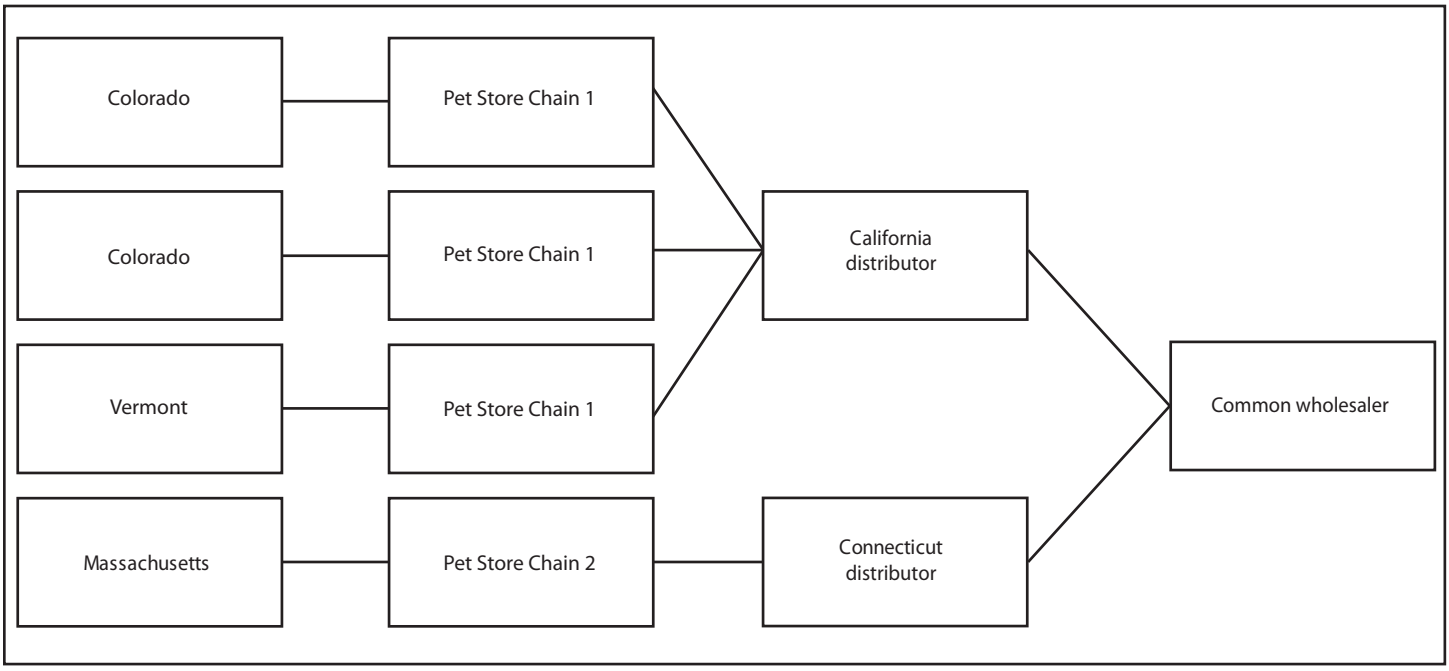
FIGURE. Traceback* of guinea pigs associated with human salmonellosis from patient to distributor of origin (n = 4) — three states, 2015–2017



* Traceback for guinea pig distribution from patients back to a common wholesaler. The Colorado and Vermont patients purchased guinea pigs from Pet Store Chain 1, which received guinea pigs from a California distributor. The Massachusetts patient purchased a guinea pig from Pet Store Chain 2, which received guinea pigs from a Connecticut distributor. Both distributors had a single common wholesaler.

