Weekly U.S. Influenza Surveillance Report | CDC

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2018-2019 Influenza Season Week 48 ending December 1, 2018

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

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.,

Synopsis:

Influenza activity in the United States increased slightly. Influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B viruses continue to co-circulate, with influenza A(H1N1)pdm09 viruses reported most commonly by public health laboratories since September 30, 2018. Below is a summary of the key influenza indicators for the week ending December 1, 2018:

- **Viral Surveillance:** Influenza A viruses have predominated in the United States since the beginning of October. The percentage of respiratory specimens testing positive for influenza in clinical laboratories remains low, but is increasing.
    - **Virus Characterization:** The majority of influenza viruses characterized antigenically and genetically are similar to the cell-grown reference viruses representing the 2018–2019 Northern Hemisphere influenza vaccine viruses.
    - **Antiviral Resistance:** All viruses tested show susceptibility to the neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir).
- **Influenza-like Illness Surveillance:** The proportion of outpatient visits for influenza-like illness (ILI) remained at 2.2%, which is at the national baseline of 2.2%. Four of 10 regions reported ILI at or above their region-specific baseline level.
    - **ILI State Activity Indictor Map:** Two states experienced high ILI activity; two states experienced moderate ILI activity; New York City and eight states experienced low ILI activity; and the District of Columbia, Puerto Rico, and 38 states experienced minimal ILI activity.
- **Geographic Spread of Influenza:** The geographic spread of influenza in one state was reported as widespread; nine states reported regional activity; 18 states reported local activity; the District of Columbia, Puerto Rico, the U.S. Virgin Islands and 22 states reported sporadic activity; and Guam did not report.
- **Influenza-associated Hospitalizations** A cumulative rate of 1.3 laboratory-confirmed influenza-associated hospitalizations per 100,000 population 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:** No influenza-associated pediatric deaths were reported to CDC for week 48.

National and Regional Summary of Select Surveillance Components

Data for current week	Predominant flu

HHS Surveillance Regions*	Out-patient ILI†	Number of jurisdictions reporting regional or widespread activity§	% respiratory specimens positive for flu in clinical laboratories‡	virus reported by public health laboratories for the most recent three weeks‡
Nation	Elevated	10 of 54	4.2%	Influenza A(H1N1)pdm09
Region 1	Normal	3 of 6	2.0%	Approximately equal Influenza A(H1N1)pdm09 and A(H3)
Region 2	Normal	1 of 4	1.9%	Influenza A(H1N1)pdm09
Region 3	Normal	0 of 6	1.0%	Influenza A(H1N1)pdm09
Region 4	Elevated	2 of 8	9.6%	Influenza A(H1N1)pdm09
Region 5	Normal	0 of 6	1.9%	Influenza A(H1N1)pdm09
Region 6	Normal	1 of 5	2.5%	Influenza A(H1N1)pdm09
Region 7	Elevated	0 of 4	2.3%	Influenza A(H1N1)pdm09
Region 8	Elevated	0 of 6	2.3%	Influenza A(H1N1)pdm09
Region 9	Elevated	2 of 5	4.4%	Influenza A(H1N1)pdm09
Region 10	Normal	1 of 4	1.6%	Influenza A(H1N1)pdm09

*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
§ 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, Guam, 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.

