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Update: Influenza A (H3N2)v Transmission and Guidelines — Five States, 2011

From August 17 to December 23, 2011, CDC received reports of 12 human infections with influenza A (H3N2)v viruses that have the matrix (M) gene from the influenza A (H1N1)pdm09 virus (formerly called swine-origin influenza A [H3N2] and pandemic influenza A [H1N1] 2009 viruses, respectively [Box]). The 12 cases occurred in five states (Indiana, Iowa, Maine, Pennsylvania, and West Virginia), and 11 were in children (*1,2*). Six of the 12 patients had no identified recent exposure to swine. Three of the 12 patients were hospitalized, and all have recovered fully.

A case in an adult male in Indiana with occupational exposure to swine was among the 12, and two children in West Virginia who regularly attended the same day care accounted for the latest cases. This report describes those cases and swine influenza virus (SIV) surveillance being conducted by the U.S. Department of Agriculture (USDA).

Case Reports

Indiana. On October 28, 2011, CDC was notified by the Indiana Department of Health of a suspected case of A(H3N2)v virus infection in an adult male. The patient experienced onset of fever, cough, shortness of breath, nausea, vomiting, and body aches on October 20, and was hospitalized for 4 days. He did not receive treatment with influenza antiviral medications and recovered fully.

On October 22, a respiratory specimen from the patient was positive for influenza at the hospital. On October 28, the virus was identified by real-time, reverse transcription–polymerase chain reaction (rRT-PCR) testing at the Indiana State Public Health Laboratory as an inconclusive influenza A virus, consistent with results seen with other recent A(H3N2)v infections. On October 31, genome sequencing at CDC confirmed the virus as A(H3N2)v with the M gene from the A(H1N1)pdm09 virus, similar to the viruses identified in the other cases of human infection in the United States since August 2011.

The patient reported direct contact with swine during his work in the week before illness onset. He said he did not wear any personal protective equipment (PPE) because the swine did not exhibit signs of illness. No illness was reported among the patient's household members or other close contacts.

West Virginia. On November 19, a child aged <5 years developed acute onset of fever after 1 week of cough and congestion. The child had been hospitalized for an unrelated condition 2 days before the onset of fever. On November 21, a respiratory specimen was collected. Rapid diagnostic tests conducted by the hospital were negative for influenza and respiratory syncytial virus, but influenza A was identified by an alternative rRT-PCR at the hospital. The specimen was forwarded to the West Virginia Office of Laboratory Services, where it was identified as a suspected influenza A (H3N2)v virus. Subsequent genome sequencing conducted at CDC confirmed the virus as A(H3N2)v with the M gene from the A(H1N1)pdm09 virus. The child, who had no recent travel or exposure to swine, was discharged on November 21, and has since recovered from the influenza illness.

An investigation was conducted to ascertain respiratory illnesses among contacts of the child that occurred during November 9–December 19. Multiple contacts, including children who regularly attended day care with the child, were found to have had respiratory illness during this period. On November 29, a second child aged <5 years who attended day care regularly with the first child and who had no recent travel or swine exposure became ill with fever, cough, diarrhea, and rhinorrhea. The second child did not seek medical care and recovered fully from the illness. A respiratory specimen obtained from the second child on December 7 was inconclusive by rRT-PCR at the West Virginia Office of Laboratory Services; however, the specimen was confirmed as influenza A (H3N2)v with the M gene from the A(H1N1)pdm09 virus via genome sequencing at CDC.

No additional A(H3N2)v cases have been identified among the other ill day care attendees or contacts of either patient. Enhanced surveillance for influenza-like illness and increased diagnostic testing of respiratory specimens is being conducted in West Virginia and adjacent counties in Maryland as part of the ongoing investigation of these cases. Currently, no evidence

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BOX. Changes in nomenclature for the swine-origin influenza A (H3N2) and pandemic influenza A (H1N1) 2009 viruses

After discussions among the World Health Organization (WHO), the World Organization for Animal Health, the Food and Agriculture Organization, CDC, and other U.S. federal agencies, swine-origin influenza viruses identified in humans will now be referred to as "variant" viruses and denoted with a "v." Influenza viruses identified in swine populations will continue to be referred to as "swine influenza" viruses.

