Untitled note

2017-2018 Influenza Season Week 46 ending November 18, 2017

All data are preliminary and may change as more reports are received.

Synopsis:

During week 46 (November 12-18, 2017), influenza activity increased in the United States.

- **Viral Surveillance:** The most frequently identified influenza virus type reported by public health laboratories during week 46 was influenza A. The percentage of respiratory specimens testing positive for influenza in clinical laboratories is increasing.
- **Novel Influenza A Virus:** One human infection with a novel influenza A virus was reported.
- **Pneumonia and Influenza Mortality:** The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System.
- **Influenza-associated Pediatric Deaths:** Five influenza-associated pediatric deaths were reported, one of which occurred during the 2016-17 season.
- **Influenza-associated Hospitalizations:** A cumulative rate of 1.4 laboratory-confirmed influenza-associated hospitalizations per 100,000 population was reported.
- **Outpatient Illness Surveillance:** The proportion of outpatient visits for influenza-like illness (ILI) was 2.0%, which is below the national baseline of 2.2%. Regions 1, 2, 4 and 6 reported ILI at or above region-specific baseline levels. Two states experienced high ILI activity, one state experienced moderate ILI activity, New York City and 4 states experienced low ILI activity, the District of Columbia and 43 states experienced minimal ILI activity, and Puerto Rico had insufficient data.
- **Geographic Spread of Influenza:** The geographic spread of influenza in two states was reported as widespread; Guam and six states reported regional activity; 20 states reported local activity; the District of Columbia, the U.S. Virgin Islands and 21 states reported sporadic activity; one state reported no activity; and Puerto Rico did not report.

National and Regional Summary of Select Surveillance Components

	Data for current week			Data cumulative since October 1, 2017 (week 40)							
HHS Surveillance Regions*	**Out-patient ILI†**	**Number of jurisdictions reporting regional or widespread activity§**	**% respiratory specimens positive for flu in clinical laboratories‡**	**A(H1N1)pdm09**	**A (H3)**	**A (Subtyping not Performed)**	**B Victoria lineage**	**B Yamagata lineage**	**B lineage not performed**	**Pediatric Deaths**
				Influenza test results from public health laboratories only						
Nation	Normal	9 of 54	5.3%	136	1,193	28 6	105	85	5	
Region 1	Elevated	1 of 6	1.7%	2	21	0 1	1	0	0	
Region 2	Elevated	0 of 4	1.8%	2	23	3 0	4	1	0	
Region 3	Normal	0 of 6	1.1%	6	40	0 0	3	0	0	
Region 4	Elevated	4 of 8	7.3%	49	133	3 0	7	26	2	
Region 5	Normal	0 of 6	1.9%	3	167	6 0	19	5	0	
Region 6	Elevated	3 of 5	6.0%	34	143	1 1	7	11	1	
Region 7	Normal	0 of 4	4.3%	6	68	12 0	13	5	0	
Region 8	Normal	0 of 6	3.4%	4	138	0 1	16	1	0	
Region 9	Normal	1 of 5	5.8%	21	340	3 2	18	35	2	
Region 10	Normal	0 of 4	4.6%	12	120	0 1	17	1	0	

*https://www.hhs.gov/about/agencies/iea/regional-offices/index.html
† Elevated means the % of visits for ILI is at or above the national or region-specific baseline
Â§ Includes all 50 states, the District of Columbia, Guam, Puerto Rico, and U.S. Virgin Islands
‡ National data are for current week; regional data are for the most recent three weeks

U.S. Virologic Surveillance:

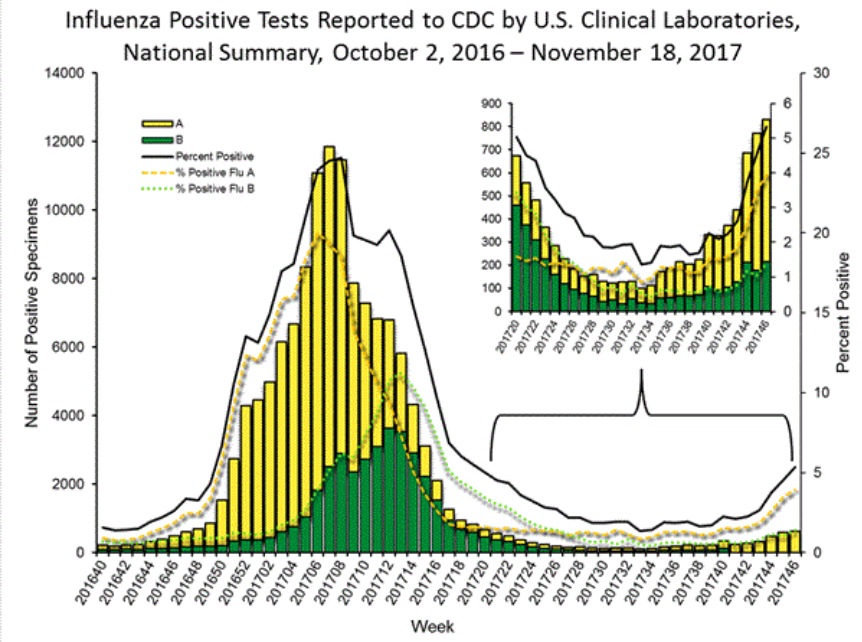
WHO and NREVSS collaborating laboratories, which include both public health and clinical laboratories located in all 50 states, Puerto Rico, and the District of Columbia, report to CDC the total number of respiratory specimens tested for influenza and the number positive for influenza by virus type. In addition, public health laboratories also report the influenza A subtype (H1 or H3) and influenza B lineage information of the viruses they test and the age or age group of the persons from whom the specimens were collected.