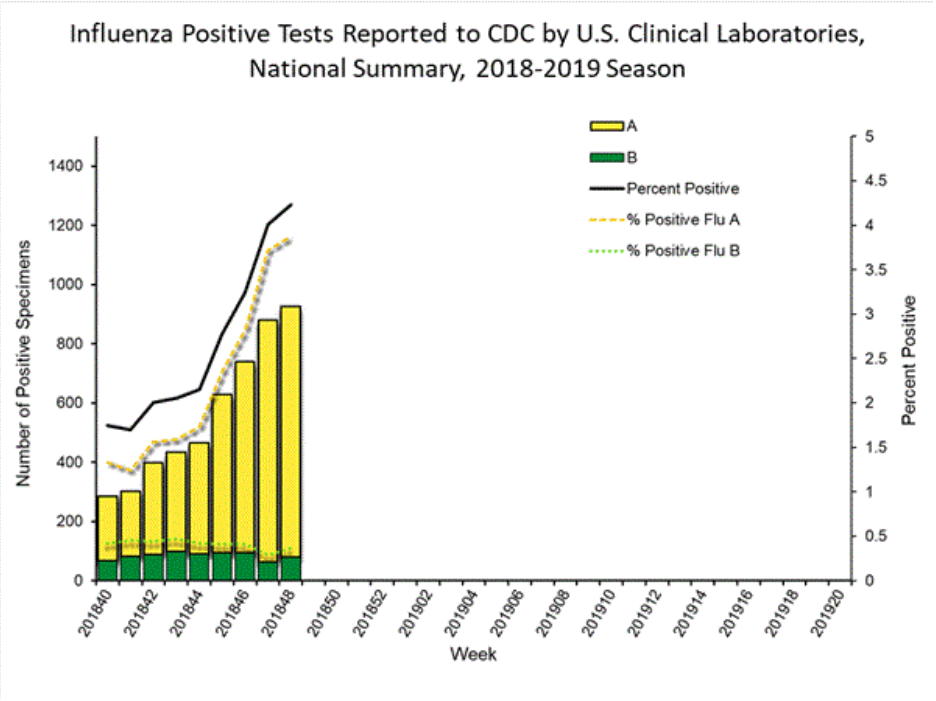
Additional virologic data, including national, regional and select state-level data, can be found at: http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html. Age group proportions and totals by influenza subtype reported by public health laboratories can be found at: http://gis.cdc.gov/grasp/fluview/flu_by_age_virus.html.

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

September 30, 2018 (Week 40)

	Week 48	Data Cumulative since
No. of specimens tested	21,851	186,197
No. of positive specimens (%)	925 (4.2%)	5,059 (2.7%)

Positive specimens by type		
Influenza A	846 (91.5%)	4,303 (85.1%)
Influenza B	79 (8.5%)	756 (14.9%)



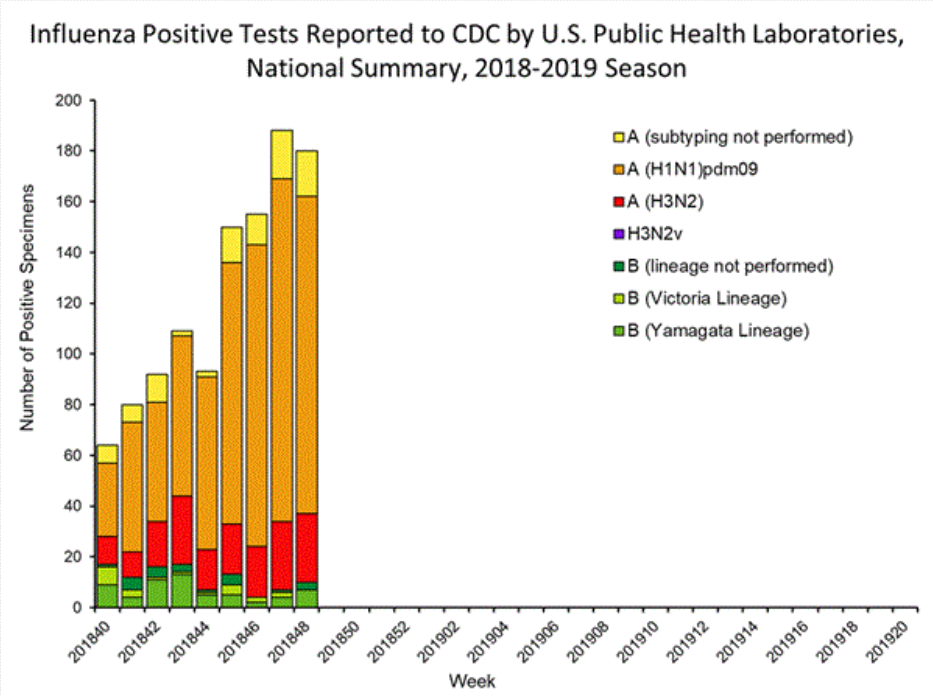
View National and Regional Level Graphs and Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/data/whoAllregt_cl48.html) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/WhoNPHL48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/FluView48.ppt)

The results of tests performed by public health laboratories are summarized below.