This change in nomenclature follows announcement by WHO of a decision to standardize nomenclature for the pandemic influenza A (H1N1) 2009 virus (which has had diverse names) as influenza A (H1N1)pdm09 (*1*).

Since August 2011, CDC has identified 12 human infections in five states with swine-origin influenza A (H3N2) viruses. Per the new naming convention, these H3N2 viruses will now be referred to as "influenza A (H3N2) variant viruses with genes from avian, swine and human viruses," and will be abbreviated as "A(H3N2)v" for scientific use and "H3N2v" for general public use. These 12 A(H3N2)v viruses also have the M gene from the A(H1N1)pdm09 virus.

Reference

1. World Health Organization. Standardization of terminology of the pandemic A(H1N1) 2009 virus. Wkly Epidemiol Rec 2011;86:480.

of additional human-to-human transmission in the community has been identified.

Influenza Surveillance of U.S. Swine

Surveillance for SIV in the United States is overseen by USDA, largely in swine that display influenza-like illness. In July 2009, USDA's Animal and Plant Health Inspection Service and the swine industry implemented a SIV surveillance program* to characterize the distribution of SIV in U.S. swine herds. To date, approximately 150 SIV isolates have undergone sequencing of three genes (hemagglutinin, matrix, and neuraminidase gene segments) and sequences have been submitted to GenBank.† Thirty isolates have been identified as A(H3N2) viruses and eight of those 30 have the M gene from the influenza A (H1N1) pdm09 virus as determined by an informal analysis of GenBank submission data by the USDA Agricultural Research Service. Further characterization and analysis are ongoing, and new submissions are added as diagnostic work is completed.

*Additional information is available at http://www.aphis.usda.gov/animal_health/animal_dis_spec/swine/siv_surv_manual.shtml.

†Available at http://www.ncbi.nlm.nih.gov/genbank.

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Editorial Note

Human infections with the influenza viruses currently circulating among swine are rare. Since 2005, only 35 cases have been reported in the United States, but the frequency with which they have been detected increased in 2011. When different influenza viruses simultaneously infect a single host (e.g., a human or swine), exchange of genetic material can occur, resulting in a new influenza virus. Depending on the antigenic distance between the new virus and recently circulating seasonal viruses, little or no immunity might exist in the human population. Influenza A (H3N2)v viruses resulted from reassortment of influenza A (H1N1)pdm09 viruses with swine influenza A (H3N2) viruses. A diagram depicting this reassortment is available online from CDC's Public Health Image Library.§ Because these viruses carry a newly identified combination of genes, little information is available regarding transmission efficiency in swine, in humans, or between swine and humans. However, the recent human cases involving swine exposure and results of SIV surveillance indicate that these viruses also currently are circulating in swine herds.

The case of influenza A (H3N2)v infection after occupational contact with swine in Indiana and the apparent limited human-to-human transmission of A(H3N2)v virus that occurred in a day care setting in West Virginia represent two different possible scenarios for transmission of this virus. Work exposure highlights the risk for interspecies influenza transmission in occupational settings where humans are exposed to swine, an association that has been described previously (*3*–*7*). To minimize the risk for interspecies influenza transmission in

§Available at http://phil.cdc.gov/phil/details.asp (image ID: 13469).

occupational settings, CDC and the Occupational Safety and Health Administration (OSHA) encourage swine workers to 1) get vaccinated against human seasonal influenza, 2) wear appropriate PPE, and 3) practice good hygiene, such as washing hands thoroughly with soap and water, when in contact with swine, especially swine that show signs of illness. The National Pork Board also recommends producers work with their veterinarian to develop appropriate prevention and control measures for influenza in swine, which can include vaccinating swine against swine influenza. Similar to humans, swine infected with influenza viruses do not always exhibit signs of infection (*8*). Persons with swine exposure in the week before onset of an illness with symptoms of influenza requiring medical care should notify their health-care provider of their swine exposures. Persons who develop symptoms of influenza after close contact with swine are recommended to stay home until well to minimize contact with persons and swine as much as possible.

Guidance materials for persons who work with swine have been published by OSHA.¶ In addition, the National Pork Board,** CDC, and the National Association of State Public Health Veterinarians have published guidance for persons exposed to swine in public settings (*9*). Clinicians should consider variant influenza virus infection in the differential diagnosis of patients with febrile respiratory illness who have been near swine whether at work or at an agricultural event, such as a fair or exhibit.