Additional virologic data, including national, regional and select state-level data, can be found at: http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html. Age group proportions and totals by influenza subtype reported by public health laboratories can be found at: http://gis.cdc.gov/grasp/fluview/flu_by_age_virus.html.

The results of tests performed by clinical laboratories are summarized below.

October 1, 2017 (Week 40)

	Week 46	Data Cumulative since
No. of specimens tested	15,584	114,844
No. of positive specimens (%)	832 (5.3%)	3,764 (3.3%)
Positive specimens by type		
Influenza A	616 (74.0%)	2,722 (72.3%)
Influenza B	216 (26.0%)	1,042 (27.7%)



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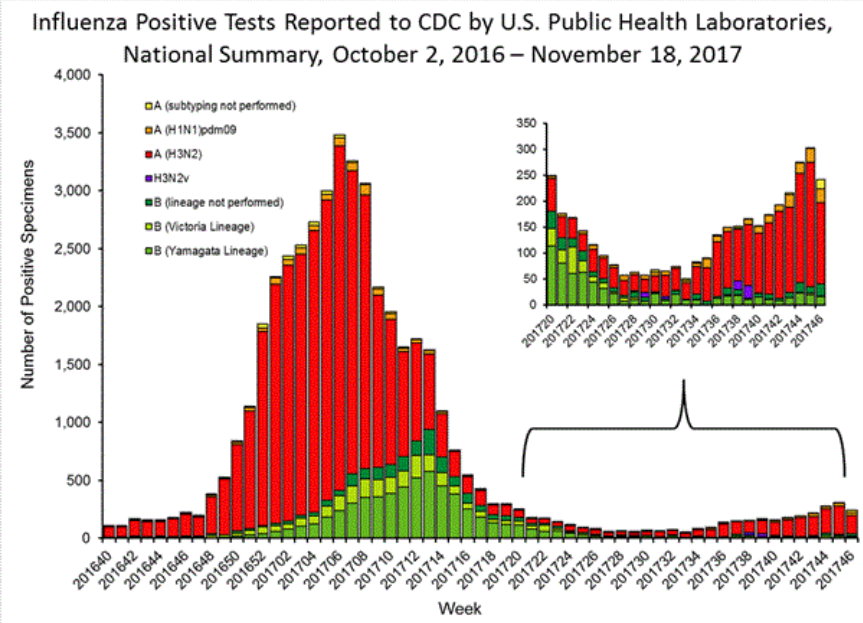
The results of tests performed by public health laboratories, as well as the age group distribution of influenza positive tests, during the current week are summarized below.

October 1, 2017 (Week 40)

	Week 46	Data Cumulative since
No. of specimens tested	937	7,642
No. of positive specimens*	241	1,554
Positive specimens by type/subtype		
Influenza A	201 (83.4%)	1,358 (87.4%)
A(H1N1)pmd09	27 (13.4%)	136 (10.0%)
H3	157 (78.1%)	1,193 (87.8%)
Subtyping not performed	17 (8.5%)	28 (2.1%)
Influenza B	40 (16.6%)	196 (12.6%)
Yamagata lineage	16 (40.0%)	105 (53.6%)
	1 (2.5%)	6 (3.1%)

Victoria lineage		
Lineage not performed	23 (57.5%)	85 (43.4%)

*The percent of specimens testing positive for influenza is not reported because public health laboratories often receive samples that have already tested positive for influenza at a clinical laboratory and therefore percent positive would not be a valid indicator of influenza activity. Additional information is available at http://www.cdc.gov/flu/weekly/overview.htm.