September 30, 2018 (Week 40)

	Week 48	**Data Cumulative since**
No. of specimens tested	670	7,809
No. of positive specimens*	180	1,111
Positive specimens by type/subtype		
(H1N1)pdm09	125 (82.2%)	740 (80.8%)
H3N2	27 (17.8%)	176 (19.2%)
Subtyping not performed	18	92
Yamagata lineage	7 (100%)	60 (74.1%)
Victoria lineage	0 (0%)	21 (25.9%)
Lineage not performed	3	22

*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.



View National and Regional Level Graphs and Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/data/whoAllregt_phl48.html) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/WhoPHL48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/FluView48.ppt)

Influenza Virus Characterization:

Close monitoring of influenza viruses is required to better assess the potential impact on public health. CDC characterizes influenza viruses through one or more tests including genomic sequencing, hemagglutination inhibition (HI) and/or neutralization assays based Focus Reduction assays (FRA). These data are used to compare how similar currently circulating influenza viruses are to the reference viruses used for developing new influenza vaccines and to monitor evolutionary changes that continually occur in influenza viruses circulating in humans. Antigenic and genetic characterization of circulating influenza viruses gives an indication of the influenza vaccine's ability to induce an immune response against the wide array of influenza viruses that are co-circulating every season. However, annual vaccine effectiveness estimates are needed to determine how much protection was 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 and to monitor the evolutionary trajectory of viruses circulating in our population. Virus gene segments are classified into genetic clades/subclades based on phylogenetic analysis. However, genetic changes that classify the clades/subclades do not always result in antigenic changes. “Antigenic drift” is a term used to describe gradual antigenic change that occurs as viruses evolve changes to escape host immune pressure. Antigenic drift is evaluated by comparing antigenic properties of cell-propagated reference viruses representing currently recommended vaccine components with those of cell-propagated circulating viruses.

CDC has antigenically or genetically characterized 163 influenza viruses collected September 30, 2018 – December 1, 2018, and submitted by U.S. laboratories, including 94 influenza A(H1N1)pdm09 viruses, 45 influenza A(H3N2) viruses, and 24 influenza B viruses.

Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 94 A(H1N1)pdm09 viruses showed that all

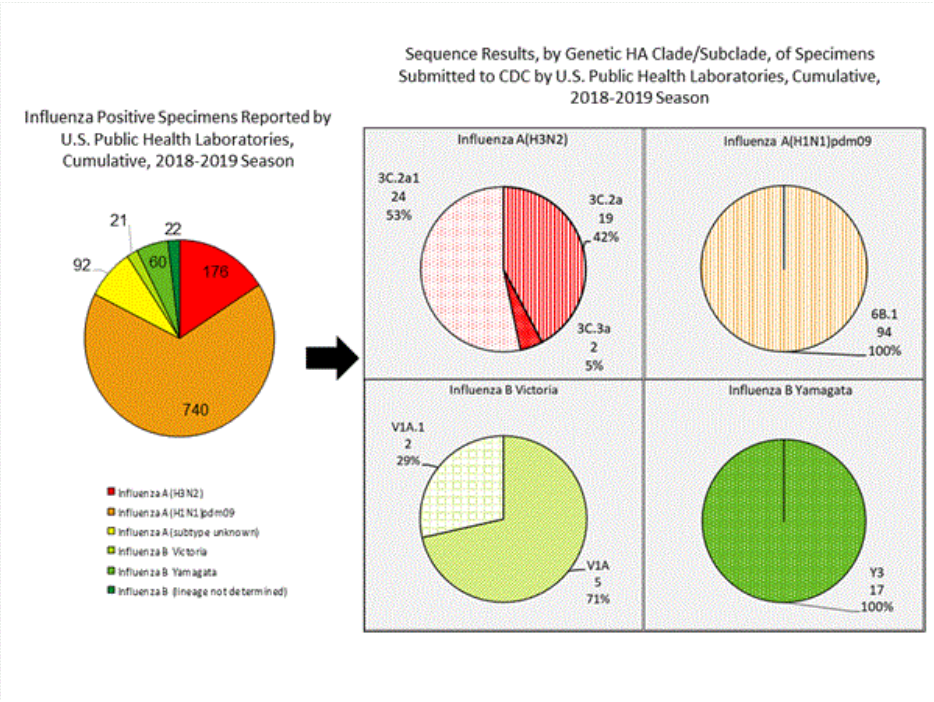
belonged to clade 6B.1. Sixty-seven A(H1N1)pdm09 viruses were antigenically characterized, and all 67 (100%) were antigenically similar (analyzed using HI with ferret antisera) to A/Michigan/45/2015 (6B.1), a cell-propagated A/Michigan/45/2015-like reference virus representing the A(H1N1)pdm09 component for the 2018-19 Northern Hemisphere influenza vaccines.