Erratum

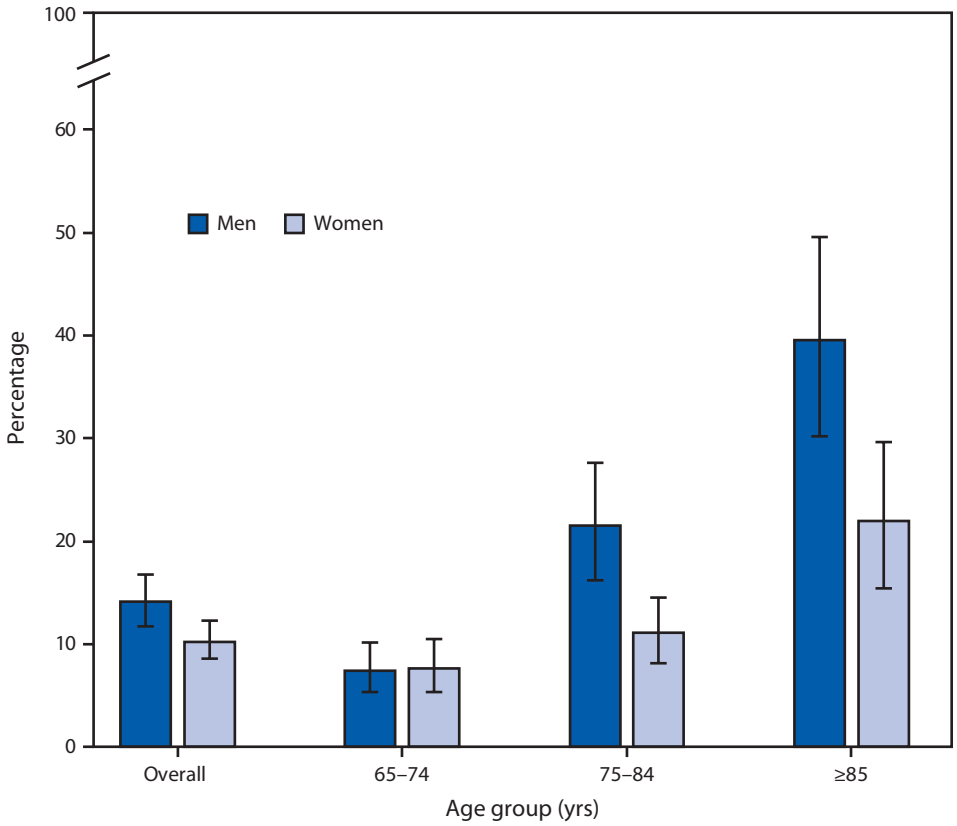
Vol. 67, No. 40

In the report "Notes from the Field: Exported Case of Sin Nombre Hantavirus Pulmonary Syndrome – Israel, 2017," on page 1129, **Maria Morales-Betoulle, PhD; Sara E. Zufan, MPH; and Shannon L.M. Whitmer, PhD,** all affiliated with the Division of High-Consequence Pathogens and Pathology, National Center for Emerging and Zoonotic Infectious Diseases, CDC, should have been included in the author list, and the affiliation for Heather Venkat, DVM, MPH should have been the **Arizona Department of Health Services**. In addition, in the first paragraph, the seventh sentence should have read "**A blood specimen collected on November 9 tested positive for SNV, with an immunoglobulin M titer of ≥1:6400 and an immunoglobulin G titer of ≥1:6400; nested reverse transcription–polymerase chain reaction (RT-PCR) followed by nucleic acid sequencing confirmed the SNV diagnosis.**"

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Prevalence* of Anemia† Among Adults Aged ≥ 65 Years, by Sex and Age Group — National Health and Nutrition Examination Survey, 2013–2016



* With 95% confidence intervals indicated with error bars.
† Anemia was defined using World Health Organization standards: hemoglobin <13 g/dL for men and <12 g/dL for women.

During 2013–2016, the prevalence of anemia among persons aged ≥65 years increased with increasing age for both men and women. Among men, the prevalence increased from 7.4% for those aged 65–74 years to 39.5% for those aged ≥85 years. The percentage of women with anemia increased from 7.6% for those aged 65–74 years to 21.9% for those aged ≥85 years. The prevalence of anemia was higher for men compared to women among those aged 75–84 years and those aged ≥85 years.

Sources: National Health and Nutrition Examination Survey, 2013–2016. https://www.cdc.gov/nchs/nhanes/index.htm; Seitz AE, et al. Anemia prevalence and trends in adults aged 65 and older: U.S. National Health and Nutrition Examination Survey: 2001–2004 to 2013–2016. https://onlinelibrary.wiley.com/doi/epdf/10.1111/jgs.15530.

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