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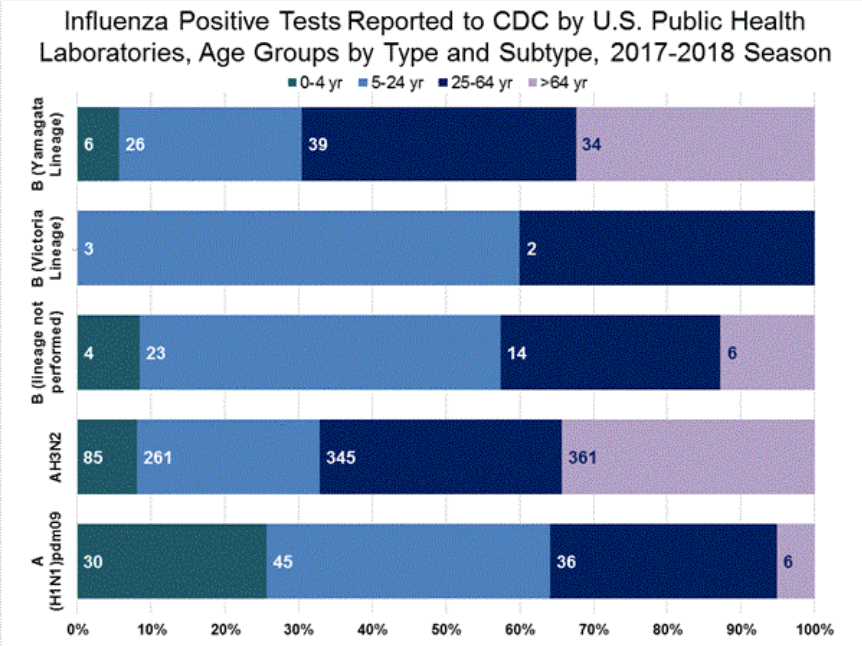

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Novel Influenza A Virus:

One human infection with a novel influenza A virus was reported from Iowa during week 46. This person was infected with an influenza A(H1N1) variant (H1N1v) virus and reported direct contact to swine during the week preceding illness onset. This patient was an adult < 50 years of age, was not hospitalized, and has fully recovered from their illness. No human-to-human transmission has been identified. This is the first H1N1v virus infection detected in the United States in 2017. This brings the total number of reported H1N1v infections in the United States since 2005 to 21.

A total of 66 variant virus infections have been reported to CDC during 2017. Sixty-one of these were influenza A(H3N2) variant (H3N2v) viruses (Delaware [1], Maryland [39], Michigan [2], Nebraska [1], North Dakota [1], Ohio [15], Pennsylvania [1], and Texas [1]), one was influenza A(H1N1) variant (H1N1v) (Iowa [1]), and four were influenza A(H1N2) variant (H1N2v) viruses (Colorado [1] and Ohio [3]). Six of these 66 infections have resulted in hospitalization; all have recovered.

Early identification and investigation of human infections with novel influenza A viruses are critical so that the risk of infection can be more fully understood and appropriate public health measures can be taken. Additional information on influenza in swine, variant influenza infection in humans, and strategies to interact safely with swine can be found at http://www.cdc.gov/flu/swineflu/index.htm.
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Influenza Virus Characterization:

CDC characterizes influenza viruses through one or more tests including genomic sequencing, hemagglutination inhibition (HI) and/or neutralization assays. These data are used to compare how similar currently circulating influenza viruses are to the reference viruses used for developing influenza vaccines, and to monitor for changes in circulating influenza viruses. Antigenic and genetic characterization of circulating influenza viruses can give an indication of the influenza vaccine's ability to produce an immune response against the wide array of influenza viruses co-circulating, but vaccine effectiveness estimates are needed to determine how much protection has been provided to the population by vaccination.

For nearly all influenza-positive surveillance samples received at CDC, next-generation sequencing is performed to determine the genetic identity of circulating influenza viruses. Viruses can be classified into genetic groups/clades based on analysis of their HA gene segments using phylogenetics and key amino acid changes (Klimov Vaccine 2012).A representative subset of influenza-positive surveillance samples are antigenically characterized. However, a proportion of influenza A(H3N2) viruses lack sufficient hemagglutination titers for antigenic characterization using hemagglutination inhibition assays. Therefore, CDC selects a representative subset of influenza A(H3N2) viruses for antigenic characterization using the virus neutralization focus reduction assay to assess the ability of various antisera to neutralize infectivity of the test viruses.

It is important to monitor circulating influenza viruses for evidence of genetic changes. However, genetic changes do not always result in antigenic change. Extensive genetic variation may exist in circulating viruses, with no evidence of substantial antigenic drift. Close monitoring of influenza viruses is required to better assess the potential impact on public health.