- **A (H3N2):** Phylogenetic analysis of the HA genes from 45 A(H3N2) viruses revealed extensive genetic diversity with multiple clades/subclades co-circulating. The HA genes of circulating viruses belonged to clade 3C.2a (n=19), subclade 3C.2a1 (n=24) or clade 3C.3a (n=2). Six A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and all 6 (100%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within 4-fold of the homologous virus titer) by ferret antisera raised against A/Singapore/INFIMH-16-0019/2016 (3C.2a1), a cell-propagated A/Singapore/INFIMH-16-0019/2016 -like reference virus representing the A(H3N2) component of 2018-19 Northern Hemisphere influenza vaccines.

Influenza B Viruses

- **B/Victoria:** Phylogenetic analysis of 7 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, however genetic subclades which are antigenically distinct have emerged. The majority of recent B/Victoria-lineage viruses belonged to a subclade of viruses with a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (V1A.1, previously abbreviated as V1A-2Del). In addition, a small number of B/Victoria-lineage viruses have a three amino acid deletion (162-164) in the HA protein (abbreviated as V1A-3Del). Three B/Victoria lineage viruses were antigenically characterized and all 3 (100%) reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) with ferret antisera raised against cell-propagated B/Colorado/06/2017-like reference virus, and belonged to clade V1A.
- **B/Yamagata:** Phylogenetic analysis of 17 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 8 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell-propagated B/Phuket/3073/2013 (Y3), the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2018-19 Northern Hemisphere quadrivalent vaccines.

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 to laboratories is that, if available, 2 influenza A(H1N1)pdm09, 2 influenza A(H3N2), and 2 influenza B viruses be submitted every other week. Therefore, the numbers of each virus type/subtype characterized should be more balanced across subtypes/lineages but will not reflect the actual proportion of circulating viruses. In the figure below, the results of tests performed by public health labs are shown on the left and CDC sequence results (by genetic clade/subclade) are shown on the right.



View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/data/Genetic48.csv) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/Genetic48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/FluView48.ppt)

Antiviral Resistance:

Testing of influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B viruses for resistance to the neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir) is performed at CDC using next-generation sequencing analysis and/or a functional assay. Neuraminidase sequences of viruses are inspected to detect the presence of amino acid substitutions,previously associated with reduced or highly reduced inhibition by any of three neuraminidase inhibitors.In addition, a subset of viruses are tested using the neuraminidase inhibition assay with three neuraminidase inhibitors. The level of neuraminidase activity inhibition is reported using the thresholds recommended by the World Health Organization Expert Working Group of the Global Influenza Surveillance and Response System (GISRS)These samples are routinely obtained for surveillance purposes rather than for diagnostic testing of patients suspected to be infected with an antiviral-resistant virus.

Reporting of baloxavir susceptibility testing for the 2018-2019 influenza season will begin later this season. More information regarding influenza antiviral drug resistance can be found here

High levels of resistance to the adamantanes (amantadine and rimantadine) persist among influenza A(H1N1)pdm09 and influenza A(H3N2) viruses (the adamantanes are not effective against influenza B viruses). Therefore, data from adamantane resistance testing are not presented below.