The A(H3N2)v cases in West Virginia involved two children who attended the same day care, but the first child was unlikely to have transmitted the virus to the second child, given the ≥10-day difference in their symptom onset dates. This represents a scenario of limited human-to-human transmission occurring in a day care setting. Therefore, clinicians also should consider the possibility of influenza A (H3N2)v infections in patients who have not had exposure to swine, particularly young children in those states where influenza A (H3N2)v cases have been reported. Clinicians who suspect variant influenza virus infection should obtain a nasopharyngeal swab, place the swab in viral transport medium, and contact their state or local health department to facilitate transport and timely diagnosis (*10*). Influenza A (H3N2)v viruses detected to date are susceptible to oseltamivir and zanamivir for the treatment of influenza. Clinicians who suspect variant influenza infection in a patient should consider treatment with these medications if clinically indicated (*10*). Because these viruses have the M gene from the influenza A (H1N1)pdm09 virus, they are resistant to amantadine and rimantadine. CDC requests that state public health laboratories notify CDC immediately of suspected variant influenza A specimens and send them to the CDC Influenza Division's Virus Surveillance and Diagnostics Branch Laboratory. Confirmed cases should be investigated thoroughly and expeditiously to ascertain whether swine-to-human or human-to-human transmission is ongoing and to limit further exposures between humans with others and swine. Such investigations require close collaboration among state, local, and federal public and animal health officials.

CDC is working with USDA and state public health and animal health experts in the locations where these cases have occurred to investigate each case fully and to enhance influenza surveillance to detect human cases of variant influenza virus infections. The CDC rRT-PCR assay that was approved by the Food and Drug Administration in September 2011 is able to identify these cases as presumptive influenza A (H3N2)v cases. These diagnostic test kits have been distributed to public health laboratories in the United States and National Influenza Centers designated by the World Health Organization in other countries. Additional rRT-PCR test enhancements to further improve detection of influenza A (H3N2)v viruses are under development.

Limited serologic studies conducted to date indicate that young children have little preexisting immunity to influenza A (H3N2)v viruses. Because the hemagglutinin genes of these viruses are related to human influenza A (H3N2) viruses

What is already known on this topic?

During August–December 2011, a total of 12 human infections with influenza A (H3N2)v viruses were identified in the United States (two from Indiana, three from Iowa, two from Maine, three from Pennsylvania, and two from West Virginia).

What is added by this report?

This report provides the new nomenclature for the virus and describes three cases, one in an adult with occupational exposure and two in children involving limited human-to-human transmission in a day care setting. It also provides an overview of the U.S. Department of Agriculture's swine influenza virus (SIV) surveillance program along with data on influenza A (H3N2) viruses in swine. Out of approximately 150 SIV isolates that have undergone sequencing of three genes (hemagglutinin, matrix, and neuraminidase gene segments), 30 have been identified as A(H3N2) viruses; eight of those 30 have the M gene from the influenza A (H1N1)pdm09 virus.

What are the implications for public health practice?

Nonhuman influenza virus infections rarely result in human-to-human transmission, but the implications of sustained ongoing transmission between humans is potentially severe; therefore, prompt and thorough identification and investigation of sporadic human infections with novel influenza viruses are needed to reduce the risk for sustained transmission.

¶ Available at http://www.osha.gov/publications/influenza-workers-pigs-factsheet.pdf.

** Additional information is available at http://pork.org/filelibrary/factsheets/swine%20health/publichealth%20influenza04726.pdf.

that circulated in the 1990s, older children and adults might have limited immunity against these viruses. Certain persons, including young children, pregnant women, persons with chronic health conditions such as asthma, diabetes, or heart and lung disease, and persons aged ≥65 years, are likely to be at greater risk for serious influenza-related complications from variant influenza viruses such as influenza A (H3N2)v. The influenza A (H3N2)v virus is different enough from current human seasonal influenza viruses that the seasonal influenza vaccine is not expected to provide significant protection.

CDC will provide routine and timely communications regarding these influenza A (H3N2)v viruses and other variant influenza viruses with the public, partners, state and local health departments, and stakeholders. Updated information and guidance documents related to A(H3N2)v viruses are available online from CDC at http://www.cdc.gov/flu/swineflu/influenza-variant-viruses.htm.

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