Genetic Characterization

During May 21 â€“ November 18, 2017, 3,298 influenza positive specimens were collected and reported by public health laboratories in the United States (Figure, left). CDC genetically characterized 665 influenza viruses [91 influenza A(H1N1)pdm09, 415 influenza A(H3N2), and 159 influenza B viruses] collected by U.S. laboratories.

Influenza A Viruses

- **A (H1N1)pdm09 [91]:** The HA gene segment of all influenza A(H1N1)pdm09 viruses analyzed showed that one virus belonged to clade 6B, with the remainder belonging to 6B.1, the same genetic clade as the vaccine reference virus, A/Michigan/45/2015.

- **A (H3N2) [415]:** Phylogenetic analysis of the HA genes indicate that multiple clades/subclades are circulating. The HA genes show extensive diversity and belong to clades 3C.2a, subclade 3C.2a1 or 3C.3a, with 3C.2a predominating. The vaccine reference virus, A/Hong Kong/4801/2014, belongs to the genetic clade 3C.2a.

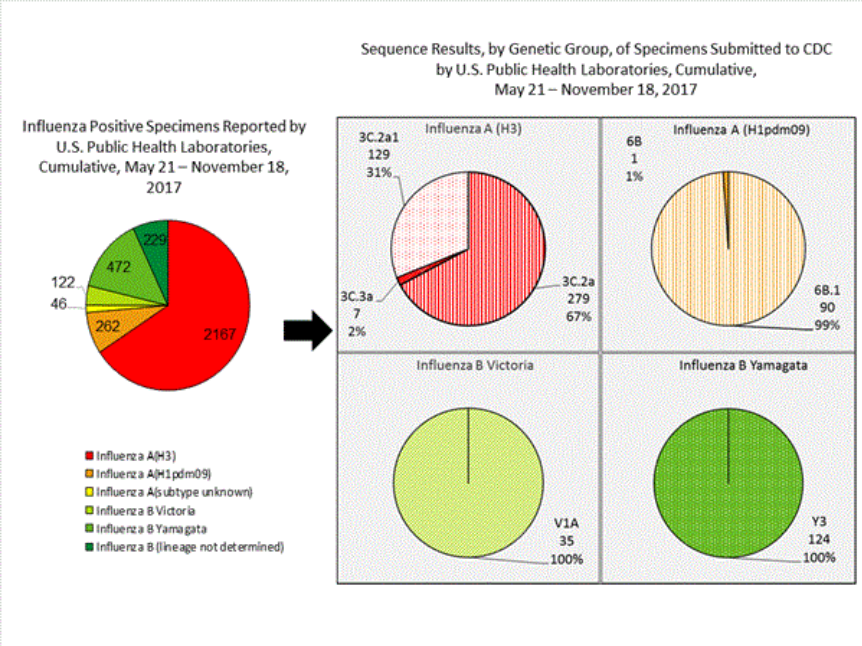
Influenza B Viruses

- **B/Victoria [35]:** The HA of influenza B/Victoria-lineage viruses all belonged to genetic group V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008.
- Two subgroups of viruses within V1A have been detected with a double or triple deletion of amino acids in the HA. The majority of the double deletion viruses were identified in the United States, while no triple deletion viruses have been identified in the United States.

- **B/Yamagata [124]:** The HA of influenza B/Yamagata-lineage viruses analyzed all belonged to genetic group Y3, the same genetic clade as the vaccine reference virus, B/Phuket/3073/2013.

The majority of U.S. viruses submitted for characterization come from state and local public health laboratories. Due to Right Size Roadmap considerations, specimen submission guidance issued to the laboratories request that, if available, 2 influenza A (H1N1), 2 A influenza (H3N2), and 2 influenza B viruses be submitted every other week. Because of this, the number of each virus type/subtype characterized should be approximately equal. In the figure below, the results of tests performed by public health labs are presented

on the left and sequence results by genetic group of specimens submitted to CDC are presented on the right.



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Antigenic Characterization

During May 21 â€“ November 18, 2017, CDC antigenically characterized 351 influenza viruses [73 influenza A(H1N1)pdm09, 145 influenza A(H3N2), and 133 influenza B viruses] collected by U.S. laboratories. Antigenic similarity is evaluated by comparing cell-propagated circulating viruses with cell-propagated reference viruses representing the recommended vaccine components of the Northern Hemisphere 2017-18 vaccine.