Assessment of Virus Susceptibility to Neuraminidase Inhibitors Using Next-Generation Sequencing Analysis and/or Neuraminidase Inhibition Assay

	Inhibition of Neuraminidase Activity by Antiviral Drug								
	Oseltamivir			Peramivir			Zanamivir		
Type/Subtype or Lineage	Virus	Reduced,	Highly Reduced,	Virus	Reduced,	Highly Reduced,	Virus	Reduced,	Highly Reduced,

	Tested (n)	Number (%)	Number (%)	Tested (n)	Number (%)	Number (%)	Tested (n)	Number (%)	Number (%)
Total Viruses	158	0 (0%)	0 (0%)	158	0 (0%)	0 (0%)	158	0 (0%)	0 (0%)
A(H1N1)pdm09	93	0 (0%)	0 (0%)	93	0 (0%)	0 (0%)	93	0 (0%)	0 (0%)
A(H3N2)	43	0 (0%)	0 (0%)	43	0 (0%)	0 (0%)	43	0 (0%)	0 (0%)
B/Victoria	7	0 (0%)	0 (0%)	7	0 (0%)	0 (0%)	7	0 (0%)	0 (0%)
B/Yamagata	15	0 (0%)	0 (0%)	15	0 (0%)	0 (0%)	15	0 (0%)	0 (0%)

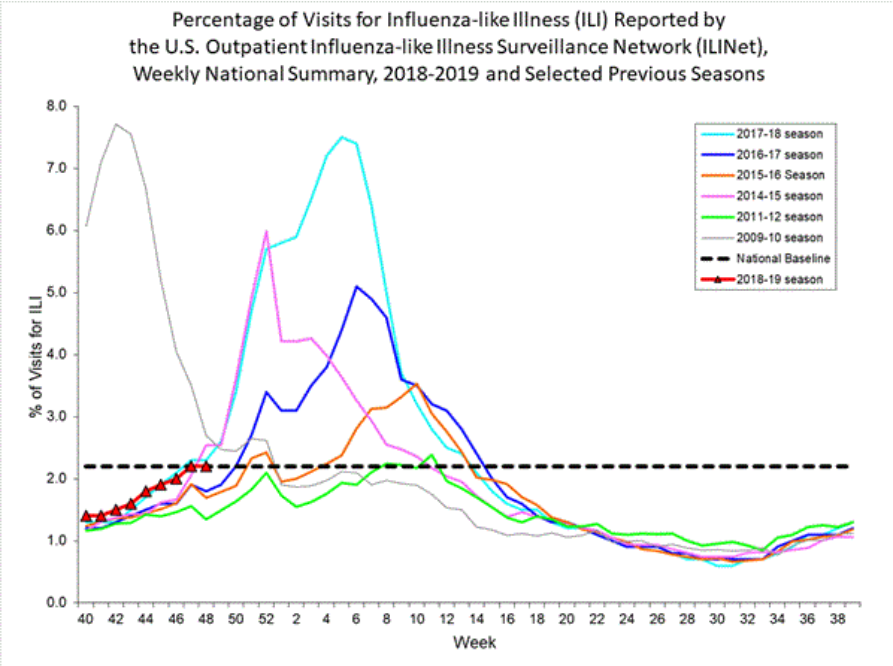
Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at high risk for serious influenza-related complications. Additional information on recommendations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

Outpatient Illness Surveillance:

Nationwide during week 48, 2.2% 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 at the national baseline of 2.2%.*(ILI is defined as fever (temperature of 100°F [37.8°C] or greater) and cough and/or sore throat.)*

On a regional level, the percentage of outpatient visits for ILI ranged from 0.8% to 3.2% during week 48. Four of 10 regions (Regions 4, 7, 8 and 9) reported a percentage of outpatient visits for ILI at or above their region-specific baseline.

Additional data on medically attended visits for ILI for current and past seasons and by geography (national, HHS region, or select states) are available on FluView Interactive http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html.



View National and Regional Level Graphs and Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/data/senAllregt48.html) | View Full

Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/ILI48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/FluView48.ppt)

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.

The ILI Activity Indicator Map displays state-specific activity levels for multiple seasons and allows a visual representation of relative activity from state to state. More information is available on FluView Interactive at https://gis.cdc.gov/grasp/fluview/main.html.