Influenza A Virus [218]

- **A (H1N1)pdm09 [73]:** 72 of 73 (98.6%) influenza A(H1N1)pdm09 viruses were antigenically characterized using ferret post-infection antisera as A/Michigan/45/2015 (H1N1)pdm09-like.
- **A (H3N2) [145]:** 141 of 145 (97.2%) influenza A(H3N2) viruses were antigenically characterized as A/Hong Kong/4801/2014-like by HI testing or neutralization testing. Among the viruses that reacted poorly with ferret antisera raised against A/Hong Kong/4801/2014-like viruses, all belong to genetic group 3C.3a.

Influenza B Virus [133]

- **Victoria Lineage [33]:** 22 of 33 (66.7%) B/Victoria-lineage viruses were antigenically characterized using ferret post-infection antisera as B/Brisbane/60/2008-like. Among the viruses that reacted poorly with ferret antisera raised against B/Brisbane/60/2008-like viruses, all were double deletion viruses.
- **Yamagata Lineage [100]:** All 100 (100%) B/Yamagata-lineage viruses were antigenically characterized using ferret post-infection antisera as B/Phuket/3073/2013-like.

Antiviral Resistance:

A total of 625 specimens collected during May 21-November 18, 2017, were tested for resistance to the influenza neuraminidase inhibitor antiviral medications currently approved for use against seasonal influenza: oseltamivir, zanamivir, and peramivir. A total of 92 influenza A(H1N1)pdm09, 383 influenza A(H3N2), and 150 influenza B viruses were found to be sensitive to all three antiviral medications. An additional one influenza A(H1N1)pmd09 virus was tested for resistance to oseltamivir and peramivir and 14 influenza A(H3N2) viruses were tested for resistance to oseltamivir and zanamivir. All were found to be sensitive to both antiviral medications.

The majority of recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications, oseltamivir, zanamivir, and peramivir; however, rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A (H1N1)pdm09

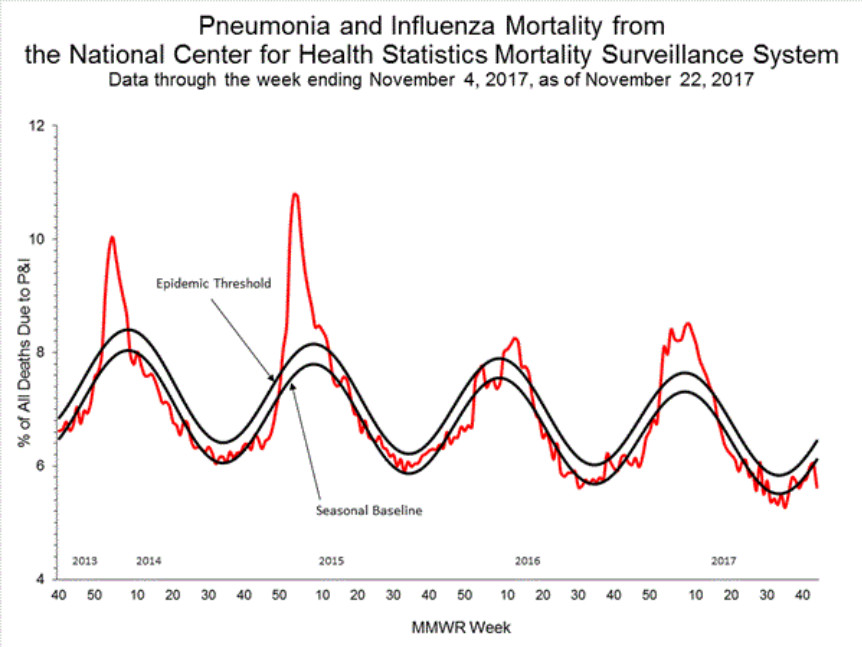
viruses and oseltamivir-resistant influenza A (H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at high risk for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at http://www.cdc.gov/flu/antivirals/index.htm.

Pneumonia and Influenza (P&I) Mortality Surveillance:

Based on National Center for Health Statistics (NCHS) mortality surveillance data available on November 22, 2017, 5.6% of the deaths occurring during the week ending November 4, 2017 (week 44) were due to P&I. This percentage is below the epidemic threshold of 6.4% for week 44.

Background: Weekly mortality surveillance data include a combination of machine coded and manually coded causes of death collected from death certificates. There is a backlog of data requiring manual coding within NCHS mortality surveillance data. The percentages of deaths due to P&I are higher among manually coded records than more rapidly available machine coded records and may result in initially reported P&I percentages that are lower than percentages calculated from final data. Efforts continue to reduce and monitor the number of records awaiting manual coding.

Region and state-specific data are available at http://gis.cdc.gov/grasp/fluview/mortality.html.



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Influenza-Associated Pediatric Mortality:

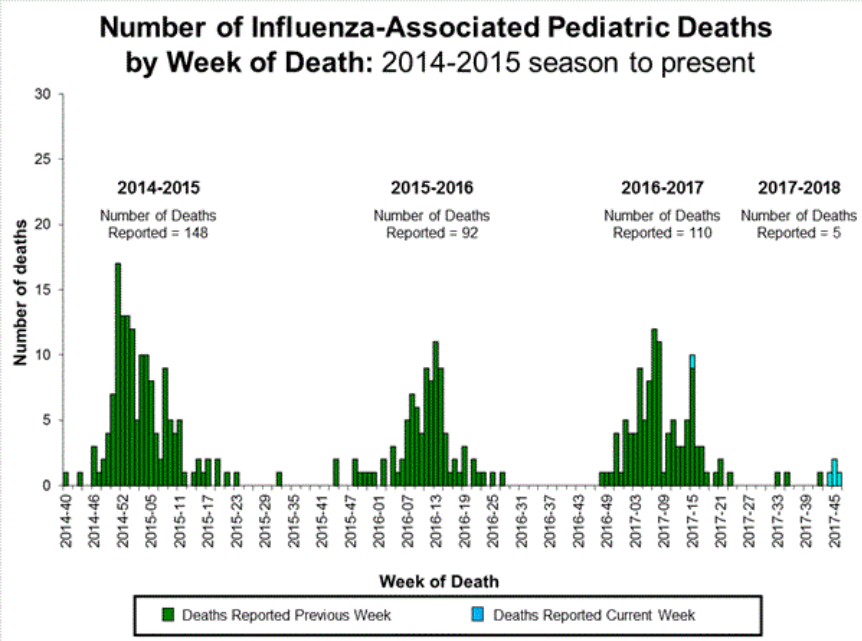
Five influenza-associated pediatric deaths were reported to CDC during week 46.

Two deaths were associated with an influenza A (H3) virus and occurred during weeks 45 and 46 (the weeks ending November 11 and November 18, 2017, respectively). One death was associated with an influenza A (H1N1)pdm09 virus and occurred during week 44 (the week ending November 4, 2017). One death was associated with an influenza A virus for which no subtyping was performed and occurred during week 44.

A total of five influenza-associated pediatric deaths have been reported for the 2017-2018 season.

One death that occurred during the 2016-2017 season was associated with an influenza A (H3) virus and occurred during week 15 (the week ending April 15, 2017). This death brings the total number of reported influenza-associated pediatric deaths occurring during that season to 110.

Additional data can be found at: http://gis.cdc.gov/GRASP/Fluview/PedFluDeath.html.



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Influenza-Associated Hospitalizations:

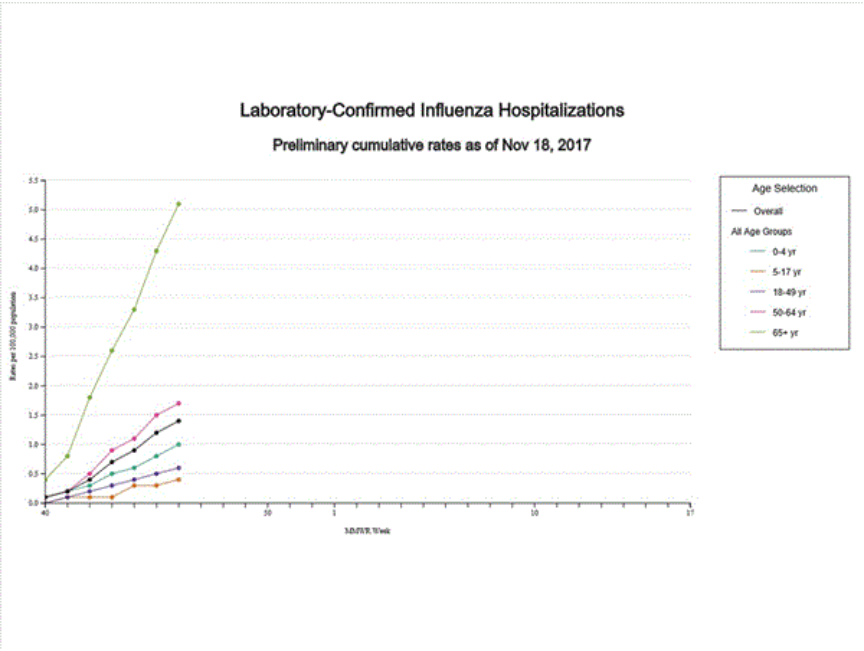
The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza-related hospitalizations in children younger than 18 years of age (since the 2003-2004 influenza season) and adults (since the 2005-2006 influenza season).