During week 48, the following ILI activity levels were experienced:

- Two states (Georgia and Louisiana) experienced high ILI activity.
- Two states (Colorado and South Carolina) experienced moderate ILI activity.
- New York City and eight states (Alabama, Arizona, Kentucky, Mississippi, New Jersey, North Carolina, Utah and Virginia) experienced low ILI activity.
- The District of Columbia, Puerto Rico and 38 states (Alaska, Arkansas, California, Connecticut, Delaware, Florida, Hawaii, Idaho, Illinois, Indiana, Iowa, Kansas, Maine, Maryland, Massachusetts, Michigan, Minnesota, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Mexico, New York, North Dakota, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Dakota, Tennessee, Texas, Vermont, Washington, West Virginia, Wisconsin, and Wyoming) experienced minimal ILI activity.

*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 displaying the influenza activity reported by state and territorial epidemiologists for the current and past seasons are available on FluView Interactive at https://gis.cdc.gov/grasp/fluview/FluView8.html

During week 48, the following influenza activity was reported:

- Widespread influenza activity was reported by one state (Massachusetts).
- Regional influenza activity was reported by nine states (California, Connecticut, Georgia, Kentucky, Louisiana, Nevada, New York, Oregon, and Vermont).
- Local influenza activity was reported by 18 states (Arizona, Colorado, Delaware, Florida, Idaho, Illinois, Michigan, Montana, New Hampshire, New Jersey, North Carolina, Ohio, Oklahoma, Pennsylvania, South Carolina, Texas, Utah, and West Virginia).

- Sporadic influenza activity was reported by the District of Columbia, Puerto Rico, the U.S. Virgin Islands and 22 states (Alabama, Alaska, Arkansas, Hawaii, Indiana, Iowa, Kansas, Maine, Maryland, Minnesota, Mississippi, Missouri, Nebraska, New Mexico, North Dakota, Rhode Island, South Dakota, Tennessee, Virginia, Washington, Wisconsin, and Wyoming).
- Guam did not report.

Influenza-Associated Hospitalizations:

The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza-related hospitalizations in select counties in the Emerging Infections Program (EIP) states and Influenza Hospitalization Surveillance Project (IHSP) states.

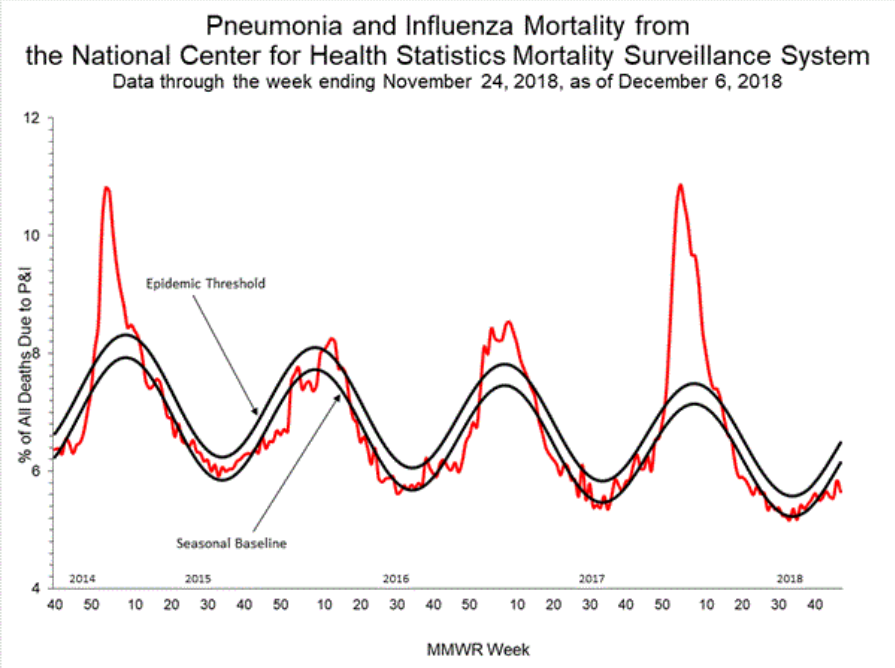
A total of 383 laboratory-confirmed influenza-associated hospitalizations were reported between October 1, 2018 and December 1, 2018. The overall hospitalization rate was 1.3 per 100,000 population. The highest rate of hospitalization was among adults aged ≥65 years (3.3 per 100,000 population) and children aged 0-4 (3.3 per 100,000), followed by adults aged 50-64 (1.4 per 100,000 population). Among 383 hospitalizations, 279 (72.8%) were associated with influenza A virus, 88 (23.0%) with influenza B virus, 9 (2.3%) with influenza A virus and influenza B virus co-infection, and 7 (1.8%) with influenza virus for which the type was not determined. Among those with influenza A subtype information, 14 (21.9%) were A(H3N2) and 49 (76.6%) were A(H1N1)pdm09 virus.