The FluSurv-NET covers more than 70 counties in the 10 Emerging Infections Program (EIP) states (CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN) and additional Influenza Hospitalization Surveillance Project (IHSP) states. The IHSP began during the 2009-2010 season to enhance surveillance during the 2009 H1N1 pandemic. IHSP sites included IA, ID, MI, OK and SD during the 2009-2010 season; ID, MI, OH, OK, RI, and UT during the 2010-2011 season; MI, OH, RI, and UT during the 2011-2012 season; IA, MI, OH, RI, and UT during the 2012-2013 season; and MI, OH, and UT during the 2013-2014, 2014-15, 2015-16, 2016-17, and 2017-18 seasons.

Data gathered are used to estimate age-specific hospitalization rates on a weekly basis, and describe characteristics of persons hospitalized with influenza illness. The rates provided are likely to be an underestimate as influenza-related hospitalizations can be missed, either because testing is not performed, or because cases may be attributed to other causes of pneumonia or other common influenza-related complications.

A total of 400 laboratory-confirmed influenza-associated hospitalizations were reported between October 1, 2017 and November 18, 2017. The overall hospitalization rate was 1.4 per 100,000 population. The highest rate of hospitalization was among adults aged â‰¥65 years (5.1 per 100,000 population), followed by adults aged 50-64 (1.7 per 100,000 population) and children aged 0-4 years (1.0 per 100,000 population). Among 400 hospitalizations, 330 (82.5%) were associated with influenza A virus, 65 (16.3%) with influenza B virus, 2 (0.5%) with influenza A virus and influenza B virus co-infection, and 3 (0.8%) with influenza virus for which the type was not determined. Among those with influenza A subtype information, 87 (91.6%) were A(H3N2) and 8 (8.4%) were A(H1N1)pdm09 virus.

Additional FluSurv-NET data can be found at: http://gis.cdc.gov/GRASP/Fluview/FluHospRates.html and http://gis.cdc.gov/grasp/fluview/FluHospChars.html.



Data from the Influenza Hospitalization Surveillance Network (FluSurv-NET), a population-based surveillance for influenza related hospitalizations in children and adults in 13 U.S. states. Cumulative incidence rates are calculated using the National Center for Health Statisticsâ€™ (NCHS) population estimates for the counties included in the surveillance catchment area.

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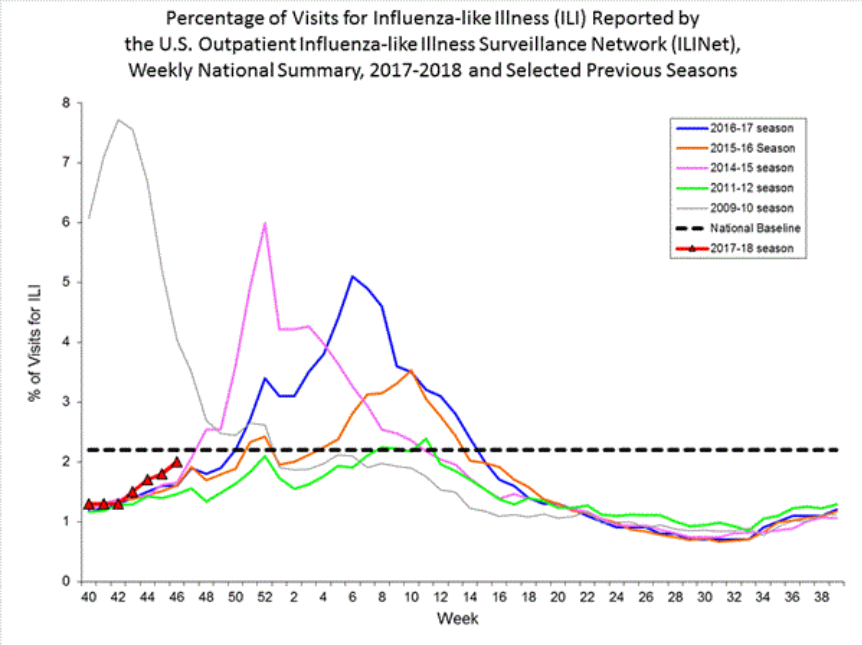
Outpatient Illness Surveillance:

Nationwide during week 46, 2.0% of patient visits reported through the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) were due to influenza-like illness (ILI). This percentage is below the national baseline of 2.2%. *(ILI is defined as fever (temperature of 100Â°F [37.8Â°C] or greater) and cough and/or sore throat.)*

Additional ILINet data, including national, regional and select state-level data, are available at http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html.



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On a regional level, the percentage of outpatient visits for ILI ranged from 0.7% to 4.5% during week 46. Regions 1, 2, 4 and 6 reported percentages of outpatient visits for ILI at or above their region specific baselines.

ILINet State Activity Indicator Map:

Data collected in ILINet are used to produce a measure of ILI activity* by state. Activity levels are based on the percent of outpatient visits in a state due to ILI and are compared to the average percent of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, which would correspond to ILI activity from outpatient clinics being below, or only slightly above, the average, to high, which would correspond to ILI activity from outpatient clinics being much higher than average.

During week 46, the following ILI activity levels were experienced:

- Two states experienced high activity (Louisiana and Mississippi)
- One state experienced moderate ILI activity (Georgia)
- New York City and four states experienced low ILI activity (Alabama, Nebraska, South Carolina, and Texas).
- The District of Columbia and 43 states experienced minimal ILI activity (Alaska, Arizona, Arkansas, California, Colorado, Connecticut, Delaware, Florida, Hawaii, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Maine, Maryland, Massachusetts, Michigan, Minnesota, Missouri, Montana, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Carolina, North Dakota, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Dakota, Tennessee, Utah, Vermont, Virginia, Washington, West Virginia, Wisconsin and Wyoming).
- Data were insufficient to calculate an ILI activity level from Puerto Rico.

Click on map to launch interactive tool

*This map uses the proportion of outpatient visits to health care providers for ILI to measure the ILI activity level within a state. It does not, however, measure the extent of geographic spread of flu within a state. Therefore, outbreaks occurring in a single city could cause the state to display high activity levels.
Data collected in ILINet may disproportionally represent certain populations within a state, and therefore, may not accurately depict the full picture of influenza activity for the whole state.
Data displayed in this map are based on data collected in ILINet, whereas the State and Territorial flu activity map is based on reports from state and territorial epidemiologists. The data presented in this map are preliminary and may change as more data are received.
Differences in the data presented here by CDC and independently by some state health departments likely represent differing levels of data completeness with data presented by the state likely being the more complete.

Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists

The influenza activity reported by state and territorial epidemiologists indicates geographic spread of influenza viruses, but does not measure the severity of influenza activity.

Additional data can be found at https://gis.cdc.gov/grasp/fluview/FluView8.html.

During week 46, the following influenza activity was reported::

- Widespread influenza activity was reported by two states (Louisiana and Oklahoma).
- Regional influenza activity was reported by Guam and six states (Arkansas, Georgia, Kentucky, Massachusetts, Mississippi, and South Carolina).
- Local influenza activity was reported by 20 states (Alabama, Alaska, Arizona, California, Colorado, Connecticut, Florida, Kansas, Maine, Maryland, Nebraska, New Hampshire, New Mexico, North Dakota, Ohio, Pennsylvania, Texas, Utah, Washington, and Wisconsin).
- Sporadic influenza activity was reported by the District of Columbia, the U.S. Virgin Islands and 21 states (Delaware, Hawaii, Idaho, Illinois, Indiana, Iowa, Michigan, Minnesota, Missouri, Montana, Nevada, New Jersey, New York, North Carolina, Oregon, Rhode Island, South Dakota, Tennessee, Vermont, Virginia, and Wyoming).
- No influenza activity was reported by one state (West Virginia).
- Puerto Rico did not report.

Additional National and International Influenza Surveillance Information

FluView Interactive: FluView includes enhanced web-based interactive applications that can provide dynamic visuals of the influenza data collected and analyzed by CDC. These FluView Interactive applications allow people to create customized, visual interpretations of influenza data, as well as make comparisons across flu seasons, regions, age groups and a variety of other demographics. To access these tools, visit http://www.cdc.gov/flu/weekly/fluviewinteractive.htm.

U.S. State and local influenza surveillance: Click on a jurisdiction below to access the latest local influenza information.

World Health Organization: Additional influenza surveillance information from participating WHO member nations is available through FluNet and the Global Epidemiology Reports.

WHO Collaborating Centers for Influenza located in Australia, China, Japan, the United Kingdom, and the United States (CDC in Atlanta, Georgia).

Europe: For the most recent influenza surveillance information from Europe, please see WHO/Europe and the European Centre for Disease Prevention and Control at http://www.flunewseurope.org/.

Public Health Agency of Canada: The most up-to-date influenza information from Canada is available at http://www.phac-aspc.gc.ca/fluwatch/

Public Health England: The most up-to-date influenza information from the United Kingdom is available at https://www.gov.uk/government/statistics/weekly-national-flu-reports

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An overview of the CDC influenza surveillance system, including methodology and detailed descriptions of each data component, is available at: http://www.cdc.gov/flu/weekly/overview.htm.