Additional FluSurv-NET data displaying hospitalization rates for the current and past seasons and different age groups, as well as data on patient characteristics (such as influenza virus type, demographic, and clinical information), are available on FluView Interactive at: http://gis.cdc.gov/GRASP/Fluview/FluHospRates.html and http://gis.cdc.gov/grasp/fluview/FluHospChars.html.

Pneumonia and Influenza (P&I) Mortality Surveillance:

Based on National Center for Health Statistics (NCHS) mortality surveillance data available on December 6, 2018, 5.7% of the deaths occurring during the week ending November 24, 2018 (week 47) were due to P&I. This percentage is below the epidemic threshold of 6.5% for week 47.

Additional pneumonia and influenza mortality data for current and past seasons and by geography (national, HHS region, or state) are available at on FluView Interactive http://gis.cdc.gov/grasp/fluview/mortality.html. Data displayed on the regional and state-level are aggregated by the state of residence of the decedent.



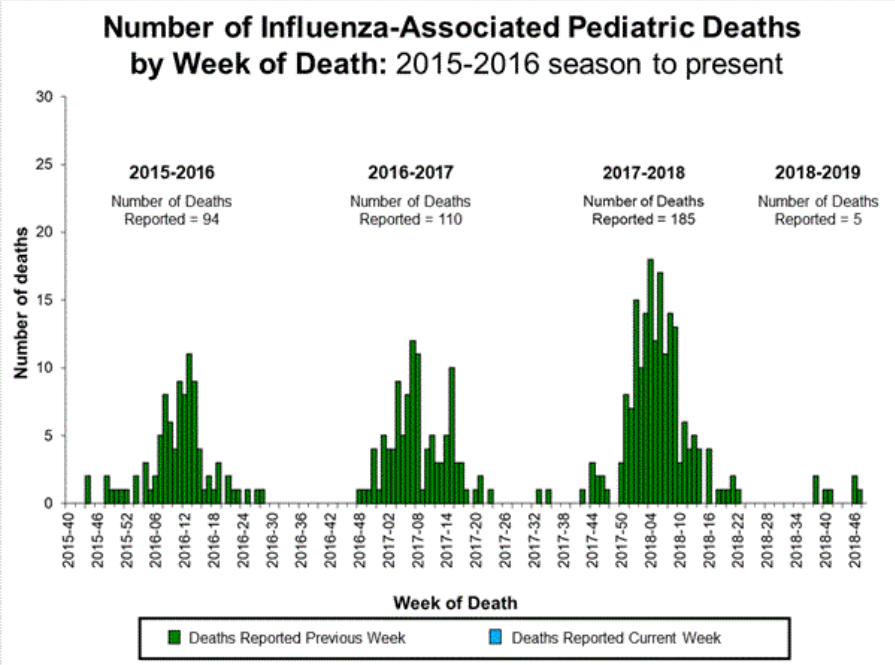
View Regional and State Level Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/data/NCHSData48.csv) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/NCHS48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/FluView48.ppt)

Influenza-Associated Pediatric Mortality:

No influenza-associated pediatric deaths were reported to CDC during week 48.

A total of five influenza-associated pediatric deaths have been reported for the 2018-2019 season.

Additional information on influenza-associated pediatric deaths including basic demographics, underlying conditions, bacterial co-infections, and place of death for the current and past seasons, is available on FluView Interactive http://gis.cdc.gov/GRASP/Fluview/PedFluDeath.html.



View Interactive Application | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/PedFlu48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2018-2019/FluView48.ppt)

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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